



```
☐ 14 3w15_A Peroxisomal targeting s 100.0 8.4E-40 2.3E-44 279.6
                                                                    32.7
                                                                           252
                                                                                  8-282
                                                                                            61-365 (368)
  15 3jro_A Fusion protein of prote 100.0
                                             1E-39 2.8E-44
                                                             303.4
                                                                     32.0
                                                                           297
                                                                                  1-297
                                                                                             1-297
                                                                                                   (753)
  16 1got B GT-beta: complex (GTP-b 100.0 1.4E-38 3.8E-43
                                                             269.4
                                                                     34.3
                                                                           249
                                                                                  2-282
                                                                                            90-340
                                                                                                   (340)
     4i0w A U3 small nucleolar RNA- 100.0
                                              2E-38 5.5E-43
                                                             268.7
                                                                     34.0
                                                                           247
                                                                                  1-284
                                                                                             6-274
                                                                                                   (343)
     4wju_A Ribosome assembly prote 100.0 2.5E-38 6.9E-43
                                                             282.1
                                                                                   2-282
                                                                                           179-514
  19 3fm0_A Protein CIAO1; WDR39,SG 100.0 1.9E-37 5.4E-42
                                                             262.6
                                                                     37.2
                                                                           258
                                                                                  2-283
                                                                                             8-281
                                                                                                   (345)
  20 3ow8_A WD repeat-containing pr 100.0 7.8E-38 2.2E-42
                                                             262.5
                                                                     33.7
                                                                           249
                                                                                  1-282
                                                                                            24-276 (321)
  21 4;73 A Coatomer subunit beta'; 100.0 1.3E-37 3.6E-42
                                                             259.0
                                                                     34.1
                                                                           249
                                                                                  2-280
                                                                                            48-298
                                                                                                   (301)
  22 5cxb B Ribosome biogenesis pro 100.0 1.1E-37
                                                      3E-42
                                                             266.7
                                                                     33.7
                                                                           254
                                                                                  1-282
                                                                                            13-369
                                                                                                   (369)
  23 lerj_A Transcriptional repress 100.0 1.7E-37
                                                    4.7E-42
                                                                           247
                                                                                           121-387
267.7
                                                                     34.9
                                                                                   7-283
                                                                                                   (393)
  24 2pbi B Guanine nucleotide-bind 100.0 2.1E-37 5.9E-42
                                                             263.4
                                                                                   2-282
                                                                                            57-354
                                                                                                   (354)
  25 3fm0 A Protein CIAO1; WDR39,SG 100.0 7.7E-37 2.1E-41
                                                                                  3-284
                                                             258.9
                                                                     37.5
                                                                           262
                                                                                            55-334
                                                                                                   (345)
  26 1k8k_C P40, ARP2/3 complex 41 100.0 3.9E-37 1.1E-41
                                                             262.4
                                                                     35.1
                                                                           270
                                                                                  2-297
                                                                                            1-287
                                                                                                   (372)
                                                                                            55-307
  27 4bh6 A APC/C activator protein 100.0 2.1E-37 5.7E-42
                                                             258.6
                                                                     32.5
                                                                           249
                                                                                  2-286
                                                                                                   (308)
  28 3ow8 A WD repeat-containing pr 100.0 4.8E-37 1.3E-41
                                                             257.8
                                                                                  2-285
                                                                                            73-321 (321)
                                                                     34.8
                                                                           249
  29 4jsn_D Target of rapamycin com 100.0 2.4E-37 6.6E-42
                                                             260.1
                                                                           258
                                                                                            34-298
                                                                                                   (326)
  30 3frx_A Guanine nucleotide-bind 100.0 8.7E-37 2.4E-41
                                                             255.8
                                                                     34.8
                                                                           247
                                                                                  2-284
                                                                                            10-266
                                                                                                   (319)
  31 41g9_A F-box-like/WD repeat-co 100.0 1.1E-36 2.9E-41
                                                             263.3
                                                                     35.8
                                                                           241
                                                                                  7-282
                                                                                           109-397
                                                                                                   (400)
  32 41g9_A F-box-like/WD repeat-co 100.0 6.5E-37 1.8E-41
                                                             264.6
                                                                     34.2
                                                                           249
                                                                                  2-282
                                                                                            48-356 (400)
                                                                                  2-282
                                                                                            57-338 (393)
  33 leri A Transcriptional repress 100.0 1.2E-36 3.3E-41
                                                             262.4
                                                                     34.1
                                                                           246
  34 4wju_A Ribosome assembly prote 100.0 1.8E-37 4.9E-42
                                                                                           135-472 (515)
                                                             276.6
                                                                     29.8
                                                                           250
                                                                                  1-282
  35 4wjs A RSA4; ribosome assembly 100.0 1.3E-36 3.6E-41
                                                             269.1
                                                                           250
                                                                                   2-282
                                                                                           150-484 (485)
  36 4all_B DNA excision repair pro 100.0 2.5E-36
                                                                           258
                                                             261.6
                                                                     35.1
                                                                                  1-284
                                                                                            35-364
                                                                                                   (408)
  37 41g8_A PRE-mRNA-processing fac 100.0 2.7E-36 7.4E-41
                                                             256.7
                                                                     34.6
                                                                           247
                                                                                  2-283
                                                                                           107-354 (354)
  38 4psw_B Histone acetyltransfera 100.0 1.1E-36
                                                      3E-41
                                                             263.3
                                                                     32.0
                                                                           249
                                                                                  2-284
                                                                                           111-383
                                                                                                   (401)
  39 3jam q RACK1; eukaryotic trans 100.0 3.9E-36 1.1E-40
                                                                                  2-282
                                                                                            11-271 (326)
                                                             252.6
                                                                     34.5
                                                                           247
     4d6v A GIB2, G protein beta su 100.0
                                              6E-36 1.6E-40
                                                             250.1
                                                                           249
                                                                                  2-282
                                                                                             8-260
                                                                     35.1
                                                                                                   (314)
  41 4ggc A P55CDC, cell division c 100.0 7.1E-36
                                                             250.4
                                                                                  2-282
                                                                                            60-312
  42 41g8_A PRE-mRNA-processing fac 100.0 5.3E-36 1.5E-40
                                                             254.9
                                                                     34.1
                                                                           241
                                                                                  8-282
                                                                                            67-311 (354)
  43 5ams A SQT1, ribosome assembly 100.0 5.6E-36 1.5E-40
                                                             261.1
                                                                     34.2
                                                                           254
                                                                                  1-282
                                                                                            57-339
                                                                                                   (431)
  44 4gga A P55CDC, cell division c 100.0
                                              1E-35 2.9E-40
                                                             258.7
                                                                     34.6
                                                                           247
                                                                                  2-282
                                                                                           140-392 (420)
                                                                                            66-381 (383)
  45 3ei3 B DNA damage-binding prot 100.0
                                              1E-35 2.9E-40
                                                             255.6
                                                                     33.7
                                                                           258
                                                                                  2-284
  46 4wjs_A RSA4; ribosome assembly 100.0 6.4E-36 1.8E-40
                                                             264.7
                                                                           253
                                                                                  1-282
                                                                                           106-442 (485)
  47 4xyh_A Kinetochore protein MIS 100.0 1.9E-36 5.2E-41
                                                             264.2
                                                                     28.5
                                                                           257
                                                                                   2-284
                                                                                           124-413
                                                                                                   (430)
  48 4j0w_A U3 small nucleolar RNA- 100.0 5.6E-36 1.5E-40
                                                             253.6
                                                                     30.2
                                                                           259
                                                                                  5-297
                                                                                            63-334
                                                                                                   (343)
  49 3jam g RACK1; eukaryotic trans 100.0 5.9E-35 1.6E-39
                                                             245.4
                                                                     36.1
                                                                           247
                                                                                  2-282
                                                                                            59-321 (326)
  50 3jb9 L PRE-mRNA-splicing facto 100.0
                                                                           253
                                                                                  1-282
                                                                                            42-297
                                             2E-37 5.4E-42
                                                             262.2
                                                                     20.5
                                                                                                   (340)
  51 4jsn_D Target of rapamycin com 100.0 8.5E-36 2.3E-40
                                                                                             3-248
                                                             250.7
                                                                     30.4
                                                                           243
                                                                                 12-282
                                                                                                   (326)
  52 4j0x_A Ribosomal RNA-processin 100.0 1.5E-35 4.1E-40
                                                             259.3
                                                                                            25-392
                                                                                                   (451)
  53 5gan_H U4/U6 small nuclear rib 100.0 3.3E-36
                                                             265.2
                                                                     28.5
                                                                           246
                                                                                   6-282
                                                                                           215-465
                                                                                                   (465)
                                                                                                   (337)
  54 1gxr A ESG1, transducin-like e 100.0 8.3E-35 2.3E-39
                                                             244.8
                                                                     35.6
                                                                           241
                                                                                  7-283
                                                                                            95-335
  55 3jb9 L PRE-mRNA-splicing facto 100.0 5.1E-37 1.4E-41
                                                             259.7
                                                                     21.5
                                                                           251
                                                                                  2-284
                                                                                            86-340
                                                                                                   (340)
                                                                                  2-283
  56 3frx A Guanine nucleotide-bind 100.0 1.3E-34 3.6E-39
                                                             242.7
                                                                     35.5
                                                                           246
                                                                                            58-315 (319)
  57 4d6v_A GIB2, G protein beta su 100.0 1.3E-34 3.5E-39
                                                                                            56-312
                                                                                                   (314)
     4yvd A Pleiotropic regulator 1 100.0 1.6E-34 4.3E-39
                                                             246.9
                                                                     35.9
                                                                           244
                                                                                  2-282
                                                                                            57-300
                                                                                                   (374)
                                                                                             7-291 (330)
  59 2hes_X YDR267CP; beta-propelle 100.0 4.9E-34 1.4E-38
                                                             238.9
                                                                           270
                                                                                  2-297
                                                                     38.0
  60 2xyi A Probable histone-bindin 100.0 1.5E-35 4.2E-40
                                                             258.4
                                                                     29.9
                                                                           263
                                                                                  2-284
                                                                                           121-409
                                                                                                   (430)
  61 5ams A SQT1, ribosome assembly 100.0 9.2E-35 2.5E-39
                                                             253.4
                                                                     34.4
                                                                           247
                                                                                  2-284
                                                                                           102-430 (431)
  62 3w15 A Peroxisomal targeting s 100.0 5E-35 1.4E-39
                                                                                             2-305 (368)
                                                             250.1
                                                                     32.1
                                                                           254
                                                                                  1-282
  63 4zox_A Ribosome assembly prote 100.0 1.5E-34 4.2E-39
                                                             247.0
                                                                           258
                                                                                   1-282
                                                                                             7-289
                                                                                                   (381)
  64 5a31_R The anaphase-promoting 100.0 5.6E-35 1.5E-39
                                                             251.4
                                                                                  2-282
                                                                                           124-372
                                                                     32.3
                                                                           244
                                                                                                   (386)
  65 Scvl_A WD repeat-containing pr 100.0 3.6E-35
                                                      1E-39
                                                             266.0
                                                                     32.4
                                                                           248
                                                                                   4-282
                                                                                            40-295
                                                                                                   (598)
  66 4gqb_B Methylosome protein 50; 100.0 8.1E-35 2.2E-39
                                                             246.0
                                                                     32.4
                                                                           253
                                                                                  2-286
                                                                                            75-332 (344)
  67 3dwl C Actin-related protein 2 100.0 1.1E-36
                                                                                  1-297
                                                      3E-41
                                                             260.5
                                                                     21.0
                                                                           268
                                                                                             3-292(377)
  68 2j04 B YDR362CP, TAU91; beta p 100.0 4.7E-36 1.3E-40
                                                             268.0
                                                                           258
                                                                                  2-286
                                                                                           200-518
                                                                                                   (524)
                                                                     25.5
  69 1k8k_C P40, ARP2/3 complex 41 100.0 6.8E-35 1.9E-39
                                                             248.5
                                                                                   2-282
                                                                                            45-358
                                                                                                   (372)
     4j0x_A Ribosomal RNA-processin 100.0 1.2E-35 3.4E-40
                                                             259.9
                                                                     27.5
                                                                           265
                                                                                   1-295
                                                                                           106-444
                                                                                                   (451)
  71 5gan H U4/U6 small nuclear rib 100.0 2.9E-35 7.9E-40
                                                             259.2
                                                                     29.9
                                                                           249
                                                                                  2-282
                                                                                           168-423 (465)
                                                                           254
                                                                                           111-384 (435)
  72 4e54 B DNA damage-binding prot 100.0 5.5E-36 1.5E-40
                                                             261.4
                                                                     25.1
                                                                                  1-282
  73 3mkg A Coatomer beta'-subunit; 100.0 5.8E-35 1.6E-39
                                                                                             5-256 (814)
                                                             273.8
                                                                     33.6
                                                                           248
                                                                                  1-282
  74 4aez_A CDC20, WD repeat-contai 100.0 1.2E-34 3.3E-39
                                                                                           128-377
                                                                                                   (401)
  75 2hes X YDR267CP; beta-propelle 100.0 3.6E-34 9.9E-39
                                                             239.7
                                                                     33.8
                                                                           258
                                                                                  2-284
                                                                                            49-327
                                                                                                   (330)
  76 5cvo_A WD repeat-containing pr 100.0 7.3E-35
                                                      2E-39
                                                             266.3
                                                                     31.9
                                                                           248
                                                                                  4-282
                                                                                           25-280 (677)
  77 5cxb_A Ribosome biogenesis pro 100.0 9.5E-35 2.6E-39
                                                             258.9
                                                                     31.8
                                                                           250
                                                                                  2-282
                                                                                           123-436
                                                                                                   (514)
  78 1r5m_A SIR4-interacting protei 100.0 2.4E-34 6.7E-39
                                                             249.4
                                                                     33.2
                                                                           254
                                                                                  1-284
                                                                                           100-424 (425)
     4zoy_A SQT1; chaperone, riboso 100.0 7.7E-34 2.1E-38
                                                             250.4
                                                                     36.7
                                                                           253
                                                                                  1-282
                                                                                             7-408
                                                                                                   (491)
  80 3k26_A Polycomb protein EED; W 100.0 2.1E-34 5.7E-39
                                                                                   7-282
                                                                                            67-363
                                                                                                   (366)
                                                                                           607-910 (1249)
  81 3sfz_A APAF-1, apoptotic pepti 100.0 2.8E-34 7.8E-39
                                                             280.1
                                                                     36.6
                                                                           249
                                                                                   1-282
  82 3gre_A Serine/threonine-protei 100.0 2.5E-35 6.8E-40
                                                             257.2
                                                                     26.2
                                                                           254
                                                                                  2-282
                                                                                            55-356
                                                                                                   (437)
  83 3i2n_A WD repeat-containing pr 100.0
                                              9E-35 2.5E-39
                                                             247.6
                                                                     28.6
                                                                           251
                                                                                  8-284
                                                                                            64-352 (357)
  84 4yvd A Pleiotropic regulator 1 100.0 1.8E-33
                                                                                  2-284
                                                                                            99-352
                                                      5E-38
                                                             240.3
                                                                     36.3
                                                                           246
                                                                                                   (374)
  85 4g56_B MGC81050 protein; prote 100.0 2.3E-34 6.4E-39
                                                                                   7-297
                                                                                            92-355
                                                             244.5
                                                                     30.3
                                                                           260
                                                                                                   (357)
  86 4ery_A WD repeat-containing pr 100.0 1.4E-33 3.9E-38
                                                             235.1
                                                                     33.7
                                                                           253
                                                                                   2-285
                                                                                            58-312
                                                                                                   (312)
  87 4gga_A P55CDC, cell division c 100.0 7.9E-34 2.2E-38
                                                             246.9
                                                                     32.8
                                                                           244
                                                                                   7-282
                                                                                           103-350
                                                                                                   (420)
  88 3gre A Serine/threonine-protei 100.0 7.6E-35 2.1E-39
                                                             254.1
                                                                     26.2
                                                                           247
                                                                                  7-282
                                                                                           109-437
                                                                                                   (437)
     4ci8 A Echinoderm microtubule- 100.0 8.9E-34 2.4E-38
                                                             259.7
                                                                     34.4
                                                                           265
                                                                                  2-297
                                                                                           292-622 (655)
  90 1gxr A ESG1, transducin-like e 100.0
                                              3E-33 8.3E-38
                                                             235.2
                                                                     34.6
                                                                           247
                                                                                  2-282
                                                                                            44-293 (337)
  91 3dwl_C Actin-related protein 2 100.0 2.9E-35
                                                                                                   (377)
  92 1r5m_A SIR4-interacting protei 100.0 6.3E-34 1.7E-38
                                                             246.8
                                                                     30.6
                                                                           249
                                                                                   1-282
                                                                                            35-358
                                                                                                   (425)
                                                                                            31-336 (368)
  93 3mmy_A MRNA export factor; mRN 100.0 4.7E-34 1.3E-38
                                                             244.1
                                                                     29.3
                                                                           248
                                                                                  1-275
  94 5dfz B Serine/threonine-protei 100.0 1.2E-36 3.4E-41
                                                             295.8
                                                                     15.0
                                                                           250
                                                                                  1-282
                                                                                          1061-1363(1460
  95 3vl1 A 26S proteasome regulato 100.0 1.1E-33 3.2E-38
                                                             245.4
                                                                     31.9
                                                                           245
                                                                                  5-283
                                                                                            92-362 (420)
     3v7d_B Cell division control p 100.0 2.6E-33
                                                                                           115-378 (464)
                                                      7E-38
                                                             246.7
                                                                     34.5
                                                                           242
                                                                                   3-282
     2pm9_A Protein WEB1, protein t 100.0 4.5E-35
                                                             254.1
                                                                                   7-284
                                                                                            65-336
                                                                                                   (416)
                                                             235.3
                                                                           253
                                                                                  2-297
  98 3odt_A Protein DOA1; ubiquitin 100.0 1.8E-33 5.1E-38
                                                                     31.5
                                                                                            52-307
                                                                                                   (313)
  99
     4ery_A WD repeat-containing pr 100.0
                                             1E-32 2.8E-37
                                                             229.9
                                                                     35.9
                                                                           250
                                                                                  2-282
                                                                                            16-265
                                                                                                   (312)
100 4ggc A P55CDC, cell division c 100.0 3.3E-33
                                                      9E-38
                                                             234.2
                                                                     33.0
                                                                                   8-282
                                                                                            24-270 (318)
  No 1
                                     PDB<sup>®</sup>
PROTEIN DATA BANK
                                                 NCBI
                                                             Pub Med
🗌 >2pm7_B Protein transport protein SEC13, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A
```

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{Saccharomyces cerevisiae} PDB: 2pm9 _B 4bzk _F 2pm6 _B 3iko _A 3mzk _A 3mzl _A 4bzk _B 4xmm _A 4xmn _A 4bzj _F
 Probab=100.00 E-value=2.3e-51 Score=341.24 Aligned_cols=297 Identities=98% Similarity=1.534 Sum_probs=0.0
                       \texttt{CceEecCCcCeeeEEEecCCCceeEEEeccCCcceeEEeeccCCcceeEEeeccCccCeEEEEeccCcceEE}
 Q ss pred
 Q Fri_Mar_04_23:
                     1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                           80 (297)
                     Q Consensus
                                                                                                           80 (297)
                     T Consensus
                                                                                                           80 (297)
                     1 MVVIANAHNEMIHDAVMDYYGKRMATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVM
 T 2pm7 B
                                                                                                           80 (297)
                       -\texttt{CEECCSCSSCEEEEEECTTSSEEEEEETTSCEEEEBCSSCBCCCEEECCCSSCEEEEEECCGGGCSEEEEEETTTEEE}
 T ss dssp
 T ss_pred
                       EEEccCCeEEEEEecccCccEEEEEeCCccCcEEEEEECCCccCc
 Q ss pred
                    81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
 Q Fri Mar 04 23:
                                                                                                          160 (297)
                                                  -----l----d--i-i-----
                       T Consensus
                    81 iWd------h---v---p---g--l-s-s-d--i-iwd------h---v-----p-----p
                                                                                                          160 (297)
                    81 IWKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPMLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                                          160 (297)
 T 2pm7_B
                       EEEBSSSCBCCCEEECCSSCEEEEECCGGGCSEEEEEETTSEEEEEEBCSSSCBCCEEEECCSSCEEEEECCCC---
 T ss_dssp
 T ss pred
                       EEEccCCceEEEEEcccCCceEEEEEcccCCccEEEEEecCCCCcceeecccCCcceeEEEE
 Q ss_pred
                       Q Fri_Mar_04_23: 161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
                                                                                                          240 (297)
                   161 -----l-tq--d--i--wd------h---v--l--s-----las-s-Dq-i-iw-----
                                                                                                          240 (297)
 Q Consensus
                       161 -----l-sgs-d--i-iwd------l-gh---V--v-sp------las-s-D--v-iWd---
 T Consensus
                                                                                                          240 (297)
                   161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYMASVSQDRTCIIWTQDNEQ
 T 2pm7_B
                                                                                                          240 (297)
 T ss dssp
                       -----CCEEEEEETTSCEEEEEETTTTEEEEEEEECCCSSCEEEEECCCCSSSEEEEEETTSCEEEEESSTT
                       T ss_pred
 Q ss_pred
                       CceeEEEecccCCceEEEEECCCCCEEEEEccCCCCEEEeeeccC
                                                                                  297 (297)
 Q Fri_Mar_04_23: 241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
 O Consensus
                   241 ----d--j-iw-----
                                                                                   297 (297)
                       .++...+....
                   241 -----y----s--g--las---d--y----w----g-w---
 T Consensus
                                                                                   297 (297)
                   241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
 T 2pm7_B
                       SCCEEEESSSSCCSSCEEEEECSSSCCEEEEETTSCEEEECTTSCEEEC---
 T ss_dssp
 T ss_pred
                       CceeeEEeccCCCCEEEEEECCCCCEEEEecCCCCEEEEEcCCCCEEEEeeccCC
 No 2
                                                                 Pub Med
33jrp_A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic
 vesicle, endoplasmic reticulum; 2.60A {Saccharomyces cerevisiae}
Probab=100.00 E-value=2.9e-48 Score=333.24 Aligned cols=297 Identities=100% Similarity=1.542 Sum probs=0.0
 Q ss_pred
                       Q Fri_Mar_04_23:
                     1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                           80 (297)
                     Q Consensus
                                                                                                           80 (297)
                       ++-++-+|...|++++|+||+||+||+||+||+||+||+||+|++-+++++||++++||++++||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||+++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||+-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||+-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||++-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+-||+
                           ----H---V--v--s-dg--lasgs-D--v-iWd-------l-gH---V--v-----g--lasgs-D--v-
                                                                                                           82 (379)
 T Consensus
                     3 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
 T 3jrp_A
                                                                                                           82 (379)
                       T ss_dssp
                       T ss pred
 Q ss_pred
                       EEEccCCeEEEEEecccCccEEEEEeCCccCccEEEEEECCCCcc
                    81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
 Q Fri Mar 04 23:
                                                                                                          160 (297)
 O Consensus
                    81 iwd-----v----v-----v-----v------
                                                                                                          160 (297)
                       T Consensus
                                                                                                          162 (379)
                    83 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
 T 3irp A
                                                                                                          162 (379)
                       EEEEETTEEEEEEECCCSSCEEEEECCCGGGCSEEEEEETTSEEEEEECCTTSCCCEEEEECCTTCEEEEEECCCC---
 T ss_dssp
                       T ss pred
                       Q ss pred
 Q Fri Mar 04 23:
                   161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
                                                                                                          240 (297)
                   240 (297)
 Q Consensus
                       T Consensus
                   163 -----l-sgs-D--i-iWd-----l-gH---V--y-sp-----las-s-D--v-iWd-----
                                                                                                          242 (379)
                   163 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
 T 3jrp A
                                                                                                          242 (379)
                       -----CTTCEEEEEETTSCEEEEEETTTTEEEEEEEECCCSSCEEEEEECCCSSSEEEEEEETTSCEEEEEESSTT
 T ss dssp
 T ss_pred
                       Q ss_pred
                       O Fri Mar 04 23: 241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHO
                                                                                  297 (297)
 Q Consensus
                   241 ~~~~d~i~iw~~~~
                                                                                   297 (297)
                        243 -----v----s-dg--las---dg-v-iW-----
 T Consensus
                                                                                   299 (379)
 T 3jrp_A
                   243 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
                                                                                  299 (379)
                       SCCERESSSSCCSSCEREERCSSSCCREERESSSSEREEREETTERREREEC-
 T ss_dssp
 T ss pred
                       CceeeeccccCCcEEEEECCCCCEEEEEecCCCcEEEEEecCCCceEEeEE
                                  PDB"
```

```
🗀 >4190_A Protein transport protein SEC13, copii coat assem protein SEC16 fusion protein; beta propeller, vesicle
 coat budding; HET: EDO; 1.60A {Komagataella pastoris}
Probab=100.00 E-value=1.6e-46 Score=319.03 Aligned_cols=288 Identities=70% Similarity=1.286 Sum probs=0.0
                 \tt ceeecCCcCeeeEEEecCCCcEeEEEecCCcceeEEeccCCcceeEEeccCCccEEEEEecCCccEEEEEccCCceEEE
Q ss pred
 Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                81 (297)
 O Consensus
               2 -----h---v-----q--l-t-s-d--v-lwd------h---v------l-s-s-D--i-i
                                                                               81 (297)
                 T Consensus
                                                                               141 (349)
                 VTIGNAHDDLIHDAVLDYYGRRLATCSSDKTIKIFEIDGENQRLVETLIGHEGPVWQVAWAHPKFGVILASCSYDGKVLI
T 4190 A
                                                                               141 (349)
                 EEEECSCSSCEEEEECTTSSEEEEEETTSEEEEEC----CEEEEEEECCSSCEEEEEECCGGGCEEEEEETTSCEEE
 T ss_dssp
                 T ss pred
                 EECCCCeEEEEEeccCcccEEEEEeCCccCceEEEEEECCCccchhhhhhhhcccceeEEEECCCcccc
Q ss pred
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
Q Fri_Mar_04_23:
                                                                               161 (297)
                                    -----l----d--i-i----
 Q Consensus
                                                                               161 (297)
                 T Consensus
                                                                               221 (349)
T 4190 A
                                                                               221 (349)
 T ss dssp
                 EEEETTEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTSEEEEEECBTTBCCSCEEEECSSSCEEEEECCCC-
 T ss_pred
                 EECCCCCceeeeeccCCCcEEEEEEcCCCCCEEEEEcCCCCcceeEEEccCCCcceeEEEccCCCcc
                 Q ss pred
              162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
Q Fri Mar 04 23:
                                                                               241 (297)
              162 -----l-tg--d-i--wd------h---v--l--s----las-s-Dg-i-iw-
Q Consensus
                                                                               241 (297)
                        T Consensus
              222 ~---
                    -----l~sgs-D--v-iWd------l-gH---V--v-sp-----las-s-D--v-iWd----
                                                                               293 (349)
              222 T-----RREVSGCONI.VKTWRYDDAAKTETEEEAFOGHSDWVRDVAWSPSRI.SKSYTATASODRTVI.TWTKDGKSN
т 4190 А
                                                                               293 (349)
                 C----CEEEEEETTSCEEEEEETTTTEEEEEEEECCCSSCEEEEEECCCSSSEEEEEETTSCEEEEEECTTCS
T ss dssp
                 C-----CEEEEEeCCCcEEEeEecCCCceeeEeeecCCCCCeeEEEECCCCCCEEEEEECCCCCC
T ss pred
Q ss_pred
                 CeeEEEecccCCceEEEEECCCCCEEEEEccCCCCEEEEECCCCcEEEeeeccC
Q Fri_Mar_04_23:
              242 PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHO
                                                            297 (297)
              242 ----d-i-iw-----
Q Consensus
                                                             297 (297)
                 .+....+...+++++|+|+|+|+++++.|++|++|+...+++|+++++..
              294 -----v-lW------w-----
T Consensus
T 4190 A
              294 KWEKQPLTKEKFPDVCWRASWSLSGNVLAISGGDNKVTLWKENIQGKWESAGEVDQ
                                                             349 (349)
T ss_dssp
                 CEEEEESCSSCCSSCEEEEECSSSCCEEEEETTSCEEEEECTTSCEEEEECC-
T ss_pred
                 CeeeeecccCCceEEEEEcCCCCEEEEEcCCCCEEEEeecCCCCEEEEEecCC
                          PDB<sup>N</sup>
PROTEIN DATA BANK
                                 NCBI Pub Med
📄 >3bgl_A Protein SEC13 homolog; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
complex, nucleus, phosphoprotein; 3.00A {Homo sapiens} PDB: 3bg0 A 5a9q 6
Probab=100.00 E-value=5.2e-45 Score=305.58 Aligned_cols=278 Identities=53% Similarity=1.036 Sum_probs=0.0
                 CGERGCCCCeeeEEEECCCCCEEEEEECCCCGEEEEECCCCGGGEEEEECCCCGCCEEEEECCCCGCCEEEEECCCCGEE
Q ss pred
Q Fri_Mar_04_23:
               1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                               80 (297)
Q Consensus
               1 -----h---v------l-s-s-b--i-
                                                                               80 (297)
                 T Consensus
                                                                                84 (316)
                5 INTVDTSHEDMIHDAQMDYYGTRLATCSSDRSVKIFDVRNGGQILIADLRGHEGPVWQVAWAHPMYGNILASCSYDRKVI
T 3bq1 A
                                                                               84 (316)
T ss_dssp
                 -----CCEEEEECGGGCEEEEETTTEEEEEEETTEEEEEEEECCSSCEEEEECCGGGSSCEEEEETTSCEE
T ss_pred
                 hhhhhhcccceEEEEEcCCCCEEEEEecCCCcEEEEEecCCCccEEEEEecCCCCCEEEEEecCCCCCEEEEE
                 EEEccCCeEEEEEeccCcccEEEEEeCCccCcEEEEEECCCc-chhhhhhhhcccceeEEEECCC---
Q ss pred
Q Fri_Mar_04_23:
               81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGT-TSPIIIDAHAIGVNSASWAPA---
                                                                               156 (297)
O Consensus
               156 (297)
               T Consensus
                                                                               164 (316)
T 3bg1_A
               85 IWREENGTWEKSHEHAGHDSSVNSVCWAPHDYGLILACGSSDGAISLLTYTGEGQWEVKKINNAHTIGCNAVSWAPAVVP
                                                                               164 (316)
T ss_dssp
                 EECCSSSCCEEEEECCGSSCCEEEECCTTTCSCEEEECSSSCEEEECCBTTSSSSCBCCCEECCCCCC
T ss_pred
                 EEECCCCceeeeEEecCCCccEEEEEECCCCCCEEEEEECCCCCceEEEEEcCCCCceeEEEeeccCccccEEeccCCCC
                 -----cccccccccCccceEEEEEcCcceEEEEEccCCceeEEEEEccCCcceeEEEECCCcc
Q ss pred
              157\ ------TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT----VLL
Q Fri_Mar_04_23:
                                                                               218 (297)
                              Q Consensus
              157 ------
                                                                               218 (297)
                           T Consensus
                                                                               228 (316)
              165 GSLIDHPSGQKPNYI-----KRFASGCDNLIKLWKEEED-GQWKEEQKLEAHSDWVRDVAWAPSIGLPT-
T 3bg1 A
                                                                               228 (316)
 T ss_dssp
                 -----CCSCCCCCC-----CBEECCBTTSBCCEEEECTT-SCEEEEECCBCSSCEEEEECCCSSCSC-
                 cccccccccccccccccccc-----ceEEEecCCCeEEEEEecCC-CceecceecccCCceeeeEecccCCCCC-
T ss_pred
                 CCEEEEECCCCeEEEECCCC-CceeEEEecccCCceEEEEECCCCCEEEEECCCCCEEEEECCCCCEEEeeeccC
Q ss pred
Q Fri Mar 04 23: 219 RSYLASVSQDRTCIIWTQDNEQ-GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
                                                                               297 (297)
 Q Consensus
              219 ---las-s-Dg-i-iw------i-----i------l-----d--i-iw------
                                                                               297 (297)
                  T Consensus
                                                                               305 (316)
T 3bg1 A
                                                                               305 (316)
                 -CEEEEETTCEEEEECSSTTCCCBCEEEE--CSSCEEEEEECTTTCCEEEEESSSCEEEEECTTSCEEEEECC-
T ss_dssp
                 T ss pred
```

```
PDB<sup>N</sup>
                                                                                       Pub Med
>4ule I Eukaryotic translation initiation factor 3 subuni; EIF3 complex, beta-propeller; 2.00A {Saccharomyces
 cerevisiae} PDB: 3zwl _B
 Probab=100.00 E-value=2.3e-41 Score=287.15 Aliqned cols=252 Identities=19% Similarity=0.322 Sum probs=0.0
                               eEecCCcCeeeEEEEcCCCCEEEEEecCCccEEEEEccCCccceeEEeccCCCCCEEEEEecCCCcCCEEEEE
 Q ss pred
 Q Fri Mar 04 23:
                                                                                                                                               82 (297)
                            3 VIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW
                                    -h---v-----g--l-t-s-d--v-lwd-------h---v------l-s-s-b--i-iw
 O Consensus
                                                                                                                                               82 (297)
                            79 (347)
 T Consensus
                            4 IKLTGHERPLTQVKYNKEGDLLFSCSKDSSASVWYS--LNGERLGTLDGHTGTIWSIDVDCF--TKYCVTGSADYSIKLW
 T 4ule I
                                                                                                                                               79 (347)
                               EEECCCSSCEEEEECTTSSEEEEEETTSCEEEEET--TTCCEEEEECCCCSCEEEEECTT--SSEEEEEETTTEEEEE
 T ss dssp
                               eEecCCcceEEEECCCCCEEEEeecCCceEEEEc--CCCceeEEEEcCCCcceEEEE
 T ss pred
 Q ss_pred
                               ECCCCeEEEEEeccCccceEEEEecCccccceEEEEECC-----CEEEEEEecCCcc------chhhhhhhccc--
 Q Fri_Mar_04_23:
                           83 KEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSD-----GKVSVVEFKENGT------TSPIIIDAHAI--
                                                                                                                                              146 (297)
                                                                                                                                              146 (297)
                           O Consensus
                           T Consensus
                                                                                                                                              154 (347)
                           80 DVSNGQ--CVATWK-SPVPVKRVEFSPC--GNYFLAILDNVMKNPGSINIYEIERDSATHELTKVSEEPIHKIITHEGLD
 T 4ule I
                                                                                                                                              154 (347)
 T ss_dssp
                               ETTTCC--EEEEE-CSSCEEEEECTT--SSEEEEEECCCTTCCCEEEEEEEECTTTCCEEEECSSCSEEECCTTSC
 T ss_pred
                               ECCCC--EEEEec-CCCceeEEEECCC--CCeEEEEeccCCCCCcEEEEEccCCcccccCCCcceeEEecCCCC
 Q ss_pred
                               Q Fri_Mar_04_23: 147 GVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS
                                                                                                                                              226 (297)
 O Consensus
                          147 \quad \text{$^{\text{-v}}$} \quad \text{$^{-v}}$} \quad \text{$^{\text{-v}}$} \quad \text{$^{\text{-v}}$} \quad \text{$^{\text{-v}}$} \quad \text{$^{\text{-
                                                                                                                                              226 (297)
                                                 T Consensus
                               ~~~~s~da---
                                                                                                                                             215 (347)
 T 4ule I
                          155 AATVAGWSTKG-----KYIIAGHKDGKISKYDVSNNY--EYVDSIDLHEKSISDMQFSPDL--TYFITSS
                                                                                                                                              215 (347)
 T ss dssp
                               CEEEEECGGG-----CEEEEEETTSCEEEEEGGGTT--EEEEEECCCSSCEEEEECTTS---SEEEEE
 T ss pred
                               ceeeeecccc---chhhhhhcccccceeeeecccc--chhhhhhcccccceeeeeccc--ceeeee
 Q ss pred
                               Q Fri_Mar_04_23: 227 QDRTCIIWTQDNEQGPWKKT-----
 Q Consensus
                          254 (297)
                               . | ++ | ++ | | +.......
                          216 -D--i-lwd------p-----g-----g------
 T Consensus
                                                                                                                               ~~~1~a--H~
                                                                                                                                              293 (347)
                          216 RDTNSFLVDVSTLOVLKKYETDCPLNTAVITPLKEFIILGGGOEAKDVTTTSANEGKFEARFYHKIFEEEIGRVQG--HF
 T 4ule I
                                                                                                                                              293 (347)
                               T ss_dssp
                               CCCceEEEEcccceEEEEEccCCCeeEEEEcCCCCeEEEeCCcccceEEeccCCCeEEEEEeehhhhhheecceEc--cc
 T ss_pred
 Q ss pred
                               CEEEEECCCCCEEEEECC
 Q Fri Mar 04 23: 255 DVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
 O Consensus
                         255 --i-----l----d--i-iw---
                                                                         284 (297)
                         ..|++++|+|+|+|+|+|+|+|+|+|
294 ~~V~~vafspdg~~laS~s~D~~vrlW~~~
 T Consensus
                                                                          323 (347)
                          294 GPLNTVAISPOGTSYASGGEDGFIRLHHFE 323 (347)
 T 4ule I
                               SCEEEEECTTSSEEEEEETTSCEEEEECC
 T ss dssp
                               eeEEEEECCCCCeEEeccCCccEEEecC
 T ss pred
                                                 PDB"
                                                                                         Pub Med
>4j87 A Coatomer subunit alpha; beta propeller domain, vesicle trafficking, protein transpor; 1.67A
  {Schizosaccharomyces pombe} PDB: 4j8b A 4j8g A
 Probab=100.00 E-value=7.4e-41 Score=281.53 Aligned_cols=268 Identities=17% Similarity=0.290 Sum_probs=0.0
                               Q ss pred
 O Fri Mar 04 23:
                          1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                                               80 (297)
                            80 (297)
 O Consensus
                               ---v---sp----l-t---dg-i-lwd------h---V----
 T Consensus
                                                                                                                                               78 (327)
                            3 MLTKFESRSSRAKGVAFHPTOPWILTSLHNGRIOLWDY-RMGTLLDRFDGHDGPVRGIAFHPT-OPIFYSGGDDYKVN
 T 4j87 A
                                                                                                                                               78 (327)
 T ss dssp
                               EEEEEEECSCEEEEECSSSSEEEEEETTSEEEEEET--TTTEEEEEEECCSSCEEEEEECSS--SSEEEEEETTSCEE
 T ss_pred
                               hheeeccCccEEEEECCCCCeEEEEcCCCCEEEEEc--CCCeEEEEEcCCCccEEEEEECCC--CCEEEEEcCCCcEE
 Q ss_pred
                               EEECCCCEEEEEEeccCCccEEEEEeCCCcCCCEEEEEECCCCcchhhhhhhhcccceeEEEECCCccc
 Q Fri_Mar_04_23:
                           81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                                                                              160 (297)
                           160 (297)
 O Consensus
                                                                    ----l-s-s-D--i-iwd-----h---
 T 4j87 A
                           79 VWNYKSRK--LLFSLCGHMDYVRVCTFHHE--YPWILSCSDDQTIRIWNWQSR--NCIAILTGHSHYVMCAAFHPSE---
                                                                                                                                              149 (327)
 T ss_dssp
                               EEETTTTE--EEEEECCCSSCEEEEEECSS--SSEEEEEETTSCEEEEETTTT--EEEEEECCCSSCEEEEEECSSS---
                               EEECCCCe--EEEEEcCCCcEEEEEEcCC--CCEEEEECCCCeEEEEECCCC--ceeeEEccCCCcEEEEEECCCC---
 T ss_pred
 Q ss_pred
                               Q Fri_Mar_04_23: 161 DGEHNGTKESRKFVTGGADNLVKIWKYN------SDAQTYVLESTLEGHSDWVRDVA 211 (297)
                          O Consensus
                                                                                                                                              211 (297)
                                           .+|++|+.|+.|++||+.
                          219 (327)
 T Consensus
                                                                                                             ----h---v--
                          150 -----DLIVSASLDQTVRVWDISGLRMKNAAPVSMSKEDQKAQAHNSISNDLFGSADAIVKFVLEGHDRGVNWCA
 т 4ј87_А
                                                                                                                                             219 (327)
 T ss dssp
                               ----SEEEEEETTSEEEEECHHHHHHHHSCCCCCGGGSCTTC-----CCSEEEEEEECCSSCEEEEE
 T ss_pred
```

```
Q ss_pred
                              O Fri Mar 04 23: 212 WSPTVLLRSYLASVSODRTCIIWTODNEOGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEP
                                                                                                                                          291 (297)
                                        ---las-s-Dg-i-iw-----i--
 O Consensus
                         212 ~s~
                                                                                                        ~1~~~~d~~i~iw~~
                                                                                                                                          291 (297)
                                       .+|++++.|+.|++|+++...
                                -p-----h-s---p---i-s---p---i-w-------h---v-------p----i-s-s-bg-i-vWd-----
 T Consensus
                         220
                                                                                                                                          293 (327)
                         220 FHPTL--PLILSAGDDRLVKLWRMTASK--AWEVDTCRGHFNNVSCCLFHPHOELILSASEDKTIRVWDLNRRTAVOT
 T 4j87 A
                                                                                                                                         293 (327)
                              ECSSS---SEEEEEETTSEEEEEECSSC---EEEEEEEECCSSCEEEEECSSSEEEEEETTSEEEEEETTTCCEEEE
 T ss_dssp
                              ECCCC---CeEEEEcCCCEEEEEEcCCc---eEEEEEEeCccCcEEEEEECCCCChhhh
 T ss pred
 Q ss_pred
 Q Fri Mar 04 23: 292 AGEVHQ 297 (297)
 O Consensus
                        292 ~~~~
                                        297 (297)
 T Consensus
                         294 ~~~~~
                                        299 (327)
                         294 FRRAND 299 (327)
 T 4j87 A
 T ss_dssp
                              EECSSC
 T ss_pred
                              hhhccc
                                               PDB'
 No 7
                                                             NCBI
                                                                                      Pub Med
🗎 >4j73_A Coatomer subunit beta'; beta propeller, dilysine motif, ER retrieVal signal, coatome recognition, protein
  transport; 1.44A {Saccharomyces cerevisiae} PDB: 4j77 _A 4j78 _A 4j81 _A 4j82 _A 4j84 _A 4j86 _A 2ynn _A 2yno _A
 Probab=100.00 E-value=9.2e-41 Score=277.97 Aligned_cols=251 Identities=17% Similarity=0.251 Sum_probs=0.0
 Q ss pred
                              Q Fri Mar 04 23:
                           1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                                           80 (297)
                                  ----h---v---
                                                    ----q--1-t-s-d--v-1wd-----h---v----
                                                                                                              -----l~s~s~D~~i~
 O Consensus
                                                                                                                                           80 (297)
                              -----h---V----fsp----l-s---dg-v-iwd------
                                                                                                                     ~~~l~sqs~d~~i~
                                                                                                                                           80 (301)
 T 4j73_A
                           5 IKKTFSNRSDRVKGIDFHPTEPWVLTTLYSGRVEIWNY--ETOVEVRSIOVTETPVRAGKFIAR--KNWIIVGSDDFRIR
                                                                                                                                           80 (301)
 T ss dssp
                              CERERERECSCEREERCSSSSERERETTSERERET--TTTERERERECCSSCREERERGG--GTERERETTSERE
                              hhhhhcCCCCceEEEECCCCCEEEEEcCCCcEEEEec--CCCceeeEecccccEEEEEeCc--CCEEEEECCCCCEE
 T ss pred
 Q ss pred
                              EEEccCCeEEEEEeccCccEEEEEECCCcCCEEEEEEECCCcchhhhhhhhhcccceeEEEECC-Cccc
 Q Fri_Mar_04_23:
                          81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAP-ATIE
                                                                                                                                          159 (297)
 Q Consensus
                          81 jwd-----v----v-----v-----
                                                                                                                                          159 (297)
                              +||+++++ .+..+..|...|.+++|+|+ +.++++++.|+.|++||+... .....+.+||...|.+++||+| +.
                          T Consensus
                                                                                                                                          153 (301)
                           81 VFNYNTGE--KVVDFEAHPDYIRSIAVHPT--KPYVLSGSDDLTVKLWNWENN-WALEQTFEGHEHFVMCVAFNPKDP--
 T 4j73 A
                                                                                                                                          153 (301)
 T ss_dssp
                              EEETTTCC--EEEEEECCSSCEEEEEECSS--SSEEEEEETTSCEEEEETTTT-TEEEEEECCCSSCEEEEEECTTCT--
 T ss_pred
                              EEECCCCC--EEEEEeCCCCCEEEEEECCC--CCEEEEECCCCCEEEEECCCCC-cchhhhcccCCCCEEEEEECCCCC--
                              Q ss pred
                         160 \verb|| EDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNE||
 Q Fri Mar 04 23:
                                                                                                                                          239 (297)
 O Consensus
                         160 -----latg-d-i-wd-----h--v-l-ss-s-Dg-i-iw----
                                                                                                                                          239 (297)
                                            ..|++|+.|+.|++||++....
                         154 -----1~sgs~D~v~iwd~~~~~~~
                                                                                                        ~-~~~l~s~s~D~~i~iwd~~
 T Consensus
                                                                                        ~~~v~~~
                                                                                                                                          218 (301)
 т 4ј73 А
                         154 -----STFASGCLDRTVKVWSLGQSTPN---FTLTTGQERGVNYVDYYPLP-DKPYMITASDDLTIKIWDYQTK
                                                                                                                                          218 (301)
                              -----TEEEEEETTSEEEEETTCSSCS--EEEECCCTTCCCEEEECCST-TCCEEEECTTSEEEEEETTTC
 T ss_dssp
                              -----CEEEEEeCCCccEEEEECCCCcc---ceeecCCcCcEEEEEEcc-CCCcEEEEECCCc
 T ss_pred
                              CCceeEEEecccCCceEEEEE
 Q ss pred
 Q Fri_Mar_04_23:
                         240 OGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
 Q Consensus
                         240 ----d-i-iw-
                                                                                        282 (297)
                                   ....+.. |...|..++|+|++++|++++.||+|++|+
 T Consensus
                         219 ~----h~~v~~~~~l~s~s~Dq~i~iWd 256 (301)
                         219 S---CVATLEG--HMSNVSFAVFHPTLPIIISGSEDGTLKIWN
 T 4i73 A
                                                                                        256 (301)
 T ss_dssp
                              C---EEEEEC--CSSCEEEEEECSSSSEEEEEETTSCEEEEE
 T ss_pred
                              c---hhhhhcC--CCCCeEEEEECCCCCEEEEE
 No 8
                                           SCOPe PROTEIN DATA BANK
                                                                            NCBI
                                                                                                     Pub Med
>vyh_c Platelet-activating factor acetylhydrolase IB alpha subunit; lissencephaly, platelet activacting factor,
  regulator of cytoplasmic dynein; 3.4A {Mus musculus} SCOP: b.69.4.1
 Probab=100.00 E-value=2.9e-41 Score=292.79 Aligned_cols=247 Identities=25% Similarity=0.425 Sum_probs=0.0
                              \texttt{CceEecCCcCeeeEEEecCCCceeEEEeccCCcceeEEeeccCCcceeEEeeccCccCeEEEEeccCcceEE}
 0 ss pred
 Q Fri_Mar_04_23:
                            1 \ \texttt{MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL}
                                                                                                                                           80 (297)
 Q Consensus
                           1 \  \  \, \sim \sim \sim \sim h \sim \sim v \sim \sim \sim -g \sim 1 - t - s - d \sim v \sim 1 w d \sim \sim \sim \sim \sim h \sim \sim v \sim \sim \sim \sim \sim 1 - s - s - D \sim i \sim 1 - t \sim v \sim \sim \sim \sim \sim 1 - s \sim s - D \sim i \sim 1 - t \sim v \sim \sim \sim \sim \sim 1 - t \sim s \sim 1 - t \sim v \sim \sim \sim \sim 1 - t \sim s \sim 1 - t \sim s \sim 1 - t \sim v \sim \sim \sim \sim 1 - t \sim s \sim 1 - t \sim v \sim 1 - t \sim 1 - t
                                                                                                                                           80 (297)
                              T Consensus
                         142 ----1--h---V--1----g--1-s-s-D--i-1Wd-------h---v--v--p------1-sgs-D--i-
                                                                                                                                         217 (410)
                         142 FERTLKGHTDSVQDISFDHSGKLLASCSADMTIKLWDF--QGFECIRTMHGHDHNVSSVSIMPN--GDHIVSASRDKTIK
 T lvyh_C
                                                                                                                                         217 (410)
 T ss dssp
                              CCEEECCCSSCEEEEECTTSSEEEEEETTSCCCEET--TSSCEEECCCCSSCEEEEECSS--SSEEEEEETTSEEE
 T ss_pred
                              EEEEEecccCcEEEEEcCCCCEEEEEcCCCcEEEEEC--CCCcEEEEEecCCCCEEEEEecCC--CCEEEEEecCCCcEE
 Q ss_pred
                              Q Fri Mar 04 23:
                          81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPA----
                                                                                                                                          156 (297)
                                                                   ----1----d--i-i-----v---
 Q Consensus
                          81 iwd~
                                                                                                                                          156 (297)
                              T Consensus
 T 1vyh_C
 T ss dssp
                              EEETTTCC--EEEEEECCSSCEEEEEECTT--SSEEEEEETTSCEEEEETTTCC--EEEEECCCSSCEEEEEECCSSCGG
```

```
T ss_pred
                 EEECCCCc--EEEEEcCCCccEEEEEECCC--CCEEEEEeCCCccEEEEECCCCC--eEEEecCCCCcEEEEEEcCcccch
                 -----ccccccccCCcceEEEEECCCceeEEEEEcCCCceeEEEEECCCCCCE
0 ss pred
 Q Fri_Mar_04_23: 157 -----TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRS 220 (297)
              Q Consensus
                                                                                220 (297)
              T Consensus
                                                                                351 (410)
              292 SISEATGSETKKSGKPG-----PFLLSGSRDKTIKMWDVSTG---MCLMTLVGHDNWVRGVLFHSGG--K 351 (410)
T lvyh C
                 GGGGCCSCC-----C-----CEEEEEETTSEEEEEETTTT---EEEEEEECCSSCEEEEEECSSS--S
T ss dssp
T ss_pred
                 hhhhhcccccccCCCC-----CEEEEEcCCCeEEEEECCCC----CEEEEEECCCC--C
                 EEEEEeCCCceeEEEEccCCCceeEEEeccccCcceEEEEE
Q ss pred
Q Fri Mar 04 23: 221 YLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
           221 ~las~s~Dg~i~iw~~~~~~~~~i~~~~i~~~~l~~~~d~i~iw~ 282 (297)
O Consensus
                 +|++|+.|+.|++|++...
T Consensus
              352 ~l~sgs~D~-i~vWd~~~~~l~~~l~~vV~l~~~~~l~sgs~Dg~i~vWd 408 (410)
              352 FILSCADDKTLRVWDYKNKR---CMKTLNA--HEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 408 (410)
T lvyh_C
                 CEEEEETTEEEEECCTTSC---CCEEECC--CSSCEEEEECSSSSCEEEEETTSEEEEEC
T ss_dssp
                 EEEEEeCCCeEEEEeCCCCe---EEEEECC--CCCcEEEEEEcCCCCeEEEee
T ss pred
                         PDB ROTEIN DATA BANK PROTEIN DATA BANK PUBMEd
No 9
>3f3f A Nucleoporin SEH1; structural protein, protein complex, nucleopori complex, nuclear pore complex, macromolecular assembly, MEM coat; 2.90A {Saccharomyces cerevisiae} PDB: 3f3g A 3f3p A 3ewe A 4xmm
 Probab=100.00 E-value=4e-40 Score=279.78 Aligned_cols=277 Identities=28% Similarity=0.587 Sum_probs=0.0
                 CceEccCcCeeeEEEccCCcEEEEEccCCcc--ceeEEccCCcCCEEEEEccCCccC
0 ss pred
Q Fri Mar 04 23: 1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETH--KLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGK
                                                                                78 (297)
               1 ~~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~h~~~v~~~~~h~~~v~~~~~l~s~s~b~~~
O Consensus
                                                                                78 (297)
               T Consensus
                                                                                82 (351)
               3 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
T 3f3f_A
                                                                                82 (351)
                 CCCEECCCSSCEEEEEECSSSSEEEEEETTSEEEEEEECSSSCCEEEEEEECCSSCEEEEEECCGGGCSEEEEEETTSC
T ss_dssp
T ss pred
                 Q ss_pred
                 EEEEEcc-----CCeEEEEEEeccCccEEEEEeCCccCCcEEEEEEecCCcchhhhhhh------
Q Fri_Mar_04_23:
              79 VLIWKEE-----NGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIID------
                                                                               142 (297)
Q Consensus
               79 i-iwd------ 142 (297)
                 83 v-iWd-----h---v--y--y-sp---g--l-s---d--v-lwd-------
T Consensus
               83 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP 162 (351)
T 3f3f_A
T ss dssp
                 EEEEEECTTSCTTSSCSEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTCEEEEEECSSTTCTTCCEEEEEEESCSCC
T ss_pred
                 --hccceeEEEECCCcccccccCCcceEEEEEECCCceeEEEEEEcCCCceeEEEEECCCCce
Q ss_pred
Q Fri_Mar_04_23: 143 --AHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT----V 216 (297)
              Q Consensus
                                                                               216 (297)
                   .|...+.+++|+|+.
              163
                             T Consensus
                                                                                230 (351)
              163 PANHLQSDFCLSWCPSR------FSPEKLAVSALEQ-AIIYQRGKD-GKLHVAAKLPGHKSLIRSISWAPSIGRWY
T 3f3f A
                                                                               230 (351)
                 CSSCSCCEEEEECCCS-----SSCCEEEEEETTE-EEEEEECTT-SCEEEEEECCCCSCEEEEEECCCSSCSS
T ss_dssp
                 CCcccCCEEEeECCCc------CCCceeEEecccc-eEEEEecCC-CcEEEEEEeCCCCcceeEEEeCCCCCCC
T ss pred
Q ss_pred
                 CCCCEEEEeCCCeEEEEEccCC------CCceeEEEecc
Q Fri_Mar_04_23: 217 LLRSYLASVSQDRTCIIWTQDNE------QGPWKKTLLKE
                                                                               250 (297)
O Consensus
              217 ~~~~las~s~Dg~i~iw~~~~~
                                                                                250 (297)
                   .+||+|+.|++|+||++...
              T Consensus
                                                                                304 (351)
T 3f3f A
              231 ---QLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE---LLSEHDD
                                                                               304 (351)
                 ---EEEEEEETTSCEEEEEEECC------CCSEEEE--EEEEECT
 T ss dssp
T ss pred
                 ccCceEEEEEcccccEEEEEcccccEEEEeeccc
Q ss pred
Q Fri Mar 04 23: 251 EKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (297)
              251 ----i----l----d--i-iw------
Q Consensus
                   |...|++++|+|+|++|++++.|++|+||+....++|+++..+.+
              305 --h---V--v-spdg-las-s-D--v-lW------------------------349 (351)
305 --HNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITA 349 (351)
T Consensus
T 3f3f A
                 --TSSCEEEEECSSSCCEEEEETTSCEEEEEECTTSCEEEEEEC-
T ss dssp
T ss_pred
                 --CCceEEEEEcCCCCEEEEecCCCeEEEehhccCCcEEEEEecc
No 10
                         SCOPe PROTEIN DATA BANK
                                           NCBI
                   435
                                                         Pub Med
>1vyh_C Platelet-activating factor acetylhydrolase IB alpha subunit; lissencephaly, platelet activacting factor,
 regulator of cytoplasmic dynein; 3.4A {Mus musculus} SCOP: b.69.4.1
Probab=100.00 E-value=6.4e-41 Score=290.63 Aligned_cols=246 Identities=22% Similarity=0.342 Sum_probs=0.0
Q ss pred
                 CeEecCCcCeeeEEEccCCCEEEEEccCCcceeEEeccCCcceeEEeccCCccCeEEE
Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                81 (297)
               2 -----h---v-----g--l-t-s-d--v-lwd------h---v------l-s-s-b--i-i
Q Consensus
                                                                                81 (297)
              T Consensus
T lvyh C
              101 KYALSGHRSPYTRVIFHPVFSVMVSASEDATIKVWDY--ETGDFERTLKGHTDSVODISFDHS--GKLLASCSADMTIKL 176 (410)
```

```
T ss_dssp
                 SCEEECCSSCEEEEECSSSSEEEEEESSSCEEEET--TTCCCCEEECCCSSCEEEEEECTT--SSEEEEEETTSCCCE
T ss_pred
                 CARACCCCCERREREECCCCCERREREACCCCARREREC--CCCCRERREACCCCCRERERECCC--CCRERREACCCCCCRER
                 Q ss_pred
                                                                                161 (297)
 Q Fri_Mar_04_23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
              O Consensus
                                                                                161 (297)
T Consensus
                                                                                246 (410)
              177 WDFQGFE--CIRTMHGHDHNVSSVSIMPN--GDHIVSASRDKTIKMWEVQTG--YCVKTFTGHREWVRMVRPNQDG----
T lvyh C
                                                                                246 (410)
                 EETTSSC--EEECCCCSSCEEEEECSS--SSEEEEEETTSEEEEEETTTC--CEEEEEECCSSCEEEEECTTS----
 T ss_dssp
                 EECCCCc--EEEEEeCCCCCEEEEEEeCC--CCEEEEEECCCC--cEEEEECCCC---
T ss pred
                 cccCCccceEEEEEcCCceEEEEEEcCCCceeEEEEEEcCCCceEEEEECCC
Q ss pred
Q Fri_Mar_04_23: 162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT------VLLRSY
                                                                                221 (297)
              T Consensus
                                                                                310 (410)
              247 -----TLIASCSNDQTVRVWVVATKE----CKAELREHRHVVECISWAPESSYSSISEATGSETKKSGKPG---PF
T lvyh_C
                                                                                310 (410)
                 -----SEEEEEETTSCEEEEETTTCC---EEEEECCCSSCEEEEECCSCGGGGGGGCCSCC-----CCE
T ss dssp
                  -----CEEEEEeCCCcEEEEECCCCC----eEEEecCCCCcEEEEEECCcccchhhhhhdcccccccCCCC---CE
 T ss_pred
                 ERRECCCCERRERCCCCCCceeREECcccCCceRREEECCCCCERRERCCCCCERRER
Q ss pred
Q Fri_Mar_04_23: 222 LASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
                                                                 282 (297)
              Q Consensus
T Consensus
              311 l~sgs~D~i~lwd~~~~~h~~~v~~v~~~g~~l~sgs~D~~i~vWd 366 (410)
              311 LISGSRDKTIKMWDVSTGM---CLMTLVG--HDNWVRGVLFHSGGKFILSCADDKTLRVWD
T 1vyh_C
                                                                 366 (410)
                 EEEEETTSEEEEEETTTTE---EEEEEEC--CSSCEEEEEECSSSSCEEEEETTTEEEEEC
T ss dssp
                 EEEEcccceeeeeeccccc---EEEEeec--cccceeeeeeccccceeeeee
T ss pred
                           PDB
                                   NCBI Pub Med
Nucleoporin SEH1; transport protein; 23.00A {Homo sapiens}
 Probab=100.00 E-value=7.4e-40 Score=279.22 Aligned_cols=281 Identities=33% Similarity=0.626 Sum_probs=0.0
Q ss_pred
                 CGERGCCCCeeeEEEECCCCCEEEEEECCCCGEEEEECCCCGCGGGGGGGCCCEEEEECCCCGCCEEEEECCCCGE
Q Fri_Mar_04_23:
              1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETH-KLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                 79 (297)
Q Consensus
                1 -----h---v-----q--l-t-s-d--v-lwd------h---v------l-s-s-D--i
                                                                                 79 (297)
                83 (360)
                4 ARSIAADHKDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKTHSGSVWRVTWAHPEFGQVLASCSFDRTA
T 5a9q 7
                                                                                 83 (360)
T ss dssp
                 CCCEECCCSSCEEEEECSSSSEEEEEETTSEEEEEECSSBCEEEEEECCSSCEEEEEECCTTTCSEEEEEETTSCE
T ss pred
                 EEEEccCC-----eEEEEEEecccCccEEEEEecCCccCcEEEEEEccCccchhhhhhhc--
Q ss_pred
Q Fri_Mar_04_23:
               80 LIWKEENG-----RWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAH---AI
                                                                                146 (297)
               Q Consensus
                                                                                146 (297)
                 84 ~iWd~~~g~~~~~~~
                                        ---V--v-fspd--g--las-s-D--v-iWd-----
T Consensus
                                                                                163 (360)
               84 AVWEEIVGESNDKLRGQSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYEAPDVMNLSQWSLQHEISCKL
T 5a9q_7
                                                                                163 (360)
                 EEEEECSSSCCCSSTTCCSEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTCEEEEEECSCSSCSSCCEEEEEEECCS
T ss_dssp
                 T ss pred
                 ceeEEECCCcccccccCCccceEEEEECCce-----EEEEEECCCCceeEEEEECCCCCCEEEEEECCCCCCCC
Q ss pred
Q Fri Mar 04 23: 147 GVNSASWAPATIEEDGEHNGTKESRKFVTGGADNL-----VKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRS
                                                                                220 (297)
 O Consensus
              220 (297)
                 T Consensus
                                                                                233 (360)
              164 SCSCISWNPSSSRAHS-----PMIAVGSDDSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL--GR
T 5a9q 7
                                                                                233 (360)
                 SCCEEECCCCTTTSC-----CEEEECCCCCSSSCCCCEEEECCSSSCSEEEECCCCCSCCCEEECCCS-SC
 T ss dssp
                 CccEEECCcccCCC-----cEEEEEcCCCCcccceEEEEEecCcCcceeEEEEEccCCCcceEEEEECCCC--CC
T ss pred
                 ---EEEEEeCCCeEEEEEccCCCc-----eeEEEecccCCceEEEEECC
Q ss pred
Q Fri Mar 04 23: 221 ---YLASVSQDRTCIIWTQDNEQGP------WKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENL
                                                                                285 (297)
              221 ----las-s-Dg-i-iw-----d--i-iw---d--i-iw--
                                                                                285 (297)
Q Consensus
              ++++++.| +++|++++.... ....+.. | ...|++++|+|++|+|++|+|++|+|+|+...
234 ~~~las~~d-v-iw~~~~~~~g-H-~V-v-fspdg~las~s-D-~v-iw~~~
234 SFHILAIATKD--VRIFTLKPVRKELTSSGGPTKFEIHIVAQFDN--HNSQVWRVSWNITGTVLASSGDDGCVRLWKANY
T Consensus
                                                                                309 (360)
T 5a9g 7
                                                                                309 (360)
                 SSEEEEEESSS--EEEEEECCCCCBTTBCCCCCEEEEEEECT--TCSCCCEEEECSSSCCEEEECTTSCEEEEECS
T ss dssp
                 ceeEEEccCC--EEEEEEcCCcccccCCCCcEEEEEEEccC--CCCceEEEEEcCCCCEEEEEcCCC
T ss pred
Q ss_pred
                 CCCEEEeeec
Q Fri Mar 04 23: 286 EGKWEPAGEV 295 (297)
Q Consensus
              286 ~~~
                          295 (297)
                  .+.|+.+..|
              310 ~~~
                         319 (360)
T Consensus
              310 MDNWKCTGIL 319 (360)
T 5a9q_7
T ss_dssp
                 SSCEEEEEE
T ss pred
                 CCCEEEEEE
                   SCOPe PROTEIN DATA BANK
```

```
🗌 >1got_B GT-beta; complex (GTP-binding/transducer), G protein, heterotrimer signal transduction; HET: GDP; 2.00A
{Bos taurus} SCOP: b.69.4.1 PDB: 1b9y A 1b9x A* 2trc B 3v5w B* 1gg2 B* 1omw B 1gp2 B 1xhm A 3ah8 B* 3krw B* 3krx B* 3psc B 3pvu B* 3pvw B* 3uzs B 1tbg A* 4kfm B* 4pnk B* 1a0r B* ...

Probab=100.00 E-value=7.6e-40 Score=277.03 Aligned_cols=249 Identities=20% Similarity=0.268 Sum_probs=0.0
                                                                                           3cik
                 Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                 81 (297)
Q Consensus
                2 -----h---v-------l-s-s-d--v-lwd------h---v-----l-s-s-D--i-i
                                                                                 81 (297)
                 123 (340)
T Consensus
               48 RRTLRGHLAKIYAMHWGTDSRLLLSASQDGKLIIWDS--YTTNKVHAIPLRSSWVMTCAYAPS--GNYVACGGLDNICSI
T 1got_B
                                                                                123 (340)
T ss dssp
                 EEEECCCSSCEEEEECTTSSEEEEEETTTEEEEET--TTCCEEEEEECSSSCEEEEEECTT--SSEEEEEETTCEEEE
T ss_pred
                 CARACTOCCCAREEEECCCCCEEEEEACCCCEEEEEC--CCCCCAREEEECCCC--CCEEEEEECCC--CCEEEEEACCCCAREEEE
                 EECCC--CeEEEEEecccCccEEEEEeCCccCcEEEEEECCCccchhhhhhhhhccceeeEEEECCCcc
Q ss_pred
Q Fri_Mar_04_23:
               82 WKEEN--GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIE
                                                                                159 (297)
O Consensus
               159 (297)
              T Consensus
                                                                                196 (340)
              124 YNLKTREGNVRVSRELAGHTGYLSCCRFLD---DNQIVTSSGDTTCALWDIETG--QQTTTFTGHTGDVMSLSLAPDT--
T 1got B
                                                                                196 (340)
                 EETTTCSBSCEEEEEECCSSCEEEEEEE---TTEEEEEETTSCEEEEETTTT--EEEEEECCCSSCEEEEECTTS-
T ss_dssp
                 EeccCCCccceeeeccCCCcEEEEEECC---CCeEEEEECCCc--cEEEEEECCCC--
T ss pred
                 Q ss pred
Q Fri_Mar_04_23:
              160 \verb|| EDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNE||
                                                                                239 (297)
                         ~~~l~tg~~d~~i~~wd~~~
                                           -----las-s-Dg-i-iw-
 Q Consensus
               160 ~~~~
                                                                                239 (297)
                         .++++|+.|+.|++||++.+. +...+|...|.+++|+|++ .+|++|+.|++|++|++|
              197 -----h---v--v--p-----l-sgs-D--v-iwd----
T Consensus
                                                                                258 (340)
              197 -----RLFVSGACDASAKLWDVREGM---CRQTFTGHESDINAICFFPNG--NAFATGSDDATCRLFDLRAD
T lgot B
                                                                                258 (340)
T ss_dssp
                 -----SEEEEEETTSCEEEEETTTCS---EEEEECCCSSCEEEEECTTS---SEEEEEETTSCEEEEETTTT
T ss_pred
                  -----CEEEEEeCCCEEEEEECCCC----eeeEEeCCcCCEEEEEcCCC---CEEEEEcCCCeEEEEEcCCC
                 CCceeEEEecccCCceEEEEE
Q ss pred
Q Fri_Mar_04_23: 240 QGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
 O Consensus
                 ~~~~~1~~~~d~~i~~~~~1~~~~d~~i~iw~
                                                   282 (297)
                   259 ----vwd 298 (340)
T Consensus
              259 Q---ELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWD 298 (340)
T 1got_B
                 E---EEEEECCTTCCSCEEEEEECTTSSEEEEEETTSEEEEE
T ss_dssp
                 C---EEEEEccCCccceEEEEECCCCCEEEEE
T ss pred
                                                  Pub Med
->4j87_A Coatomer subunit alpha; beta propeller domain, vesicle trafficking, protein transpor; 1.67A
 {Schizosaccharomyces pombe} PDB: 4j8b A 4j8g A
 Probab=100.00 E-value=4.6e-39 Score=270.62 Aligned_cols=251 Identities=22% Similarity=0.349 Sum_probs=0.0
Q ss pred
                 Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                 81 (297)
               Q Consensus
                                                                                 81 (297)
T Consensus
                                                                                121 (327)
               46 LDRFDGHDGPVRGIAFHPTQPIFVSGGDDYKVNVWNY--KSRKLLFSLCGHMDYVRVCTFHHE--YPWILSCSDDQTIRI
т 4ј87_А
                                                                                121 (327)
                 EERRECCSSCEEEEECSSSSEEEEETTSCEEEETT-TTTEEEEEECCCSSCEEEEECSS-SSEEEEETTSCEEE
T ss_dssp
                 EEEEcCCCceeeeecccceeeeecccceeeeec--ccceeeeeccccceeeeeccc--cceeeeecccceeee
T ss pred
Q ss_pred
                 EECCCCEEEEEEcccCccEEEEEeCCccCccEEEEEEcccc
Q Fri Mar 04 23:
               82 WKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEF----- 130 (297)
               O Consensus
              197 (327)
T Consensus
              122 WNWQSRN--CIAILTGHSHYVMCAAFHPS--EDLIVSASLDQTVRVWDISGLRMKNAAPVSMSKEDQKAQAHNSISNDLF 197 (327)
T 4j87 A
T ss_dssp
                 EETTTTE--EEEEECCCSSCEEEEECSS--SSEEEEEETTSEEEEEECHHHHHHHHSCCCCCGGGSCTTC-----
                 T ss_pred
Q ss_pred
                 cCCCcchhhhhhhhccceeEEEECCCccccccCCccceEEEEEeCCCceeEEEEEecCCCceeEEEE
 Q Fri Mar_04 23: 131 KENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDV
                                                                                210 (297)
              O Consensus
                                                                                210 (297)
              T Consensus
                                                                                262 (327)
              198 GSADAIVKFVLEGHDRGVNWCAFHPTL------PLILSAGDDRLVKLWRMTASKAW-EVDTCRGHFNNVSCC
T 4j87_A
                 --CCSEEEEEECCSSCEEEEECSSS-----SEEEEEETTSEEEEEECSSCEE-EEEEECCSSCEEEE
T ss_dssp
T ss pred
                 Q ss pred
                 EECCCCCCCEEEEEecCCCceeEEEeccCCCceeEEEeccCCCceEEEEECCCCCEEEEEEC
              211\ \texttt{AWSPTVLL}{\textbf{R}} \texttt{SYLASVSQD}{\textbf{R}} \texttt{TCIIWTQDNEQGPW}{\textbf{K}} \texttt{TLLKEEKFPDVLW}{\textbf{R}} \texttt{ASWSLSGNVLALSGGDN}{\textbf{K}} \texttt{VTLW}{\textbf{KEN}}
Q Fri_Mar_04_23:
                                                                            284 (297)
              284 (297)
              T Consensus
T 4j87 A
                 EECSSS---SEEEEETTSEEEEEETTTCC---EEEEEEC--SSCCEEEEEECSSSSCEEEEE-TTEEEEEEEC
T ss dssp
                 EECCCC---CEEEEEECCCCeEEEEECCCCC---hhhhhhh--cCCcEEEEEECCCceEEEEEcC
 T ss pred
```

```
PDB<sup>IM</sup>
PROTEIN DATA BANK
                                                  Pub Med
□ >3w15_A Peroxisomal targeting signal 2 receptor; beta-propeller, targeting signal recognition, cytosol; 1.80A
 {Saccharomyces cerevisiae}
 Probab=100.00 E-value=8.4e-40 Score=279.63 Aligned cols=252 Identities=21% Similarity=0.374 Sum probs=0.0
                  CCCeeeEEEECC-CCCEEEEEECCCCcceeEEEccCCccceeEEeccCCccCEEEEEccCCccEEEEEccCCc
Q ss pred
Q Fri Mar 04 23:
                                                                                   86 (297)
                8 HNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEEN
                8 h---v-----g--l-t-s-d--v-lwd-------h---v-----l-s-s-D--i-iwd---
O Consensus
                                                                                   86 (297)
                  |...|.+++|+| ++++|++++.|++|+||+. ....++.|++||++++.|++||+++.|++||+++.|++||+++|
                   ~~~v~~v~-sp~~~~las~s~D~~i~lWd~~~~~~~~l~gh~~~V~~v~-sp~~~~l~s~s~D~ti~lWd~~
T Consensus
                                                                                  138 (368)
                61 TQDCLFDLAWNESHENQVLVAQGDGTLRLFDTT-FKEFPIAIFKEHEREVFSCNWNLVN-RQNFLSSSWDGSIKIWSPLR
T 3w15 A
                                                                                  138 (368)
                  ESSCEEEEECTTCTTEEEEEETTSEEEEEETT-SCSSCSEEEECCSSCEEEEECSSS-SSCEEEEETTSCEEECTTC
T ss dssp
T ss pred
                  cCCcceEEEeCCCCCEEEEEcCCCcEEEEECC-CCCCceeehhccCcEEEEECcCC-CCEEEEecCCCeEEEEeCCC
Q ss_pred
                  Q Fri_Mar_04_23:
               87 GRWSOIAVHAVH-----SASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPI
                                                                                  139 (297)
                                                                                  139 (297)
O Consensus
               87 ~~~~~~~
                           ~______l~~~d~~i~i~~~~~~~~~~~
                                                ...|.+++|+|++ +.+|++++.|+.|++||++......
               139 ------las-s-D--i-l\d-----
T Consensus
                                                                                  215 (368)
               139 KQ--SLMTLTPRPLEITKMVDPLNAIILKKKSFTGISKNRNCVYQAQFSPHD-QNLVLSCSGNSYASLFDIRLPSGKNQN
T 3w15 A
                                                                                  215 (368)
T ss_dssp
                  SS--CSEEECCCCHHHHHHSCTTGGGSCC------CCEEEEEECSSC-TTEEEEEETTSEEEEEETTSCTTSSEE
T ss_pred
                  Cc--ceeecCCccceeccccccccccccCCCcEEEEECCCC-CCEEEEEccCCCcccc
Q ss_pred
                  hhhh-ccceeEEEECCCccccccCCccce-EEEEEeCCceEEEEEcCCCceeE-----EEEEe-ccCCCEEEE
 Q Fri_Mar_04_23:
               140 \ \mathtt{IIDA-HAIGVNSASWAPATIEEDGEHNGTKESR-KFVTGGADNLVKIWKYNSDAQTYV------LESTL-EGHSDWVRDV}
                                                                                  210 (297)
               O Consensus
                                                                                  210 (297)
                       ~~~v~~~~sp~~----
                                        ----valasqs-D--i-lWd-----v
T Consensus
                                                                                  282 (368)
T 3w15 A
               216 NFLVHSGLEALTCDFNKYR------PYVVATGGVDNAIRIWDIRMLNKNPGQLHNSSCINEIPNAHGLAIRKV
                                                                                  282 (368)
T ss dssp
                  EEECSTTSCEEEEEECSSC-----TTEEEEEETTSCEEEEETTC-----CEEEEETTSSSSCEEEE
T ss pred
                  eeEecCCcceEEEecCCCC------CCEEEEecCCCcEEEEECCcccCCcCcccchhhhccCcccccccc
Q ss pred
                  EECCC-CCCCEEEEEeCCCeEEEEEccCCCCcee------EEEeccccCCceEEEEEECC--CCEEEEEcC
Q Fri_Mar_04_23: 211 AWSPT-VLLRSYLASVSQDRTCIIWTQDNEQGPWK------KTLLKEEKFPDVLWRASWSLS--GNVLALSGG
 Q Consensus
               ---i----1----
                                                                                  274 (297)
               T Consensus
                                                                                  357 (368)
               283 TWSPHHS---NILMSASYDMTCRIWRDLSNDGAKETYKTNSTDATKGSIFNFTQ--HSEFVFGADWSLWGKPGYVASTAW
T 3w15 A
                                                                                  357 (368)
                  EECSSCT---TEEEEEETTSCEEEEECTTC------CCTTTSTTTTEEEEECC--CSSCEEEEEECSSSSTTEEEEEET
 T ss_dssp
 T ss_pred
                  Q ss pred
                  CCCEEEE
Q Fri Mar 04 23: 275 DNKVTLWK 282 (297)
                         282 (297)
              275 d~~i~iw~
O Consensus
                  |++|+||+
T Consensus
               358 D~~v~~W~ 365 (368)
               358 DGNLFVWN 365 (368)
T 3w15 A
T ss_dssp
                  TSEEEEEE
T ss pred
                  CCCEEEE
                            PDB'
No 15
                                                   Pub Med
>3jro A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic
 vesicle, endoplasmic reticulum, transport, membrane, mRNA transport; 4.00A {Saccharomyces cerevisiae}
Probab=100.00 E-value=1e-39 Score=303.37 Aligned_cols=297 Identities=100% Similarity=1.542 Sum_probs=0.0
Q ss pred
                  CceEccCcceeEEEccCccEEEEEccCccceEEEEccCccceeEE
O Fri Mar 04 23:
                1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                   80 (297)
                    ----h---v-----g--l-t-s-d--v-lwd-------h---v------l-s-s-b--i-
O Consensus
                                                                                   80 (297)
                  1 ----1-gH---V--1-s-dg-latg--dg-I-vwd------1-h---V--1-fs-----1-s-s-Dg-I-
1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
T Consensus
                                                                                   80 (753)
T 3jro A
                                                                                   80 (753)
                  -----CCCCEEECCCSSSCCEEEETTTEEEEEEEETTBEEEEEECCCSSCEEEEEECCTTSCSEEEEEETTSCEE
T ss dssp
                  T ss pred
                  EEECCCCEEEEEEeccCCccEEEEEeCCCcCCCEEEEEECCCCcchhhhhhhhcccceeEEEECCCccc
Q ss pred
Q Fri_Mar_04_23:
               81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                  160 (297)
               O Consensus
                                                                                  160 (297)
                  T Consensus
                81 vWd------h---v--l--s----g--l-s---dg-i-iwd------
                                                                     ~~v~~l~~sp
T 3jro A
                81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                  160 (753)
T ss_dssp
                  EEEEETTEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTSEEEEEECCSSCCCCEEEECCSSCEEEEECCC---
T ss_pred
                  Q ss_pred
                  Q Fri_Mar_04_23: 161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
                                                                                  240 (297)
               O Consensus
                                                                                  240 (297)
                                                                                  240 (753)
T Consensus
T 3jro_A
               161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
                                                                                  240 (753)
 T ss dssp
                  ----CGGGCCEEEEETTSCEEEEEETTTTEEEEEEEECCCSSCEEEEEECCCSSSEEEEEEESSSS
 T ss_pred
                  CCCCCCCCCEEEEEcCCCccEEEEecCCcccceEeEecCCccceEEEEecCCCCCCEEEEEecCCCC
```

```
Q ss_pred
                  297 (297)
Q Fri Mar 04 23: 241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
O Consensus
               241 ~~
                     ....i.
                                             --d--i-iw-----
                                                                  297 (297)
                   .++....+....|.+++|+|+|++++.||.|++|+....+...+..
               241 -----v--v--spdg--l-s-s-dg-i-iwd----g----
T Consensus
               241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (753)
T 3jro A
                  SCCBCCBSSSSCCSSCCCCEEECTTTCCEEEECSSSCEECCBCCSSSCCBCCCCBC-
T ss_dssp
                  CccchhcccccCcCceEEEEEcCCCCEEEEEecCCCcchhhceeecc
T ss pred
                            SCOPe PROTEIN DATA PANE
No 16
                                                               Pub Med
>1got B GT-beta; complex (GTP-binding/transducer), G protein, heterotrimer signal transduction; HET: GDP; 2.00A
{Bos taurus} SCOP: b.69.4.1 PDB: 1b9y A 1b9x A* 2trc B 3v5w B* 1gg2 B* 1omw B 1gp2 B 1xhm A 3ah8 B* 3cik 3krw B* 3krx B* 3psc B 3pvu B* 3pvw B* 3uzs B 1tbg A* 4kfm B* 4pnk B* 1a0r B* ...

Probab=100.00 E-value=1.4e-38 Score=269.36 Aligned_cols=249 Identities=17% Similarity=0.285 Sum_probs=0.0
                  ceEecCCcCeeeEEEccCCcEEEEEccCC--CcceeEEeccCCCCEEEEEccCCcCCEEEEE
Q ss pred
O Fri Mar 04 23:
                 2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEG--ETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                      79 (297)
                 2 ~~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~_~~~~h~~~v~~~~~~~~~~l~s~s~D~~i
                                                                                      79 (297)
 Q Consensus
                  +..+..|...|.+++|+|+|++|++|++|++|++|++|...|.++|...|.++.|.+|
T Consensus
                166 (340)
T 1got B
                                                                                     166 (340)
                  EEEEECSSSCEEEEEECTTSSEEEEEETTCEEEEEETTCSBSCEEEEEEECCSSCEEEEEEE---TTEEEEEETTSCE
T ss dssp
                  T ss pred
Q ss_pred
                  EEEEccCCeEEEEEecccCccEEEEEeCCccCcEEEEEECCCCcEEEEEECCCCcchhhhhhhhhccceeeEEEECCCcc
Q Fri Mar 04 23:
                80 LIWKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIE
                                                                                     159 (297)
                80 ~iwd~~~
                                           -----l----d--i-i------
                                                                                     159 (297)
O Consensus
                         ----v---
                  ++||+++++ ....+..|...|.+++|+|+ +.++++++.|+.|++||++... ....+.+|...|.+++|+|++
               167 ~lwd~~~~~h~~~v~~l~~~~~l~sgs~d~~v~~wd~~~~~h~~~v~~v~~v~~
T 1got B
               167 ALWDIETGO--OTTTFTGHTGDVMSLSLAPD--TRLFVSGACDASAKLWDVREGM--CROTFTGHESDINAICFFPNG--
                                                                                     238 (340)
T ss dssp
                  ERRETTTTE--ERRECCCSSCERERECTT--SSERERETTSCERERETTTCS--ERRECCCSSCERERECTTS--
                  EEEECCCCc--EEEEEeCCCCcEEEEEECCC--CCEEEEEECCCCe--eeeEEeCCcCCEEEEEECCCC-
T ss pred
Q ss pred
                  Q Fri_Mar_04_23:
               160 EDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNE
                                                                                     239 (297)
Q Consensus
               160 -----l-tq--d--i--wd-------h---v--l--s-----las-s-Dq-i-iw----
                                                                                     239 (297)
                           .+|++|+.|++|++|++|++|++....
                      -----v-l~sgs~D~v~iwd~~~~~~~v~~~~v~~~~s~g---~l~g~~d~~i~vwd~
T Consensus
                                                                                     302 (340)
                  ----NAFATGSDDATCRLFDLRADQEL--MTYSHDNIICGITSVSFSKSG---RLLLAGYDDFNCNVWDALKA
T 1got B
                                                                                     302 (340)
T ss_dssp
                  -----SEEEEEETTSCEEEEETTTTEEE-EEECCTTCCSCEEEEEECTTS---SEEEEEETTSEEEEEETTTC
T ss_pred
                   CCceeEEEecccCCceEEEEE
Q ss pred
               240 QGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Fri Mar 04 23:
               240 ----d-i-iw
                                                       282 (297)
O Consensus
                   . ...+.. |...|.+++|+|+|++|++|+.|++|+|
               303 -----1---h---v---s-dg--l-sgs-D--i-iWd 340 (340)
T Consensus
               303 D---RAGVLAG--HDNRVSCLGVTDDGMAVATGSWDSFLKIWN
T 1got B
                                                       340 (340)
                   C---EEEEEC--CSSCEEEEECTTSSCEEEEETTSCEEEEC
 T ss_dssp
                   c---cceEecC--CCCeEEEEECCCCCEEEEcCC
T ss_pred
                             PDB"
No 17
                                    NCBI Pub Med
>4j0w_A U3 small nucleolar RNA-interacting protein 2; beta-propeller, WD domain, RNA binding protein,
 preribosome; 1.70A {Homo sapiens} PDB: 4jxm _A
Probab=100.00 E-value=2e-38 Score=268.67 Aligned cols=247 Identities=19% Similarity=0.268 Sum probs=0.0
                  CceEccCccceeEEEEccCccEEEEEeccCccceeEEecc------cccccEEEEEeccCcccCE
Q ss pred
Q Fri_Mar_04_23:
                 1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLT-----GHEGPVWRVDWAHPKFGTI
                                                                                      69 (297)
                 O Consensus
                                                                                      69 (297)
                 +|...|.+++|+++ +++
T Consensus
                                                                    ~qh~~~v~~~~s~d--q~~
                                                                                      81 (343)
T 4j0w A
                 6 DIRVLRGHQLSITCLVVTPDDSAIFSAAKDCSIIKWSV-ESGRKLHVIPRAKKGAEGKPPGHSSHVLCMAISSD-GKY
                                                                                      81 (343)
 T ss_dssp
                   TCEEEECCSSCEEEEECTTSSEEEEEETTSCEEEEET--TTCCEEEEECCC-----CCCSCCSSCEEEEECTT--SCE
                   T ss_pred
0 ss pred
                  EEEECCCCeEEEEEccCCceEEEEEecccCccEEEEEeCcccCceEEEEEccCccchhhhhhhhccccee
Q Fri_Mar_04_23:
                70 LASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVN
                                                                                     149 (297)
                70 l-s-s-D-i-iwd------v----v-------l-----d--i-i------
                   82 lasgs-d--i-iwd-----h---v--v--v-----l-s-s-D--v-iWd-----h---v-
T Consensus
                                                                                     155 (343)
                82 LASGDRSKLILIWEAOSCO--HLYTFTGHRDAVSGLAFRRG--THOLYSTSHDRSVKVWNVAEN--SYVETLFGHODAVA
T 4j0w A
                                                                                     155 (343)
T ss_dssp
                  EEEEETTSCEEEEETTTTE--EEEEECCCSSCEEEEECTT--SSEEEEEETTSEEEEEEGGGT--EEEEEECCSSCCC
T ss pred
                   EEEecCCCEEEEEECCCCc--cccccCccceEEEEECCC--CCEEEEecCCCCEEEeeCCCC--cceEEEeCCCCccE
Q ss_pred
                  EEEECCCccccccccccccccccceEEEEEEcCCcceEEEEEEcCCCcceEEEEEEcCCCcccCcCCCCCEEEEEECCCC
Q Fri_Mar_04_23: 150 SASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDR
                                                                                     229 (297)
                            Q Consensus
               150 ~
                                                                           ~~~las~s~Dq
                                                                                     229 (297)
                                  .++++|+.|+.|++||+...
                                                     ....+.+|...|.+++|++.
               T Consensus
                                                                                     213 (343)
T 4j0w A
T ss dssp
                  EEEECSSS-----TEEEEECBTTCEEEEEETTTT----EEEEEECSSSCEEEEEEET---TEEEEEETTS
```

```
T ss_pred
                 EEEecCCC-----CEEEEEcCCCeEEEEcCCC----ccEEEecCCCcEEEEEcCC----CEEEEE
                 eEEEEEccCCCceeEEEeccccCce-----EEEEEECCCCCEEEEEEC
0 ss pred
 Q Fri_Mar_04_23: 230 TCIIWTQDNEQGPWKKTLLKEEKFPDV------LWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
              230 ~i~iw~~~~d~~i~iw~~~
                                                                      284 (297)
                                               |.+++|+|++++|++++.|++|+||+..
                 +|++||+.... ....+.. ....
              214 ~v~lwd~~~~~
T Consensus
                                             ---v---s----lasgs-d--v-lW---
                                                                      274 (343)
              214 SVALWGLSKKR---PLALQRE--AHGLRGEPGLEQPFWISSVAALLNTDLVATGSHSSCVRLWQCG 274 (343)
T 4j0w A
                 CEEEEESSCSS---CSEEETT--TTCEESSTTCCEECCCCEEEECTTSSEEEEEEEC
T ss dssp
T ss_pred
                  eEEEEECCCC---cceeehh--hhcCCCCcccccceEEeeecCCCCEEEEeCCC
                           PDB"
No 18
                                   NCBI Pub Med
->4wju_A Ribosome assembly protein 4; ribosome biogenesis ribosome assembly, biosynthetic protein; 2.80A
 {Saccharomyces cerevisiae} PDB: 3j65 _q 4wjv _A*
Probab=100.00 E-value=2.5e-38 Score=282.06 Aligned_cols=249 Identities=28% Similarity=0.452 Sum_probs=0.0
                 ceEecCCcCeeeEEEEcCCCCEEEEEecCCcceee-EEeccCCcccee-EEeccCccceeEEEEecC-----CccCCEEEEEcC
0 ss pred
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLI-DTLTGHEGPVWRVDWAH-----PKFGTILASCSY
                                                                                 75 (297)
                2 ~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~h~~~v~~~h~~~v~~~
 Q Consensus
                                                                                 75 (297)
              T Consensus
                                                                                 256 (515)
              179 MHTLKGHYNWVLCVSWSPDGEVIATGSMDNTIRLWDP--KSGQCLGDALRGHSKWITSLSWEPIHLVKPGSKPRLASSSK
T 4wju A
                                                                                 256 (515)
T ss_dssp
                 EEEECCCSSCEEEEECTTSSCEEEEETTSCEEEECT--TTCCBCSSCBCCCSSCEEEEEECCGGGSCTTSCCCEEEEET
                  eEEEcCCCCcEEEEECCCCCEEEEEeCCCcEEEEEC
T ss pred
                 CCeEEEEEccCCeEEEEEecccCccEEEEEEcCccCcEEEEEEccC-----
Q ss pred
O Fri Mar 04 23:
               76 DGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKE-----
O Consensus
                                         ----d--i-i--
                                                                                132 (297)
                 |++|++||+..+. ....+.+|...|.+++|+++ + .+++++.|+.|++||+..
T Consensus
              257 DGTLKIWDTVSRV--CQYTMSGHTNSVSCVKWGGQ--G-LLYSGSHDRTVRVWDINSQGRCINILKSHAHWVNHLSLSTD 331 (515)
T 4wju_A
                  TSCEEEEETTTTE--EEEECCCCSSCEEEEEECTT--S-EEEEEETTSCEEEEEGGGTTEEEEEECCCSSCEEEEEESSH
T ss_dssp
T ss pred
                  Q ss_pred
                  -----CCcchhhhhhhccceeEEEEC
Q Fri_Mar_04_23: 133 ----NGTTSPIIIDAHAIGVNSASWA
                                                                                 154 (297)
Q Consensus
              154 (297)
                                               ----l-s-s-d--i-lwd-----h
                                                                                 411 (515)
T 4wju_A
              332 YALRIGAFDHTGKKPSTPEEAQKKALENYEKICKKNGNSEEMMVTASDDYTMFLWNPLKSTKPIARMTGHQKLVNHVAFS
                                                                                 411 (515)
T ss dssp
                 HHHHHTTCCTTCCCCSSHHHHHHHHHHHHHHHBSSSSBCCCEEEEETTSCEEEECTTTCSSCSEEECCCSSCEEEEEC
T ss pred
                 CCEEEEecCCCCccCChHHHHHHhhhhhhhhheeccCCCCceEEEEEcCCCCeEEEEECCCCCEEEEEEC
                 Q ss_pred
 \texttt{Q} \ \texttt{Fr\bar{i}\_Mar\_04\_23:} \ \ 155 \ \ \texttt{PATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVR} DVAWSPTVLLRSYLASVSQDRTCIIW \\ 
                                                                                 234 (297)
                 -----l-tq--d--i--wd------h---v--las-s-Dq-i-iw
 Q Consensus
              155
                                                                                 234 (297)
                             .+|++|+.|+.|++||.+.++ ++..+.+|...|.+++|+|++ ++|++++.|++|++|
                          -----h---v-vw
T Consensus
              412 pdg-
                                                                                 471 (515)
T 4wju_A
                     -----RYIVSASFDNSIKLWDGRDGK----FISTFRGHVASVYQVAWSSDC---RLLVSCSKDTTLKVW
                                                                                 471 (515)
                  TTS-----SEEEEEETTSCEEEEETTTCC---EEEEECCCSSCEEEEEECTTS---SEEEEEETTSEEEEE
T ss_dssp
                  T ss pred
                 EccCCCceeEEEecccCCceEEEEE
Q ss pred
              235 TQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Fri Mar 04 23:
              235 ----d-i-iw- 282 (297)
 O Consensus
                  |++... |...|++++|+|+|+|++|+++++|++|+
              472 d--t---l---h---V--v-spdg--lasg--D--v-lW-
T Consensus
                                                        514 (515)
              472 DVRTRK---LSVDLPG--HKDEVYTVDWSVDGKRVCSGGKDKMVRLWT
T 4wiu A
                                                        514 (515)
                  ETTTTE---EEEEEEC--CSSCEEEEEECTTSCEEEEE
 T ss dssp
                  ECCCCc---eeeEcCC--CcCcEEEEECCCCCEEEECCC
T ss pred
                          PDB<sup>IN</sup>
PROTEIN DATA BANK
No 19
                                            Pub Med
Sfmo_A Protein CIA01; WDR39,SGC,WD40,CIA01, nucleus, WD repeat, biosynthetic prote structural genomics,
 structural genomics consortium; 1.70A {Homo sapiens}
Probab=100.00 E-value=1.9e-37 Score=262.59 Aligned_cols=258 Identities=30% Similarity=0.488 Sum_probs=0.0
Q ss pred
                 ceEecCCcC-eeeEEEEcCCCCEEEEEecCCccEEEEEccCCccceeEEec-cCCCCEEEEEEccCCccEEEEEccCCce
Q Fri_Mar_04_23:
                2 VVIANAHNE-LIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLT-GHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                 79 (297)
O Consensus
                2 \  \  \, \hbox{$\sim\sim\sim\sim-h\sim-v\sim\sim\sim\sim-l-s\sim d\sim v-l$ with $d\sim\sim\sim\sim-h\sim v\sim\sim\sim\sim-l-s\sim s\sim b-i$}
                                                                                 79 (297)
                 8 -----h----v--l--s--q--las---d--i-iw-------h---v---sp-----l-s-s-d--v
                                                                                 85 (345)
T Consensus
T 3fm0_A
                8 LGRVPAHPDSRCWFLAWNPAGTLLASCGGDRRIRIWGTEGDSWICKSVLSEGHQRTVRKVAWSPC--GNYLASASFDATT
                                                                                 85 (345)
T ss dssp
                 T ss_pred
                  eeeccccCceEEEEECCCCEEEEEecCCceEEEEEcCCCceEEEEEEcCCcc
Q ss pred
                 EEEEccCCeEEEEEeccCcceEEEEEeCCccCcEEEEEECCCcc
Q Fri Mar 04 23:
               80 LIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGT-TSPIIIDAHAIGVNSASWAPATI
                                                                                 158 (297)
               158 (297)
 Q Consensus
                 ++||.+.+.....+..|...|.+++|+|+ +.+|++++.|+.|++|++....
               T Consensus
                                                                     ~~~77~~~
                                                                                 162 (345)
T 3fm0 A
               86 CIWKKNODDFECVTTLEGHENEVKSVAWAPS--GNLLATCSRDKSVWVWEVDEEDEYECVSVLNSHTODVKHVVWHPSO-
                                                                                 162 (345)
```

```
T ss_dssp
                  EEEEECCC-EEEEEECCCSSCEEEEECTT--SSEEEEEETTSCEEEEEECTTSCEEEEEECCCSCEEEEEECSSS-
T ss_pred
                  Q ss_pred
 Q Fri_Mar_04_23: 159 EEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDN
                                                                                  238 (297)
               O Consensus
                                                                                  238 (297)
T Consensus
                                                                                  225 (345)
                     -----ELLASASYDDTVKLYREEED--DWVCCATLEGHESTVWSLAFDPSG---QRLASCSDDRTVRIWRQYL
T 3fm0 A
                                                                                  225 (345)
                  -----SCEEEEETTSCEEEEEETT-EEEEEEECCCSSCEEEEECTTS---SEEEEEETTSCEEEEEEEC
 T ss_dssp
                  -----CEEEEEeCCCEEEEEECCCC--cEEEEEeCCCC--CEEEEEeCCC
T ss pred
                  CCC-----ceeEEEecccCCceEEEEECCCCCEEEEEE
Q ss pred
Q Fri_Mar_04_23: 239 EQG------PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE 283 (297)
               239 ~~~-----
                                       ----i-----1----d--i-iw-- 283 (297)
               T Consensus
                                                                281 (345)
               226 PGNEQGVACSGSDPSWKCICTLSGF--HSRTIYDIAWCQLTGALATACGDDAIRVFQE
T 3fm0 A
                                                                281 (345)
T ss dssp
                  TTCTTCCCCC---CEEEEEEECSS--CSSCEEEEECTTTCCEEEEETTSCEEEEE
 T ss_pred
                  CcccceeeecCCCcceEeeEeccc--cCCcEEEEEEcCCCceEEEEEE
No 20
                           PDB"
                                    NCBI
                                             Pub Med
🗌 >30w8_A WD repeat-containing protein 61; structural genomics consortium, SGC, transcriptio; 2.30A {Homo sapiens}
  Probab=100.00 E-value=7.8e-38 Score=262.54 Aligned cols=249 Identities=22% Similarity=0.354 Sum probs=0.0
0 ss pred
                  CceEccCcceeEEEccC----CCEEEEEccCcceeEEeccCccceeEEeccCcccCEEEEEccCC
Q Fri Mar 04 23:
                1 MVVIANAHNELIHDAVLDYY----GKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYD
                                                                                  76 (297)
O Consensus
                     \cdots \sim h \sim \sim v \sim \sim \sim \sim \sim ---g \sim 1 \sim t \sim s \sim d \sim \sim v \sim 1 w d \sim \sim \sim \sim \sim \sim h \sim \sim v \sim \sim \sim \sim \sim \sim \sim 1 \sim s \sim s \sim D
                                                                                   76 (297)
                  T Consensus
               24 ------gh---v--v----s-s-s-d
                                                                                 101 (321)
               24 LFKQEQAHDDAIWSVAWGTNKKENSETVVTGSLDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHT--LPIAASSSLD
T 3ow8 A
                                                                                 101 (321)
                  EEEETTSSSSCEEEEEC-----CEEEEEETTSCEEEEEEETTEEEEEEECCCSSCEEEEEECSS-SSEEEEEETT
T ss dssp
T ss pred
                  EEeehhcCCCcEEEEEecCCCCCCEEEEEeCCCcceeeEEEeCCCcceeEEEEcCC--CCEEEEEeCCC
Q ss_pred
                  Q Fri_Mar_04_23:
               77 GKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPA
                                                                                  156 (297)
Q Consensus
               156 (297)
               175 (321)
               102 AHIRLWDLENGK--QIKSIDAGPVDAWTLAFSPD--SQYLATGTHVGKVNIFGVESGK--KEYSLDTRGKFILSIAYSPD 175 (321)
T 3ow8 A
T ss dssp
                  SERREETTTTE--ERREECCTTCCCCERECTT--SSEREEECTTSEEEREETTTCS--REEREECSSSCEREERECTT
T ss pred
                  CCEEEEECCCc--EEEEEeCCCcEEEEEECCC--CCEEEEECCCC--eeEEecCCCCeEEEEECCCC
                  Q ss_pred
Q Fri_Mar_04_23: 157 TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQ
                                                                                  236 (297)
               157 -----l-tq--d--i--wd------h---v--l-s-s----las-s-Dq-i-iw--
 O Consensus
                                                                                  236 (297)
                          T Consensus
                                                                                  235 (321)
                     -----KYLASGAIDGIINIFDIATG----KLLHTLEGHAMPIRSLTFSPDS---QLLVTASDDGYIKIYDV
T 3ow8 A
                                                                                  235 (321)
                  S-----SEEEEETTSCEEEEETTTT----EEEEEECCCSSCCCEEECTTS---CEEEEECTTSCEEEEET
T ss_dssp
                  C-----CEEEECCCCCEEEECCCC----CEEEECCCCC---CEEEECCCC---CEEEEECCCC
T ss pred
                  CCCCceeEEEecccCCceEEEEECCCCCEEEEE
Q ss pred
Q Fri_Mar_04_23: 237 DNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
 O Consensus
               237 ----d--i-w-
                                                       282 (297)
                     ....+.. +...|.+++|+|++++|++++.|+.|++|+
               236 ~~~~l~vvd 276 (321)
T Consensus
T 3ow8_A
               236 QHAN---LAGTLSG--HASWVLNVAFCPDDTHFVSSSSDKSVKVWD
                                                       276 (321)
                  TTCC---EEEEECC--CSSCEEEEEECTTSSEEEEEETTSCEEEEE
 T ss dssp
                  CCCc---eEEEecC--CCCcEEEEEcCCCCEEEEe
T ss pred
                           PDB<sup>IN</sup>
PROTEIN DATA BANK
                                    NCBI
                                             Pub Med
No 21
       Coatomer subunit beta; beta propeller, dilysine motif, ER retrieVal signal, coatome recognition, protein
 transport; 1.44A {Saccharomyces cerevisiae} PDB: 4j77 _A 4j78 _A 4j81 _A 4j82 _A 4j84 _A 4j86 _A 2ynn _A 2yno _A
Probab=100.00 E-value=1.3e-37 Score=258.99 Aligned cols=249 Identities=20% Similarity=0.256 Sum probs=0.0
Q ss pred
                  ceEecCCcCeeeEEEccCCcEEEEEccCCcceEEEeccCccceeEEeccCCccCeEEEE
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                  81 (297)
O Consensus
                2 -----h---v-----g--l-t-s-d--v-lwd-----h---v----h---v------l-s-s-D--i-i
                                                                                  81 (297)
                  T Consensus
                                                                                  123 (301)
т 4ј73_А
               48 VRSIQVTETPVRAGKFIARKNWIIVGSDDFRIRVFNY--NTGEKVVDFEAHPDYIRSIAVHPT--KPYVLSGSDDLTVKL
                                                                                  123 (301)
T ss_dssp
                  EEEEECCSSCEEEEEEGGGTEEEEEETTSEEEEET--TTCCEEEEEECCSSCEEEEEECSS--SSEEEEEETTSCEEE
T ss_pred
                  eeEeccccccEEEEEeCCCCEEEEECCCCcEEEEEC--CCCcEEEEEeCCCCcEEEEECCC--CCEEEEECCCCcEEE
                  {\tt EEccCCeEEEEEecccCccEEEEEECCCccCeEEEEEECCCcceEEEEEECCCccc} \\
Q ss pred
 Q Fri_Mar_04_23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED 161 (297)
                  82 wd~~~~~
                                                                                 161 (297)
T Consensus
               124 Wd-----h---v--v--v--p----1-sgs-D--v-iwd-----v---v---v----
                                                                            ~---- 196 (301)
```

```
124 WNWENNW-ALEOTFEGHEHFVMCVAFNPKD-PSTFASGCLDRTVKVWSLGQS-TPNFTLTTGQERGVNYVDYYPLP---- 196 (301)
T 4j73 A
T ss_dssp
                 EETTTTT-EEEEEECCCSSCEEEEECTTC-TTEEEEEETTSEEEEEETTCS-SCSEEEECCCTTCCCEEEECCST----
T ss_pred
                 EECCCC-chhhhcccCCcEEEEEEcCCC-CCEEEEEECCC-CcCeeecCCcCcEEEEEEcC----
                 Q ss pred
 Q Fri_Mar_04_23: 162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                             241 (297)
Q Consensus
              241 (297)
                    ++.+++|+.|+.|+.|++||++.+. ++..+|...|.+++|+|++ .+|++|+.||+|+.||
                    -----l-s-s-D--i-iwd------h---v-----l-s-s-Dg-i-iWd-
                                                                             261 (301)
T Consensus
              197 -----DKPYMITASDDLTIKIWDYQTKS----CVATLEGHMSNVSFAVFHPTL---PIIISGSEDGTLKIWNSSTYK-
T 4j73_A
                                                                             261 (301)
                 -----TCCEEEEECTTSEEEEEETTTCC---EEEEEECCSSCEEEEEECSSS---SEEEEEETTSCEEEEETTTCC-
T ss_dssp
                 -----CCCEEEEECCCCcEEEEECCCC---hhhhhcCCCCCeEEEEECCCC---CEEEEECCCCeEEEEECCCce-
T ss_pred
                 ceeEEEecccCCceEEEEEECCCCC--EEEEEcCCCCEEE
Q ss_pred
Q Fri_Mar_04_23: 242 PWKKTLLKEEKFPDVLWRASWSLSGN--VLALSGGDNKVTL
                                               280 (297)
              242 ----d--i-i
O Consensus
                                                280 (297)
                  ....+.. +...+++++|+|++++ +|++|+.||.+.+
------asg---g----
                                                298 (301)
T Consensus
T 4j73 A
              262 -- VEKTLNV--GLERSWCIATHPTGRKNYIASGFDNGFTVL 298 (301)
                 --EEEEECC--SSSSEEEEEC----CCEEEEETTEEEEE
T ss_dssp
                 --eEEeccc--CCccEEEEEecCCCCceEEEE
T ss pred
                          PDB"
No 22
                                  NCBI
                                                Pub Med
Scxb_B Ribosome biogenesis protein ERB1; ribosome assembly, WD40, beta-propeller, ubiquitin-like DOMA protein
binding; 2.10A {Chaetomium thermophilum} PDB: 5cxc _B 5cyk
                                             _B
Probab=100.00 E-value=1.1e-37 Score=266.68 Aligned_cols=254 Identities=19% Similarity=0.237 Sum probs=0.0
Q ss_pred
                 CceEccCcCeeeEEEccCccEEEEEccCcccEEEEEccCcccceeEEcccCccceeEEcccCccc-------
Q Fri_Mar_04_23:
              1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGH-EGPVWRVDWAHPKF------
                                                                              66 (297)
O Consensus
               1 ~~~~~h~~~v~~~~~g~l-t~s~d~~v~lwd~~~~~~h-~~v~~~~~h-~~v~~~~~
                                                                              66 (297)
              ---v--rspdg----la--
T Consensus
                                                                             90 (369)
              13 QQTIFRGHEGRVRSVAIDPTGVALATGGDDGTVRVWEL--LTGRQVWSVKLNGDEAVNTVRWRPTKDTFILAAAAGEDIF
T 5cxb B
                                                                             90 (369)
                 EEEEECCCSSCEEEEECTTSSEEEEETTSEEEEET--TTCCEEEEEESCTTSCEEEEEECSCTTCCCEEEEETTEEE
 T ss_dssp
T ss_pred
                 Q ss pred
Q Fri_Mar_04_23:
                                                                              69 (297)
 Q Consensus
                                                                              69 (297)
T Consensus
                                                                             170 (369)
              91 LMIPTHPSVTPALDOASRDILNAGFGHATNGKOOANLPPGKEPPGKWARPGTRLEDEGVLLRITVRSTIKAISWHRRGDH
T 5cxb B
                                                                             170 (369)
                 EECCCCTTCCHHHHHHHHHHHTTC------CCCEEECCCHHHHHTTEEEEEECSSCCCEEECTTSSE
T ss dssp
                 T ss pred
                 Q ss pred
Q Fri Mar 04 23:
              70 LASCSYD---GKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAI
                                                                             146 (297)
              Q Consensus
                                                                             146 (297)
                 171 las-s-d----v--w------
                                        ---v---fsp---g--l-----i-lwd------
T Consensus
                                                                             243 (369)
              171 FATVSPSGQRSSVAIHTLSKHL--TQIPFRKLNGLAQTASFHPL--RPLFFVAT-QRSIRCYDLQKLE--LVKIVQPGAK
T 5cxb_B
                                                                             243 (369)
                 EEEECGGGTTSCEEEEETTTTE--EECCCCCCSSCEEEEECSS--SSEEEEEE-SSCEEEEETTTTS--CSEEECCCCS
T ss_dssp
                 EEEEcCCCCceEEEEeCCCcc--ccccccCCCCEEEEEECCC--CCEEEEEc-CCEEEEEECcCCc--eeeeecCCCc
T ss pred
Q ss_pred
                 ceeEEECCCcccccccCCcceEEEEEeCCceEEEEEEcCCCceeEEEEEccCCCcEeEEEE
Q Fri_Mar_04_23: 147 GVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSP-TVLLRSYLASV
                                                                             225 (297)
              147 ~v~~~~~h~~v~l~s~~~las~
                                                                             225 (297)
O Consensus
              304 (369)
T Consensus
              244 WISSFDVHPGG-----DNLVVGSYDKRLLWHDLDLSNR---PYKTMRFHTEAIRAVRFHKGGL---PLFADA
T 5cxb_B
T ss_dssp
                 SEEEEEECTTS----SEEEEEETTSCEEEEETTTCSS---CSEEECCCSSCEEEEEECCSSC--SEEEEE
                 CEEEEECCCC-----CEEEEecCCCcEEEEeccccc--hhhhhccccccEEEEECCCCC--CEEEEE
T ss_pred
Q ss_pred
                 Q Fri_Mar_04_23: 226 SQDRTCIIWTQ----DNEQGPWKKTLLKEEKFPD----VLWRASWSLSGNVLALSGGDNKVTLWK
                                                                  282 (297)
              226 s-Dg-i-iw----d--i-iw-
                                                                  282 (297)
O Consensus
              T Consensus
                                                                  369 (369)
              305 SDDGSLQIFHGKVPNDQLENPTIVPVKMLKGHKVVNKLGVLDIDWHPREPWCVSAGADGTARLWM
T 5cxb B
                                                                  369 (369)
                 ETTSEEEEEEECCSSTTSCCEEEEEEEECCCCBTTBCEEEEECSSSSCEEEEETTSCEEEEC
T ss_dssp
T ss pred
                 SCOPe PROTEIN DATA BANK
No 23
                                                        Pub Med
->lerj_A Transcriptional repressor TUP1; beta-propeller, transcription inhibitor; 2.30A {Saccharomyces cerevisiae}
SCOP: b.69.4.1 PDB: 5afu _3*
Probab=100.00 E-value=1.7e-37 Score=267.67 Aligned_cols=247 Identities=27% Similarity=0.403 Sum probs=0.0
Q ss pred
                 Q Fri Mar 04 23:
               7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEEN
                                                                              86 (297)
 O Consensus
               86 (297)
```

```
T Consensus
             121 ~~~~v~~v~~spdg~~lasgs~d~~i~iwd~~~~~~~h~~~v~~l~~~p~~~~~l~s~s~D~~v~iWd~~~ 196 (393)
             121 SSDLYIRSVCFSPDCKFLATGAEDRLIRIWDI--ENRKIVMILQGHEQDIYSLDYFPS--GDKLVSGSGDRTVRIWDLRT 196 (393)
T lerj_A
T ss dssp
                CCCCBEEEEECTTSSEEEEEETTSCEEEEET-TTTEEEEEECCCSSCEEEEEECTT-SSEEEEEETTT
                CCCceEEEEECCCCEEEEECCCCeEEEEECCCCCEEEEECCC--CCCEEEEECCCCCEEEEEECCCC
T ss pred
Q ss_pred
                87 GRWSQIAVHAVHSASVNSVQWAP-HEYGPLLLVASSDGKVSVVEFKENGTTSPIIID----AHAIGVNSASWAPATIEE 160 (297)
Q Fri_Mar_04_23:
Q Consensus
              160 (297)
                  T Consensus
                                                                              268 (393)
             197 G---QCSLTLSIEDGVTTVAVSPGD--GKY1AAGSLDRAVRVWDSETGFLVERLDSENESGTGHKDSVYSVVFTRDG---
T---EEFEEEECSSCEFEEEECSTT--CCEFEEEFTTSCEFEEETTTCCFEEEEC-----CCCSSCEFEEEECTTS---
T lerj A
T ss dssp
                T ss_pred
                ccccCCccceEEEEEeCCcceEEEEEECCCCc-----eeEEEEEeccCCccEeEEEECCCCCCCEEEEEECCCCeEE
Q ss_pred
Q Fri_Mar_04_23: 161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQ------TYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCI 232 (297)
            O Consensus
                                                                              232 (297)
T Consensus
                                                                              335 (393)
             269 -----QSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQND---EYILSGSKDRGVL
T lerj_A
                                                                              335 (393)
                -----CEEEEEETTSEEEEEEC------CEEEEEECCSSCEEEEEECGGG---CEEEEEETTSEEE
T ss_dssp
                -----CEEEEEeCCCeEEEEECCCCcccccCCCCCceeEEEEeccCCceEEEEECCCC---CEEEEEeCCCeEE
T ss pred
                EEEccCCCCceeEEEecccCCceEEEEEC-----CCCCEEEEEC
Q ss pred
Q Fri_Mar_04_23: 233 IWTQDNEQGPWKKTLLKEEKFPDVLWRASWS-----LSGNVLALSGGDNKVTLWKE 283 (297)
             233 iw----d--i-iw--
O Consensus
             387 (393)
T Consensus
T lerj_A
             336 FWDKKSGN---PLLMLQG--HRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKY 387 (393)
                EEETTTCC---EEEEEC--CSSCEEEEECSSCTTCTTCEEEEEEETTSEEEEEE
T ss dssp
T ss_pred
                EEECCCCc---EEEEEec--CCCCEEEEEeccCCCCCCCCEEEEEccCCCCEEeccc
                         SCOPe PROTEIN DATA BANK
No 24
                                          NCBI
                                                   Pub Med
      Guanine nucleotide-binding protein subunit beta 5; helix WRAP, RGS domain, DEP domain, DHEX domain, GGL
domain, propeller, signaling protein; 1.95A {Mus musculus} SCOP: b.69.4.0
Probab=100.00 E-value=2.1e-37 Score=263.43 Aligned_cols=252 Identities=17% Similarity=0.239 Sum_probs=0.0
                ceEecCCcCeeeEEEEcCCCCEEEEEeccCCccee-----
Q ss pred
Q Fri_Mar_04_23:
             2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKL-----
                                                                               45 (297)
O Consensus
              2 ~~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~~~~
                                                                               45 (297)
                ...+.+|...|++++|+|++++|++|++|++|++|
              57 ---1-gH---V----s-d---1-sgs-Dg-i-iWd------v----v----sp-g--1-----d----v----
T Consensus
                                                                              136 (354)
T 2pbi_B
              57 RRTLKGHGNKVLCMDWCKDKRRIVSSSQDGKVIVWDSFTTNKEHAVTMPCTWVMACAYAPSGCAIACGGLDNKCSVYPLT
                                                                              136 (354)
                EEEEECCSSCEEEEECTTSSEEEEEETTSEEEEEETTTCCEEEEEECSSSCCCEEEECTTSSEEEEESTTSEEEEEECC
T ss dssp
T ss_pred
                eeEecCCCccEEEEECCCCCEEEEEcCCCccEEEEcCCCcceeEeccCcceEEecccCceEEecccCceEEEEECc
                -----eeecccccceeeeecccccceeeeecccccccc
Q ss pred
Q Fri Mar 04 23:
              46 -----IDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPL
                                                                              115 (297)
              46 -----h---v------l-s-s-D--i-iwd------
                                                                              115 (297)
Q Consensus
                        T Consensus
             137 -----h---v----h---v-----h---v-----h---v----
                                                                              212 (354)
             137 FDKNENMAAKKKSVAMHTNYLSACSFTNS--DMOTLTASGDGTCALWDVESGO--LLOSFHGHGADVLCLDLAPSETGNT
T 2pbi B
                                                                              212 (354)
                CCTTCCSGGCEEEEECSSCEEEEECSS-SSEEEEEETTSEEEEEETTTCC-EEEEEECCSSCEEEEECCCSSCCE
T ss dssp
T ss_pred
                cccccccceEeeeccCceEEEEEccC--CCEEEEEccCCcEEEEEcccCc--EEEEEccCCCcEEEEEeccCCCCCE
Q ss_pred
                ERREECCCREREERecCCCcchhhhhhhaccceererecCCccccccccCCcccerererecCCccere
Q Fri Mar 04 23: 116 LLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAOTYV
                                                                              195 (297)
             195 (297)
O Consensus
             ..|++|+.|+.|++||++.....
T Consensus
T 2pbi_B
             213 FVSGGCDKKAMVWDMRSGO--CVOAFETHESDVNSVRYYPSG-----DAFASGSDDATCRI,YDLRADREV-
                                                                              275 (354)
                EEEEETTSCEEEEETTTCC--EEEEECCCSSCEEEEEECTTS-----SEEEEEETTSCEEEEETTTTEEE-
T ss_dssp
                T ss pred
                Q Fri Mar 04 23: 196 LESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGD 275 (297)
             196 ------h---v--las-s-Dg-i-iw-------i-----i-------la----d 275 (297)
O Consensus
                276 -----s-g---l-g-d-i-vwd------h---v---s-g-l-sgs-b 347 (354)
T Consensus
             276 AIYSKESIIFGASSVDFSLSG---RLLFAGYNDYTINVWDVLKGS---RVSILFG--HENRVSTLRVSPDGTAFCSGSWD
T 2pbi B
T ss_dssp
                EEECCTTCCSCEEEEECTTS---SEEEEEETTSCEEEEETTTCS---EEEEECC--CSSCEEEEECTTSSCEEEEETT
T ss_pred
                eEecCCcccceEEEECCCC---CEEEEEECCCcEEEEECCC--CCCceeEEEECCCCCEEEEE
Q ss_pred
               CCEEEEE
Q Fri_Mar_04_23: 276 NKVTLWK 282 (297)
O Consensus
             276 ~~i~iw~ 282 (297)
               ++ | ++ | +
             348 ~~i~i\(\vec{w}\)~ 354 (354)
T Consensus
T 2pbi_B
             348 HTLRVWA 354 (354)
T ss_dssp
                SEEEEEC
T ss pred
                CCEEEeC
```

```
PDB<sup>™</sup>
                                           Pub Med
No 25
>3fm0_A Protein CIAO1; WDR39,SGC,WD40,CIAO1, nucleus, WD repeat, biosynthetic prote structural genomics,
 structural genomics consortium; 1.70A {Homo sapiens}
Probab=100.00 E-value=7.7e-37 Score=258.92 Aligned_cols=262 Identities=26% Similarity=0.452 Sum_probs=0.0
                 eEecCCcCeeeEEEccCCcEEEEEccCCcceeEEEccCCccceeEEeccCCccCEEEEE
Q ss pred
Q Fri_Mar_04_23:
              3 VIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW
                                                                                82 (297)
               3 -----h---v-----g--1-t-s-d--v-lwd------h---v------
                                                                                82 (297)
Q Consensus
               T Consensus
                                                                               132 (345)
T 3fm0 A
                                                                               132 (345)
                 EECSSCSSCEEEEECTTSSEEEEEETTSCEEEEEECCC-EEEEEECCCSSCEEEEEECTT--SSEEEEEETTSCEEEE
T ss dssp
T ss_pred
                 EEecCCCCcEEEEEcCCCCEEEEEECCCeEEEEEcCCCCceEEEEEcCcCccEEEEE
Q ss_pred
                 ECCCC-PEREREPCCCCCCEERERECCCCCCEERERECCCCCCChbhbbbbbbbcccceeRERECCCccccc
Q Fri Mar 04 23:
               83 KEENG-RWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED 161 (297)
                                      -----l----d--i-i-----
               83 d-----v-----
O Consensus
                                                                               161 (297)
                 |++.+ ......+..|...|.+++|+|+ +.+++++.|+.+++|+......+.+|...|.+++|+|++
                                      -------h---v----
T Consensus
              133 d-----
                                                                               206 (345)
              133 EVDEEDEYECVSVLNSHTQDVKHVVWHPS--QELLASASYDDTVKLYREEEDDWVCCATLEGHESTVWSLAFDPSG----
T 3fm0 A
                                                                               206 (345)
                 T ss_dssp
                 ECCCCCcceeEEEeccCCcceEEEEECCC--CCEEEEEECCCCEEEEEECCCCcEEEEEEeccCcccEEEEEECCCC----
T ss pred
                 ccccCccceEEEEEcCcccEEEEEEcCCc-----eeEEEEEecc-CCCcEeEEEEECCCC
Q ss pred
Q Fri_Mar_04_23: 162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQ------TYVLESTLEG-HSDWVRDVAWSPTVLLRSYLASVSQDR 229 (297)
              162 -----larg-d-i-wd-----larg-d-i-wd------larg-s-pg 229 (297)
O Consensus
                       .+|++|+.|+.|++|+.....
T Consensus
              T 3fm0 A
              207 -----QRLASCSDDRTVRIWRQYLPGNEQGVACSGSDPSWKCICTLSGFHSRTIYDIAWCQLT---GALATACGDD
T ss dssp
                 -----SEEEEEETTSCEEEEEECTTCTTCCCCC---CEEEEEEECSSCSSCEEEEEECTTT---CCEEEEETTS
T ss_pred
                 -----CEEEEEeCCCEEEEEeCcCCcccceeeecCCCcceEeeEecccCCcEEEEEEcCCC---ceEEEEeCCC
Q ss_pred
                 eEEEEEccCCCcee----EEEeccccCceEEEEECC-CCCEEEEEEC
 Q Fri Mar 04_23: 230 TCIIWTQDNEQGPWK----KTLLKEEKFPDVLWRASWSL-SGNVLALSGGDNKVTLWKEN 284 (297)
              230 -j-jw----d--j-jw---d--j-jw---
              T Consensus
                                                                334 (345)
              275 AIRVFQEDPNSDPQQPTFSLTAHLHQAHSQDVNCVAWNPKEPGLLASCSDDGEVAFWKYQ 334 (345)
T 3fm0 A
                 CEEEEECTTSCTTSCCEEEEEEETTSSSSCEEEEEECSSSTTEEEEEETTSCEEEEEEC
T ss_dssp
T ss pred
                 CEEEEECCCCCcccceeeeccccccccceeEEEecCCCCCeEEEEEcC
                          SCOPe PROTEIN DATA BANK
No 26
       P40, ARP2/3 complex 41 kDa subunit, P41-ARC; beta-propeller, structural protein; 2.00A {Bos taurus} SCOP:
b.69.4.1 PDB: 1tyq C* 1u2v C* 2p9i C* 2p9k C* 2p9l C 2p9n C* 2p9p C* 2p9s C* 2p9u C* 3ukr C* 3dxm C* 3rse C* 3uku C* 3ule C* 4jd2 C*
Probab=100.00 E-value=3.9e-37 Score=262.39 Aligned cols=270 Identities=21% Similarity=0.305 Sum probs=0.0
                 Q ss pred
Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                81 (297)
Q Consensus
               2 -----h---v------l-s-s-D--i-i
                                                                                81 (297)
                 78 (372)
T Consensus
                1\ \mathtt{MAYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPD--SNRIVTCGTDRNAYV}
T 1k8k C
                                                                                78 (372)
                 -CEESCSSCCCEEECTTSSEEEECSSSEEEEEEETTEEEEEEECCSSCEEEEEETT-TTEEEEEETTSCEEE
T ss_dssp
T ss_pred
                 CCCCCCCCCerrereccCCCcerrereccCCcrrereccCCCcceeeeccCCCCcrrereccCCC---CCrrereccCCCcerre
Q ss_pred
                 EECCCCeEEEEEecccCcceEEEEEcCcccCcEEEEEECCCcc
Q Fri_Mar_04_23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGT--TSPIIIDAHAIGVNSASWAPATIE
                                                                               159 (297)
               O Consensus
                                                                               159 (297)
                 T Consensus
                                                                               154 (372)
T 1k8k C
               79 WTLKGRTWKPTLVILRINRAARCVRWAPN--EKKFAVGSGSRVISICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNS--
                                                                               154 (372)
 T ss_dssp
                 EEEETTEEEEEEECCCCSSCEEEEEECTT--SSEEEEEETTSSEEEEEEETTTTEEEEEEECTTCCSCEEEEEECTTS--
                 EECCCCccccccccCCCCCcEEEECCC--CCEEEEECCCCeEEEEECCCCccceeeeeecCCCCCEEEEEECCCC--
T ss_pred
                 cccccCCccceEEEEEeCCccEEEEEEcCCC------ceeEEEEEEccCCCcEeEEEE
0 ss pred
Q Fri_Mar_04_23:
              160 EDGEHNGTKESRKFVTGGADNLVKIWKYNSDA------QTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASV
                                                                               225 (297)
              160
                 -----h--v-1-tg--d--i--wd------las-
                                                                               225 (297)
                      T Consensus
                                                                               220 (372)
              155 -----VLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMFESSSSCGWVHGVCFSANG---SRVAWV
T 1k8k C
                                                                               220 (372)
T ss dssp
                 -----SEEEEEETTSCEEEEECCCTTTSCCCCCBTTBSCCCTTCEEEECCCCSSCEEEEEECSSS--SEEEEE
T ss_pred
                 Q ss_pred
                 eCCCeEEEEEccCCCCceeEEEecccCCCceEEEEEECCCCCEEEEEECC-CCcEEEeeeccC
Q Fri_Mar_04_23: 226 SQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENL-EGKWEPAGEVHQ 297 (297)
              Q Consensus
                                                                          297 (297)
                 T Consensus
              221 SHDSTVCLADADKKM---AVATLAS-ETLPLLAVTFTTESSLVAAG-HDCFPVLFTVDSAAGKLSFGGRLDV
 T 1k8k C
                                                                         287 (372)
T ss dssp
                 ETTTEEEEEGGGTT---EEEEEEC--SSCCEEEEEEETTEEEEE-TTSSCEEEEEETTTEEEECCCCCC
```

```
T ss_pred
                          SCOPe PROTEIN DATA BANK
                                                                  NCBI
                                                                                       Pub Med
>4bh6_A APC/C activator protein CDH1; anaphase promoting complex, ACM1, cell cycle, ubiquitination; HET: SEP;
 2.90A {Saccharomyces cerevisiae} SCOP: b.69.4.0
 Probab=100.00 E-value=2.1e-37 Score=258.63 Aligned cols=249 Identities=22% Similarity=0.339 Sum probs=0.0
                          \tt ceEecCCcCeeeEEEecCCCcEeEEEeccCCcceeEEeccCCccceeEEeccCCccCEEEEEeccCcccEEEEEccCCceEEE
 Q ss pred
                                                                                                                         81 (297)
 Q Fri Mar 04 23:
                       2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                       Q Consensus
                                                                                                                         81 (297)
 T Consensus
                                                                                                                        128 (308)
 T 4bh6 A
                       55 VVHLCDTENEYTSLSWIGAGSHLAVGQANGLVEIYDV--MKRKCIRTLSGHIDRVACLSWN----NHVLTSGSRDHRILH
                                                                                                                        128 (308)
                          EEEEEECSSCEEEEECTTSSEEEEEETTSCEEEEET--TTTEEEEEEECCCSSCEEEEEE----TTEEEEEESSSCEEE
 T ss dssp
 T ss pred
                          eEEEeccCCCceEEEECCCCCEEEEeccCCEEEEec--CCcceeeEeccCCCceEEEECC----CCEEEEEccCCCCEEE
                          {\tt EEccCCeEEEEEeccCcccEEEEEEcCCcccEEEEEEcCCccceEEEEEEccCccchhhhhhhhccceeeEEEECCCccccc}
 0 ss pred
 Q Fri_Mar_04_23:
                       82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                                                                        161 (297)
                                      Q Consensus
                       82 wd~~~~~
                                                                                                                        161 (297)
                          129 wd------h---v--v--s-----las-s-D--v-iwd------h---v--v--sp----
 T Consensus
                                                                                                                        200 (308)
                      129 RDVRMPD-PFFETIESHTQEVCGLKWNVA--DNKLASGGNDNVVHVYEGTSKS--PILTFDEHKAAVKAMAWSPHKR---
 T 4bh6 A
                                                                                                                        200 (308)
 T ss_dssp
                          EETTSSS-SCSEEECCCSSCEEEEECSS-SCEEEEETTSCEEEEETTCSS-CSEEECCCSSCEEEEECCSST---
                          EECCCCc-ccceeeccCCCEEEEEECC--CCEEEEECCCCEEEEeCCCCC--cEEEECCCcceEEEEEECCCCC--
 T ss pred
                          ccccCccceEEEEe--CCceEEEEEEcCCCceeEEEEEeccCCcEeEEEECCCCCCEEEE--EeCCCeEEEEEcc
 Q ss pred
 Q Fri Mar 04 23: 162 GEHNGTKESRKFVTGG--ADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLAS--VSQDRTCIIWTQD
                                                                                                                        237 (297)
 O Consensus
                                  -----l-tg---d--i--wd---------h----y--l--s-----las---s-Dg-i-iw-
                                                                                                                        237 (297)
                                     .++++|+ .|++|+++| ....+. +...+.++|+|++ ...++ ++.|+.|++|+.
                               ----vas---s-D--i-iWd-------v---v----s----l----g--d--i-lwd--
 T Consensus
                                                                                                                        263 (308)
                      201 -----GVI.ATGGGTADRRI.KIWNVNTS---IKMSDID-SGSOICNMVWSKNT---NELVTSHGYSKYNI.TI.WDCN
 T 4bh6 A
                                                                                                                        263 (308)
                          -----teeeeectttceeeeetttt----eeeeeee-cssceeeeecss---sceeeecttccceeecss
 T ss_dssp
 T ss pred
                           Q ss_pred
                          CCCCceeEEEecccCCceEEEEECCC
 Q Fri_Mar_04_23: 238 NEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLE 286 (297)
 Q Consensus
                      238 ----d-i-iw----
                                                                                    286 (297)
                      ... ...+.. | ... | .+++ | + | + | +++++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | ++ | + | + | ++ | ++ | ++ | ++ | + | + | + | + | + | + | + | + | + | 
                                                                                     307 (308)
                      264 SMD---PIAILKG--HSFRVLHLTLSNDGTTVVSGAGDETLRYWKLFDK 307 (308)
 T 4bh6 A
 T ss dssp
                          SCC---EEEEECC--CSSCEEEEECTTSSEEEEEETTTEEEEEECCCC
 T ss pred
                          CCc---eeEEEcC--CCCcEEEEEECCCCCEEEEEccCCC
                                        PDB<sup>IN</sup>
PROTEIN DATA BANK
 No 28
                                                     NCBI
                                                                           Pub Med
                                                                  🗎 >30w8_A WD repeat-containing protein 61; structural genomics consortium, SGC, transcriptio; 2.30A (Homo sapiens)
   Probab=100.00 E-value=4.8e-37 Score=257.75 Aligned cols=249 Identities=20% Similarity=0.384 Sum probs=0.0
                          Q ss pred
 Q Fri_Mar_04_23:
                        2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                                                         81 (297)
 Q Consensus
                        2 -----h---v-----g--l-t-s-d--v-lwd-----h---v-----h---v-----l-s-s-D--i-i
                                                                                                                         81 (297)
                          ~~~~~spd--g~~l~~~~dg~i~i
 T Consensus
                                                                                                                        148 (321)
                       73 \ \ \underline{\text{QWSLEGHQLGVVSVDISHTLPIAASSSLDAHIRLWDL--ENGKQIKSIDAGPVDAWTLAFSPD--SQYLATGTHVGKVNI}}
 T 3ow8 A
                                                                                                                        148 (321)
                          EEEECCCSSCEEEEECSSSSEEEEETTSEEEEET--TTTEEEEEEECCTTCCCCEEECTT--SSEEEEECTTSEEEE
 T ss_dssp
 T ss_pred
                          Q ss_pred
                          EECCCCeEEEEEecccCccEEEEEeCCccCcEEEEEECCCCCCEEEEEECCCCcchhhhhhhhcccceeEEEECCCcccc
 Q Fri_Mar_04_23:
                       82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                                                                        161 (297)
                       82 wd-----v---v----v----v----
 O Consensus
                                                                                                                        161 (297)
                          T Consensus
                                                                                                                        218 (321)
 T 3ow8 A
                      149 FGVESGK--KEYSLDTRGKFILSIAYSPD--GKYLASGAIDGIINIFDIATG--KLLHTLEGHAMPIRSLTFSPDS----
                                                                                                                        218 (321)
 T ss_dssp
                          EETTTCS--EEEEEECSSSCEEEEECTT--SSEEEEEETTSCEEEEETTTT--EEEEEECCCSSCCCEEECTTS----
                          EECCCCc--eeEEecCCCCeEEEEEcCC--CCEEEEEcCCC--cEEEEecCCCCeEEEEEcCCC---
 T ss_pred
 0 ss pred
                          Q Fri_Mar_04_23:
                      162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                                                                        241 (297)
                      241 (297)
                                    .+|++|+.|+.|++||++... +...+|...|.+++|+|++ .+|+++.|+.|+.|++|++...
 T Consensus
                               -----l-s--d-i-iwd------h---v---s----l-s-s-d-i-vwd-----
                                                                                                                        281 (321)
                      219 -----QLLVTASDDGYIKIYDVQHAN----LAGTLSGHASWVLNVAFCPDD---THFVSSSSDKSVKVWDVGTRT-
 T 3ow8 A
                                                                                                                        281 (321)
 T ss dssp
                          -----CEEEEECTTSCEEEEETTTCC---EEEEECCCSSCEEEEECTTS---SEEEEEETTSCEEEEETTTTE-
 T ss pred
                          -----CEEEEECCCCeEEEEECCCC----eEEEecCCCCcEEEEEECCCC---CEEEEECCCCc-
 Q ss_pred
                          CeeEEEeccCCCceEEEEECCCCCEEEEECCC
 Q Fri_Mar_04_23: 242 PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENL 285 (297)
                      242 ----d--i-iw----
 Q Consensus
                                                                              285 (297)
                            ....+.. +...|++++|+|++++.|+.|+.|++|+.+.
 T Consensus
                      282 --CVHTFFD--HQDQVWGVKYNGNGSKIVSVGDDQEIHIYDCPI 321 (321)
 т 3ow8 A
 T ss dssp
                          --EEEEECC--CSSCEEEEEECTTSSEEEEEETTCCEEEEECC-
```

```
T ss_pred
                           --ceeeecC--ccceEEEEECCCCCEEEEEcCCCEEEEE
                                         PDB<sup>™</sup>
PROTEIN DATA BANK
                                                      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=100.00 E-value=2.4e-37 Score=260.13 Aligned_cols=258 Identities=16% Similarity=0.292 Sum_probs=0.0
                           Q ss pred
 Q Fri Mar 04 23:
                        1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                             80 (297)
                        Q Consensus
                                                                                                                             80 (297)
                       T Consensus
                                                                                                                           110 (326)
 T 4jsn_D
                       34 CTRTVOHODSOVNALEVTPDRSMIAAAGYO-HIRMYDLNSNNPNPIISYDGVNKNIASVGFHED--GRWMYTGGEDCTAR
                                                                                                                           110 (326)
                           EEEEEECTTSCCCEEEECTTSSEEEEECBS-CEEEEESSSCSCCCSEEECCCCSBEEEEECTT--SSEEEEEETTSEEE
 T ss dssp
 T ss pred
                           EEEEecCCCCCEEEEECCCCCEEEecCCC-cEEEEECCCCCccceEecccCCcceeEEEEcCC--CCEEEEEcCCCEEE
                           EEEccCCeEEEEEeccCccEEEEEECCCccCcEEEEEECCCcchhhhhhhhhcccceeEEEECCCccc
 0 ss pred
 Q Fri_Mar_04_23:
                       81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                                                            160 (297)
                       81 iwd-----d--i-i----
 Q Consensus
                                                                                                                            160 (297)
                           +||++++.. ......|...|..+++|+|+ +..+++|+.|+.|++||++... ....+..+..+..+.++|+|++
                      111 iwd-----p-----l--g--dg-i-iwd------i----i
 T Consensus
                                                                                                                            182 (326)
                      111 IWDLRSRNL-QCQRIFQVNAPINCVCLHPN--QAELIVGDQSGAIHIWDLKTDH--NEQLIPEPEVSITSAHIDPDA---
 T 4jsn D
                                                                                                                           182 (326)
 T ss_dssp
                           EEETTSCCS-SCSEEEECSSCEEEEECTT-SSEEEEEETTSCEEEEETTTCC-EEEECSSTTSCEEEEECTTS---
                           EEECCCCce-eEEEeeccCCcEEEEEEcCC--CCEEEEEcCCCceEEEEECCCC--eeEeccCCCcceEEEEECCCC---
 T ss pred
                           ccccCCccceEEEEeCCceEEEEEcCCC----ceeEEEEEeccCCcEeEEEECCCCCCEEEEEE
 Q ss pred
 Q Fri Mar 04 23: 161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDA----QTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQ
                                                                                                                           236 (297)
 O Consensus
                      236 (297)
                                T Consensus
                                                                                                                           249 (326)
                      183 -----SYMAAVNSTGNCYVWNLTGGIGDEVTQLIPKTKIPAHTRYALQCRFSPDS---TLLATCSADQTCKIWRT
 T 4jsn_D
                                                                                                                           249 (326)
                           -----seeeeettsceeeeecccggscceeeeeecccssceeeeectts---seeeeeettteeeeet
 T ss dssp
 T ss pred
                            Q ss_pred
                           ccccceeEEEecc---ccccceEEEEEcccccEEEEE
 Q Fri_Mar_04_23: 237 DNEQGPWKKTLLKE---EKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
 Q Consensus
                      237 ----d-i-iw-
                                                                                      282 (297)
                      250 SNFSLMTELSIKSGNPGESSRGWMWGCAFSGDSQYIVTASSDNLARLWC 298 (326)
 T 4jsn D
 T ss dssp
                           TTCCEEEEECCCSSTTSCCCCCEEEEECTTSSEEEEETTSEEEEE
 T ss pred
                           CCCceeeeeeccCCCCcccceEEEEECCCCCEEEEE
                                         SCOPe POB®
 No 30
                                                                    NCBI
                                                                                           Pub Med
>3frx A Guanine nucleotide-binding protein subunit beta- like protein; RACK1, WD40, beta propeller, ribosome,
 translation, acetylation; 2.13A {Saccharomyces cerevisiae} SCOP: b.69.4.0 PDB: 1vwv h 1vxv s 1vxy s 1vw9 h 3izb
  302z T 3030 T 3u5c g 3u5g g 4byl 6 4byt 6 4ujp h 4uer R 4uji G* 4ujf h 4ujn G* 4ujk h 4ujs G*
 Probab=100.00 E-value=8.7e-37 Score=255.84 Aligned_cols=247 Identities=19% Similarity=0.308 Sum_probs=0.0
                           ceEecCCcCeeeEEEccC-CCCEEEEEecCCCc=--cceeEEeccCCCCEEEEEccCCC
 Q ss pred
 Q Fri_Mar_04_23:
                         2 VVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGET---HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDG
                                                                                                                             77 (297)
                               77 (297)
                       T Consensus
                                                                                                                             87 (319)
                       10 RGTLEGHNGWVTSLATSAGQPNLLLSASRDKTLISWKLTGDDQKFGVPVRSFKGHSHIVQDCTLTAD--GAYALSASWDK
 T 3frx A
                                                                                                                             87 (319)
                           T ss dssp
                           EEEEcccceeEeEecCCCccEEEEEcCCCeEEEEEccCCcccCCCceEecCCCcceEeEEECCC--CCEEEEEECCC
 T ss pred
                           eEEEEEccCCeEEEEEecccCccEEEEEecCccCcEEEEEECCCC
 Q ss pred
 Q Fri_Mar_04_23:
                       78 KVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPAT
                                                                                                                            157 (297)
                       78 ~i~iwd~~
                                                                 ----d--i-i---
                                                                                                                            157 (297)
 Q Consensus
                           +|++||+++++ .+..+..|...|.+++|+|+ +...++++..|+.|++|++... ....+..+..|...+..+++|.|..
                        88 ~v~iwd~~~~-_~~h~~~v~~~~~1~s~s~d~~i~vwd~~~~~-
 T Consensus
                                                                                                                            160 (319)
                        88 TLRLWDVATGE--TYQRFVGHKSDVMSVDIDKK--ASMIISGSRDKTIKVWTIKGQ---CLATLLGHNDWVSQVRVVPNE 160 (319)
 T 3frx_A
                           EEEEEETTTTE--EEEEEECCSSCEEEEECTT--SCEEEEETTSCEEEETTSC---EEEEECCCSSCEEEEECCC-
 T ss_dssp
                           eEEEEECCCc--eeeEecCCCceEEEEEcCC--CCEEEEEECCCc---cEEEEEecCCceeeEEEecCC
 T ss pred
 Q ss pred
                           cccccccCccce-----EEEEEeCCceEEEEEEcCCCceeEEEEEeccCCccEeEEEECCCCCCCEEEEEE
 Q Fri_Mar_04_23: 158 IEEDGEHNGTKESR-----KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTC
                                                                                                                           231 (297)
                      231 (297)
 O Consensus
                                         . .++++.|+.|++|++.....+.+|....++|++...++|++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|+++...+|++...+|++...+|++...+|+++...+|++...+|++...+|++...+|++...+|++...+|++...+|++...+|++...+|+++...+|++...+|++...+|++...+|++...+|++...+|++...+|++...+|++...+|++...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|
 T Consensus
                      161 -----KADDDSVTIISAGNDKMVKAWNLNQF----QIEADFIGHNSNINTLTASPDG---TLIASAGKDGEI ------CCEEEEEETTSCEEEEETTTT---EEEEEECCCCSCEEEEEECTTS---SEEEEEETTCEE
 T 3frx A
 T ss_dssp
 T ss_pred
                           -----CCCCCCCEEEEEeCCCc---eeeEEecCCCceEEEEECCCC---CEEEEEeCCCEE
 Q ss pred
                           EEEEccCCCceeEEEeccccCceEEEEECccccEEEEEcccccCceEEEEEC
 Q Fri_Mar_04_23: 232 IIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
                      232 ~iw~~~~~~d~i-iw~~ 284 (297) ++||+... +...+.+++|+|++..+++++++++...
 O Consensus
```

```
221 ~iwd~~~~-i~v~~~sp~~~la~~~~-i~v~~~ 266 (319)
T Consensus
T 3frx A
              221 MIWNI AAKK----AMYTLSAODEVFSLAFSPNRYWLAAATATG-IKVFSLD 266 (319)
T ss dssp
                 EEEETTTTE----EEEEEECCSCEEEEEECSSSSEEEEETTE-EEEEEET
                 EEEECCCCh----hheeecCCCCEEEEEECCCCceEEeecc
T ss pred
                           PDB™
PROTEIN DATA BANK
No 31
                                   NCBI Pub Med
>41g9 A F-box-like/WD repeat-containing protein TBL1XR1; structural genomics consortium, SGC, WD40 repeats,
 unknown F; 2.28A {Homo sapiens}
 Probab=100.00 E-value=1.1e-36 Score=263.28 Aligned_cols=241 Identities=25% Similarity=0.460 Sum_probs=0.0
                 CCcCeeeEEEcCCCCEEEEEcCCCcceeEEeccCCccceeEEeccCCccCEEEEEcCCCccCEEEEEccCCccCeEEEEccCCccc
0 ss pred
Q Fri Mar 04 23:
              7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEEN
                                                                                86 (297)
O Consensus
               7 ~h~~~v~~~~~~g~~l~t~s~d~~v~lwd~~~~~~h~~~v~~~~~~~l~s~s~D~~i~iwd~~~
                                                                                86 (297)
                 T Consensus
T 41q9 A
                 CSSCCEEEEECTTSSEEEEEETTSEEEEEET--TSCEEEEEEECSSCEEEEEECSS--SSEEEEETTSCEEEEETTT
T ss dssp
                 CCCCCEEEEECCCCCEEEEECCC---CCCEEEEECCC---CCCEEEEECCC--CCEEEEECCC
T ss pred
Q ss_pred
                 Cerere.....EecccCccrerereccccere
              87 GRWSQIA-----VHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSV
Q Fri_Mar_04_23:
                                                                               127 (297)
Q Consensus
               87 ~~~~~
                                                               ----l----d--i-i
                                                                               127 (297)
                                             .+..|...|.+++|+|+ +..+|++++.|+.|++
T Consensus
                      261 (400)
              184 GEAKQQFPFHSAPALDVDWQSNNTFASCSTDMCIHVCKLGQDRPIKTFQGHTNEVNAIKWDPT--GNLLASCSDDMTLKI
T 41q9 A
T ss dssp
                 TEEEEEECCCSSCEEEEEESSSSEEEEEETTSCEEEEETTCSSCSEEECCCSSCEEEEECTT--SSEEEEEETTSEEEE
                 CcceeccCCCcceEEEecCCCeEEEECCCcceEEEECCCccceeecCCccEEEEEECCC--CCEEEEEECCCcEEE
T ss pred
Q ss_pred
                 EEecCCCcchhhhhhhhccceeEEEECCCcccccccCCcce-----EEEEEECCCceEEEEE
Q Fri_Mar_04_23: 128 VEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESR------KFVTGGADNLVKIWKYNSDAQTYVLES
                                                                               198 (297)
              198 (297)
O Consensus
              T Consensus
                                                                               322 (400)
              262 WSMKQDN--CVHDLQAHNKEIYTIKWSPTG------PGTNNPNANLMLASASFDSTVRLWDVDRG----ICIH 322 (400)
T 41g9_A
T ss_dssp
                 EETTCSS--CSEEEECCSSCEEEEECSCS-----TTSSSTTSCCCEEEEETTTSCEEEEETTTT---EEEE
                 EECCCCc--eeeehhhCCCcEEEEEECCCC----cEeE
T ss pred
                 EcccCCceeEEEECCCCCCCEEEEEecCCCeeEEEEccCCCCceeEEEEcccCCCceEEEEECCCCCEE
Q ss pred
 Q Fri_Mar_04_23: 199 TLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKV
              O Consensus
T Consensus
T 41a9 A
                 EECCCCSCEEEEECTTS---SEEEEEETTSEEEEEETTTCC-----EEEEEECSSCEEEEEECTTSSEEEEEETTSCE
T ss dssp
T ss_pred
                 EECCCCceEEEEECCCC---CEEEEEECCCCcEEEEECCCCc-----eEEEECCCCCEEEEEEECCCCEEEEEECCCCC
Q ss pred
                 EEEE
Q Fri Mar 04 23: 279 TLWK 282 (297)
             279 ~iw~
                     282 (297)
 Q Consensus
T Consensus
              394 ~vwd 397 (400)
T 41g9 A
              394 CVLD 397 (400)
T ss dssp
                 EEEE
T ss_pred
                         PDE NCBI Pub Med
No 32
>41g9_A F-box-like/WD repeat-containing protein TBL1XR1; structural genomics consortium, SGC, WD40 repeats,
 unknown F; 2.28A {Homo sapiens}
Probab=100.00 E-value=6.5e-37 Score=264.62 Aligned_cols=249 Identities=24% Similarity=0.413 Sum_probs=0.0
                 Q ss pred
Q Fri Mar 04 23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTL-----TGHEGPVWRVDWAHPKFGTI
                                                                                69 (297)
               Q Consensus
                                                                                69 (297)
                 T Consensus
               125 (400)
               48 AVVLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNSE--GTL EEEECCCSSCEEEEEECSSSSEEEEETTSEEEEEECCC-----CEEEEECC------CCSSCCEEEEEECTT--SSE
T 41g9_A
                                                                               125 (400)
T ss dssp
T ss pred
                 eEEEEcccCCEEEEECCCCCEEEEEcCCCcCCcceeeEeeecccccccCccceeEEEECCC--CCE
Q ss_pred
                 EEEECCCC+EEEEEccCC+EEEEEecccCccEEEEEECCCcCCCEEEEEECCCCEEEEE
Q Fri Mar 04 23:
              70 LASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGT------
                                                                               135 (297)
               70 l~s~s~D~i~iwd~~~~~~v~~~~v~~~~l~~~~d~i~i~~~~~~
O Consensus
                                                                               135 (297)
              T Consensus
                                                                               200 (400)
T 41g9 A
              126 LATGSYDGFARIWTKDGN---LASTLGOHKGPIFALKWNKK--GNFILSAGVDKTTIIWDAHTGEAKOOFPFHSAPALDV
                                                                               200 (400)
T ss_dssp
                 EEEEETTSEEEEETTSC---EEEEEECSSCEEEEECSS--SSEEEEETTSCEEEEETTTTEEEEECCCSSCEEEE
                 EEEEECCCeEEEEcCCCc---EEEEeccCCccEEEEEECCC--CCEEEEEeCCCeEEEEeCCCccceeccCCCCCCEEE
T ss pred
 Q ss_pred -----chhhhhhhcccceeEEEEECCCccccccCCccceEEEEEECCC Q Fri_Mar_04_23: 136 ------TSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSD 190 (297)
O Consensus
              136 -----l-tg-d-i-wd---
                                                                               190 (297)
```

```
....+.+|...|.+++|+|++
                                                                  .+|++|+.|+.|++||++..
               T Consensus
                                                                                   267 (400)
               201 DWOSNNTFASCSTDMCIHVCKLGODRPIKTFOGHTNEVNAIKWDPTG-----NLLASCSDDMTLKIWSMKOD
T 41q9 A
                                                                                   267 (400)
                  EESSSSEEEEETTSCEEEEETTCSSCSEEECCCSSCEEEEECTTS-----SEEEEEETTSEEEEEETTCS
T ss dssp
 T ss_pred
                  CGeeFFFFFECCCCCCCEEFFFFCCCCCCCCC-----FFFFFECCCCEFFFFFCCCCCCCGeeFFFFECCCCCCCEFFFFF
Q ss pred
Q Fri Mar 04 23: 191 AQTYVLESTLEGHSDWVRDVAWSPTVLLRS-----YLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRAS
                                                                                   261 (297)
               191 ~~~~~h~~v~~l~~s~~~~~las~s~Dg~i~iw~~~~~~~i~
Q Consensus
                                                                                   261 (297)
               T Consensus
                                                                                   335 (400)
T 41q9 A
                                                                                   335 (400)
                  S----CSEEEECCSSCEEEEECSCS---TTSSSTTSCCCEEEEETTSCEEEEETTTTE---EEEEECC--CCSCEEEEE
T ss dssp
T ss pred
                  c---eeeehhhCCCcEEEEEECCC---CCCCCCcceEEEEECCCCc--EeEEEcc--CCceEEEEE
Q ss pred
                  ECCCCEEEEEcCCCCEEEEE
Q Fri Mar 04 23: 262 WSLSGNVLALSGGDNKVTLWK 282 (297)
               262 ~~~~~l~~~~d~~i~iw~ 282 (297)
Q Consensus
                  |+|+|++++.|+.|+|+
T Consensus
               336 ~spdg~~l~s~s~dg~v~iwd 356 (400)
               336 FSPDGRYLASGSFDKCVHIWN
T 41g9 A
                                   356 (400)
T ss_dssp
                  ECTTSSEEEEEETTSEEEEEE
T ss_pred
                  ECCCCCEEEEecCCccEEEe
                                     PDB<sup>™</sup>
PROTEIN DATA BANK
                                              NCBI
                          SCOPe
                                                             Pub Med
>lerj_A Transcriptional repressor TUP1; beta-propeller, transcription inhibitor; 2.30A {Saccharomyces cerevisiae}
SCOP: b.69.4.1 PDB: 5afu _3*
Probab=100.00 E-value=1.2e-36 Score=262.38 Aligned_cols=246 Identities=22% Similarity=0.369 Sum_probs=0.0
                  ceEecCCcCeeeEEEEcCCCCEEEEEecCCcceeEEeccCCccceeEEeccCCcc
Q Fri Mar 04 23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGP-----VWRVDWAH
                                                                                    63 (297)
                Q Consensus
                                                                                    63 (297)
                  -----h---V--v-fspdg--la-g-----v----g-----l--
T Consensus
                                                                            ~~v~~sp
                                                                                   133 (393)
T lerj A
                57 LHKSLDHTSVVCCVKFSNDGEYLATGC-NKTTQVYRV--SDGSLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFSP
                                                                                   133 (393)
T ss_dssp
                  EEEEEECSSCCCEEECTTSSEEEEC-BSCEEEET--TTCCEEEEECC------CCCCBEEEEECT
T ss_pred
                  eEEecCCCCeEEEEECCCCCEEEEEc-CCceEEEEC--CCCcEEEEECcccccCccccccCCCcceEEEEECCC
                  \verb| CccCCEEEEEccCCeEEEEEcccCceEEEEEeccCccEEEEEEeccCccEEEEEEeccCcchhhhhhhh
Q ss_pred
Q Fri_Mar_04_23:
                64 PKFGTILASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA
                                                                                   143 (297)
                64 -----l-s-s-D--i-iwd-------v-----v-----l----d--i-i------
O Consensus
                                                                                   143 (297)
               T Consensus
                                                                                   204 (393)
               134 D-GKFLATGAEDRLIRIWDIENRK-IVMILQGHEQDIYSLDYFPS-GDKLVSGSGDRTVRIWDLRTG--QCSLTLS
T lerj A
                                                                                   204 (393)
                  {\tt T--SSEEEEETTSCEEEEETTTE--EEEEECCCSSCEEEEECTT--SSEEEEEETTSEEEEEETTT---EEEEEEE
T ss_dssp
                  C--CCEEEEECCCCeEEEEECCCC--EEEEecCCCCCEEEEEEcCC--CCEEEEEECCCC---eEEEEE
T ss pred
                  Q ss pred
Q Fri_Mar_04_23:
               144 \hspace{0.1cm} \textbf{HAIGVNSASWAP-ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE-----GHSDWVRDVAWSPT} \\
                                                                                   215 (297)
                           --~~~~~~~~h~~v~l~tg~d~~i~~wd~~~~~~~~~~~h~~~v~l~~s~~
 Q Consensus
                                                                                   215 (297)
                  +...+..++|+| ++
                                      .+|++|+.|+.|++||.+.+.
                                                          +...+. +|...|.+++|+|+
                            ----l-sg--d--i-iwd------h---v----s-d
T Consensus
               205 ~~~v~~~~
                                                                                   267 (393)
               205 IEDGVTTVAVSPGDG-----KYIAAGSLDRAVRVWDSETGF---LVERLDSENESGTGHKDSVYSVVFTRD
T lerj A
                                                                                   267 (393)
 T ss dssp
                  CSSCEEEEECSTTC-----CCESEEEETTSCEEEEETTTCC---EEEEEC-----CCCSSCEEEEEECTT
                  T ss_pred
                  CCCCCEEEEEecCCCeEEEEEccCC------CCceeEEEecccCCCeEEEEE
Q ss pred
Q FTI MAT 04 23: 216 VLLRSYLASVSQDRTCIIWTQDNE-----QGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                  ~~~~las~s~Dg~i~iw~~~~~d~~i~iw~
                                                                                282 (297)
O Consensus
               216
               T Consensus
               268 G---QSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIG---HKDFVLSVATTQNDEYILSGSKDRGVLFWD 338 (393)
T lerj A
                  S---SEEEEETTSEEEEEC-----CEEEEEC---CSSCEEEEECGGGCEEEEETTSEEEEE
T ss dssp
                  C---CEEEEEeCCCeEEEEECCCCcccccCCCCCeeEEEEec---cCCcEEEEEECCCCCEEEEEE
T ss pred
                            PDB"
                                              Pub Med
No 34
>4wju_A Ribosome assembly protein 4; ribosome biogenesis ribosome assembly, biosynthetic protein; 2.80A
 {Saccharomyces cerevisiae} PDB: 3j65 _q 4wjv _A*
Probab=100.00 E-value=1.8e-37 Score=276.57 Aligned_cols=250 Identities=22% Similarity=0.442 Sum_probs=0.0
Q ss_pred
                  CceEccCcceeEEEccCcceEEEEccCcceEEEEccCccceeEEccCcccEEEEEccCcccEEEEEccCcceE
O Fri Mar 04 23:
                1 MVVIANAHNELIHDAVLDYYGKR-LATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                    79 (297)
O Consensus
                1 -----h---v-----g---l-t-s-d--v-lwd-----h---v----h---v------l-s-s-D--i
                                                                                    79 (297)
               T Consensus
                                                                                   210 (515)
               135 SSSAIAGHGSTILCSAFAPHTSSRMVTGAGDNTARIWDC--DTQTPMHTLKGHYNWVLCVSWSPD--GEVIATGSMDNTI
T 4wju A
                                                                                   210 (515)
                  ECCCBCCCSSCEEEEECSSCSSEEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEECTT--SSCEEEETTSCE
T ss dssp
                  eeeeecCCccEEEEEccCCcceEEEEecCCceEEEEEc--CCccEeEEEcCCCccEEEEECCC--CCEEEEECCCCeE
T ss_pred
Q ss pred
                  EEEEccCCeEEEE_EEecccCccEEEEEEcCC-----ccCCcEEEEEECCCCEEEEEEecCCCcchhhhhhhaccceeeEE
Q Fri_Mar_04_23: 80 LIWKEENGRWSQI-AVHAVHSASVNSVQWAP-----HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSA 151 (297)
```

```
Q Consensus
 T Consensus
                           211 RLWDPKSGQ--CLGDALRGHSKWITSLSWEPIHLVKPGS--KPRLASSSKDGTIKIWDTVSR--VCQYTMSGHTNSVSCV
 T 4wju A
                                                                                                                                                       284 (515)
                                 EEECTTTCC--BCSSCBCCCSSCEEEEECCGGGSCTTS--CCCEEEEETTSCEEEEETTTT--EEEEECCCCSSCEEEE
 T ss dssp
                                 EEEECCCC--CcceecCCCceEEEEEcccccCCCC--CcEEEEEECCCC--eEEEEecCCCCEEEE
 T ss pred
                                 EECCCcccccccCCcceEEEEEeCCc-----
 Q ss pred
 Q Fri_Mar_04_23: 152 SWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSD-----
                                                                                                                                                       190 (297)
 Q Consensus
                                                         ----l-tg--d--i--wd--
                                                                                                                                                      190 (297)
                           T Consensus
                                                                                                                                                ~~~ 350 (515)
                           285 KWGGQG-----LLYSGSHDRTVRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHTGKKPSTPE 350 (515)
 T 4wju A
 T ss_dssp
                                 EECTTS-----EEEEEETTSCEEEEEGGGTTEEEEECCCSSCEEEEEESSHHHHHHTTCCTTCCCCSSHH
 T ss_pred
                                 EECCCc-----eEEEEeCCCeEEEEECCCCceeeEeccCCceeEEEEecCCCcccCChH
 Q ss_pred
                                 -----CceeEEEEEccCCCccEeEEEeccCCcceEEEE
 232 (297)
 Q Consensus
                           191 -----las-s-Dg-i-
                                                                                                                                                       232 (297)
                                 T Consensus
                                                                                                                                                       427 (515)
                           351 EAQKKALENYEKICKKNGNSEEMMVTASDDYTMFLWNPLKSTKPIARMTGHQKLVNHVAFSPDG---RYIVSASFDNSIK
 T 4wju_A
                                                                                                                                                       427 (515)
                                 HHHHHHHHHHHHBSSSSBCCCEEEEETTSCEEEECTTTCSSCSEEECCCSSCEEEEECTTS---SEEEEEETTSCEE
 T ss_dssp
                                 HHHHHhhhhhhhheeccCCCCceEEEEEcCCCeEEEecccCCCeEEEEEcCCcCCEEEEEECCCC---CEEEEEeCCCeEE
 T ss pred
 Q ss_pred
                                EEEccCCCceeEEEecccCCceEEEEECCCCCEEEEE
 Q Fri_Mar_04_23: 233 IWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
 O Consensus
                           233 iw----d--i-iw-
                                                                                                           282 (297)
                           T Consensus
                           428 LWDGRDGK---FISTFRG--HVASVYQVAWSSDCRLLVSCSKDTTLKVWD 472 (515)
 T 4wju_A
 T ss_dssp
                                 EEETTTCC---EEEEECC--CSSCEEEEEECTTSSEEEEEETTSEEEEE
                                 EEECCCCc---EEEEEcC--CcCcEEEEECCCCCEEEEE
 T ss_pred
 No 35
                                                 PDB NCBI Pub Med
🗌 >4wjs_A RSA4; ribosome assembly, ribosome biogenesis, biosynthetic protein; 1.80A {Chaetomium thermophilum}
 Probab=100.00 E-value=1.3e-36 Score=269.07 Aligned_cols=250 Identities=27% Similarity=0.427 Sum_probs=0.0
 Q ss pred
                                 ceEecCCcCeeeEEEecCCCCEEEEEecCCCcceeEEeccCCCCCEEEEEccCC
 Q Fri_Mar_04_23:
                             2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAH----PKFGTILASCSYDG
                                                                                                                                                        77 (297)
 O Consensus
                             2 -----h---v------q--1-t-s-d--v-lwd------h---v------1-s-s-D-
                                                                                                                                                        77 (297)
                                T Consensus
                                                                                                                                                      228 (485)
                           150 KFTLKGHTGWVLGVSWSPDGKYLATCSMDTTVRVWDPESGK-QVNQEFRGHAKWVLALAWQPYHLWRDGTARLASASKDC
 T 4wjs_A
                                                                                                                                                       228 (485)
                                 EEEECCCSSCEEEEECTTSSCEEEEETTSCEEEEETTTTE-ECSSCBCCCSSCEEEEEECCGGGCBTTBCEEEEEETTS
 T ss_dssp
                                 ceEeCCCCCCEEEEEECCCCCEEEEEECCCceEEEEECCCc-cccccCCCccEEEEEecccCCCCCCEEEEEeCCC
 T ss pred
                                 eEEEEEccCCeEEEEEeccCccEEEEEEcCccCcEEEEEecC------
 Q ss pred
 Q Fri_Mar_04_23:
                           78 KVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKE-----
                            Q Consensus
                                                                                                                                                       132 (297)
                           + | + | | | +++++ ....+.. | .... | .++... | ++ | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++... | ++...
 T Consensus
                                                                                                                                                       303 (485)
 T 4wjs_A
                           229 TVRIWLVNTGR--TEHVLSGHKGSVSCVKWGG---TDLIYTGSHDRSVRVWDAVKGTLVHNFTAHGHWVNHIALSSDHVL 303 (485)
 T ss dssp
                                 CEEEEETTTTE--EEEEECCCSSCEEEEEECT---TSEEEEEETTSCEEEEETTTTEEEEEECCCSSCEEEEETTHHHH
                                 CEEEEECCCC--eeEeccCCCceEEEEECC---CCeEEEECCCCeEEEEECCCCeEEeEECCCCeE
 T ss_pred
 Q ss pred
                                 -----CCcchhhhhhhcccceeEEEECCC
 O Fri Mar 04 23: 133 -----NGTTSPIIIDAHAIGVNSASWAPA
                                                                                                                                                      156 (297)
 O Consensus
                                                                                                                                                       156 (297)
 T Consensus
                                                   -----l-s-s-d-i--wd------h---v--y--spd 383 (485)
                           304 RTAYHDHTKEVPGTEEERRAKAKERFEKAAKIKGKVAERLVSASDDFTMYLWDPTNNGSKPVARLLGHQNKVNHVQFSPD 383 (485)
 T 4wjs A
                                 HTTTCCTTCCCCSSHHHHHHHHHHHHHHHHHEETTEECCCEEEEETTSCEEEECHHHHTTSCSEEECCCSSCEEEEEECTT
 T ss dssp
                                 EEEecCCccccCchhhhHHHHhhhhhhhhhccCCcccEEEEEeCCCEEEEEecCCCCCccceEecCCCCCEEEEEECCC
 T ss_pred
 Q ss_pred
                                 Q Fri_Mar_04_23: 157 TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQ
                                                                                                                                                       236 (297)
                           157 ~
                                          Q Consensus
                                                                                                                                                       236 (297)
                                           .+|++|+.|+.|++||...++ ++..+.+|..+|.++|+|++ ++|++++.|++|++
                                                -----spd-----las-s-d--i-lwd------l--h---v----spd-----l-s-s-D--i-vwd-
                                                                                                                                                       443 (485)
                           384 G-----TLIASAGWDNSTKLWNARDGK----FIKNLRGHVAPVYQCAWSADS---RLVVTGSKDCTLKVWNV
 T 4wjs A
                                                                                                                                                       443 (485)
 T ss_dssp
                                 S-----SEEEEETTSCEEEEETTTCC---EEEEECCCSSCEEEEECTTS--SEEEEEETTSCEEEEET
 T ss_pred
                                 C-----CEEEEEcCCCcEEEEECCCC---EEEEEcCCCC---CEEEEEcCCCeEEEEEC
                                 ccccceeeeeecccccceeeeeeccccceeeee
 Q ss_pred
 Q Fri_Mar_04_23: 237 DNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
                                                                                                      282 (297)
 Q Consensus
                           237 ----d-i-iw-
                                                                                                      282 (297)
                           +... +... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | 
 T Consensus
                                                                                                      484 (485)
 T 4wjs_A
                           444 RTGK---LAMDLPG--HEDEVYAVDWAADGELVASGGKDKAVRTWR
                                                                                                      484 (485)
 T ss_dssp
                                 TTTE---EEEEECC--CSSCEEEEEECTTSSEEEEEETTCCEEEEE
 T ss pred
                                 CCCc---EeEecCC--CCccEEEEEcCCCCEEEECCCCCEEeCC
```

```
PDB<sup>N</sup>
No 36
                                               Pub Med
🗆 >4a11_B DNA excision repair protein ERCC-8; DNA binding protein, DNA damage repair; HET: DNA; 3.31A {Homo
 sapiens}
Probab=100.00 E-value=2.5e-36 Score=261.60 Aligned_cols=258 Identities=19% Similarity=0.279 Sum_probs=0.0
                 Q ss pred
Q Fri_Mar_04_23:
               1 MVVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGETHKLIDTLT-----GHEGPVWRVDWAHPKFGT
                                                                              68 (297)
               68 (297)
                   .++.+|...|++++|+| +|++|++|+.|++|+|||+.....
              T Consensus
                                                             ~~~h~~~V~~v~~~p~~-~~
                                                                             113 (408)
              35 DRDVERIHGGGINTLDIEPVEGRYMLSGGSDGVIVLYDLENSSRQSYYTCKAVCSIGRDHPDVHRYSVETVQWYPHD-TG
T 4a11 B
                                                                             113 (408)
                 T ss dssp
T ss_pred
                 EEEEEcCCCeEEEEEccCCeEEEEEeccCccEEEEEeCC---ccCCcEEEEEECCCEEEEEEccCCcchhhhhhhhcc
Q ss_pred
O Fri Mar 04 23:
              69 ILASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAP---HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHA
                                                                             145 (297)
               145 (297)
 Q Consensus
                +|++++.|++|++||+++|| + +......+..+|
T Consensus
              186 (408)
              114 MFTSSSFDKTLKVWDTNTI.---OTADVFNFEETVYSHHMSPVSTK--HCLVAVGTRGPKVOLCDLKSGS--CSHTLOGHR
T 4a11 B
                                                                             186 (408)
                 CEEEEETTSEEEEEETTTT---EEEEEEECSSCEEEEECSSCSS--CCEEEEEESSSSEEEEESSSSC--CCEEECCCC
T ss dssp
                 EEEEECCCCeEEEeECCCC---eEEEEEeccCceeeEEeccCCCC--CcEEEEECCCCcEEEEECCCCc--ccEEEECCCC
T ss pred
Q ss_pred
                 CCPPEREECCCCCCCCCCCCCCCCPEREERECCCCCPPEREERECCCCCPPEREE.....ECCCCCCEPEREE
Q Fri Mar 04 23: 146 IGVNSASWAPATIEEDGEHNGTKESR-KFVTGGADNLVKIWKYNSDAQTYVLES-----TLEGHSDWVRDVAW
                                                                             212 (297)
              146 ~~v~~~
                         212 (297)
O Consensus
                 ..|.+++|+|++
                                   . + | ++ | +. | +. | ++ | | ++.......
              187 ~~v~~v~~sp~~--
                                   ----lasgs-D--v-iWd------
                                                                 ----h---V--1-f
T 4all B
              187 OEILAVSWSPRY------DYILATASADSRVKLWDVRRASGCLITLDOHNGKKSOAVESANTAHNGKVNGLCF
                                                                             253 (408)
T ss_dssp
                 SCEEEEECSSC-----TTEEEEEETTSCEEEEETTCSSCCSEECCTTTTCSCCCTTTSSCSCSCEEEEE
                 T ss pred
Q ss pred
                 CCCCCCCEEEEeccCceeeeeecccc------
 Q Fri_Mar_04_23: 213 SPTVLLRSYLASVSQDRTCIIWTQDNEQ------GPWKKTLL
                                                                             248 (297)
Q Consensus
              213 s----las-s-Dg-i-iw------
                                                                             248 (297)
                 +|++ .+|+++.|++|++||+....
              254 spdg---~l~s~s~D~~v~lWd~~~~
                                                                     ---g--
T Consensus
                                                                          ~1
              {\tt 254~TSDG---LHLLTVGTDNRMRLWNSSNGENTLVNYGKVCNNSKKGLKFTVSCGCSSEFVFVPYGSTIAVYTVYSGEQITML}
T 4a11 B
                                                                             330 (408)
T ss_dssp
                 CTTS---SEEEEEETTSCEEEEETTTCCBCCCCCCCCCCCCCCCCSSCCCEECCSSSCEEEEEETTEEEEEETTTCCEEEEE
T ss_pred
                 cccCCceEEEEECCCCCEEEEECC
Q ss pred
              249 KEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
Q Fri Mar 04 23:
              249 ----i---i-----l----d--i-iw---
O Consensus
                                            284 (297)
                 .. |...|++++|+|+|+++++.|++|+||+..
              331 ~g--h---V--v-fspdg--l-s-s-D--i-lW---
T Consensus
                                            364 (408)
              331 KG--HYKTVDCCVFQSNFQELYSGSRDCNILAWVPS 364 (408)
T 4all B
 T ss_dssp
                 CC--CSSCEEEEEETTTTEEEEEETTSCEEEEEC
                 hc--ccCcceEEEEcCCCCEEEEecCCC
T ss_pred
                          PDB"
                                  NCBI
No 37
                                                Pub Med
>41g8_A PRE-mRNA-processing factor 19; structural genomics consortium, SGC, WD40 repeat, DNA bindin; 1.89A {Homo
 sapiens}
Probab=100.00 E-value=2.7e-36 Score=256.67 Aligned cols=247 Identities=18% Similarity=0.246 Sum probs=0.0
                 CeEecCCcCeeeEEEEcCCCCEEEEEecCCcceeEEeccCCccceeEEeccCCccCEEEEEecCCccCEEEEE
Q ss_pred
Q Fri Mar 04 23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                              81 (297)
               2 ~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~h~~~v~~~~~~l~s~s~b~~i~i
O Consensus
                                                                              81 (297)
                 T Consensus
                                                                             182 (354)
T 41q8 A
              107 LATLKGHTKKVTSVVFHPSQDLVFSASPDATIRIWSV--PNASCVQVVRAHESAVTGLSLHAT--GDYLLSSSDDQYWAF
                                                                             182 (354)
 T ss_dssp
                 EEEECCCSSCCCEEECTTSSEEEEECTTSCEEEET--TTTEEEEEECCCSSCEEEEEECTT--SSEEEEEETTSEEEE
                 EEEEcCCCCEEEEEccCCCEEEEecCCCcEEEeeC--CCCeeeEEEecCCC--CCEEEEE
T ss_pred
0 ss pred
                 {\tt EEccCCeEEEEEeccCcccEEEEEEcCCcccEEEEEEcCCccceEEEEEEccCccchhhhhhhhccceeeEEEECCCccccc}
Q Fri_Mar_04_23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                             161 (297)
               82
                 161 (297)
                 T Consensus
                 254 (354)
              183 SDIOTGRVLTKVTDETSGCSLTCAOFHPD--GLIFGTGTMDSOIKIWDLKER--TNVANFPGHSGPITSIAFSENG---
T 41g8 A
                                                                             254 (354)
T ss_dssp
                 EETTTCCEEEEECTTTCCCEEEEEECTT--SEEEEEETTSCEEEEETTTT--EEEEEECCCCSCEEEEEECTTS----
T ss pred
                 EECCCCcEEEEecCCCCcceEEEEECCC--CCEEEEECCCC--ceEEEECCCCC--ceEEEECCCC----
Q ss_pred
                 Q Fri_Mar_04_23:
              162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE-GHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ
                                                                             240 (297)
                       Q Consensus
              162
                                                                             240 (297)
                       .+|++|+.|+.|++||++..
                                       T Consensus
                     ----1~s~s~d~~v~lwd~~~~
                                                ----v---s--g-----i----d----v
              255 -----YYLATAADDSSVKIWDLRKI.---KNFKTLOLDNNFEVKSLIFDOSG--TYLALGGTD--VOLYICKOWT
T 41g8_A
                                                                             316 (354)
T ss dssp
                 -----SEEEEEETTSEEEEEETTTT----EEEEEEECCTTCCEEEEEECTTS---SEEEEEESS-EEEEETTTTE
```

```
T ss_pred
                  -----CEEEEEeCCCEEEEEECCCC---ceeEEEecCCCCeEEEEECCCC---CEEEEECCC-eEEEEcCCCce
                  CceeEEEeccCCCceEEEEE
0 ss pred
 Q Fri_Mar_04_23: 241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE
                                                     283 (297)
               241 ----d--i-iw--
                                                     283 (297)
                   ....+.. |...|.+++|+|++++|++++.||+|++|+
               T Consensus
               317 ---EILHFTE--HSGLTTGVAFGHHAKFIASTGMDRSLKFYSL
T 41q8 A
                                                     354 (354)
                  ---EEEEECC--SSSCEEEEEECGGGSCEEEEETTSCEEEEEC
T ss_dssp
                  ---EEEEEeC--CCccEEEEECCCCCEEEEECCCcEEEecC
T ss_pred
                            PDB"
No 38
                                    NCBI
                                                   Pub Med
                                             >4psw B Histone acetyltransferase type B subunit 2; HAT WD40, histone acetyltransferase, accoa, phosphorylation,
 cytoplasmatic, transferase; HET: TPO COA; 2.10A {Saccharomyces cerevisiae} PDB: 4psx _B*
Probab=100.00 E-value=1.1e-36 Score=263.33 Aligned_cols=249 Identities=18% Similarity=0.252 Sum_probs=0.0
                  ceEecCCcCeeeEEEEcCC-CCEEEEEecCCccEEEEEccCCccceeEEeccCCcCCEEEEEecCCccCe
0 ss pred
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYY-GKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGT-ILASCSYDGKV
                                                                                   79 (297)
                2 \  \  \, \sim \sim \sim \sim h \sim \sim v \sim \sim \sim -g \sim 1 - t - s - d \sim v - 1 w d \sim \sim \sim \sim \sim h \sim \sim v \sim \sim \sim \sim \sim -1 - s - s - D \sim i 
 Q Consensus
                                                                                   79 (297)
               T Consensus
                                                                                  185 (401)
               111 ITAKYEHEEEITRARYMPODPNIVATINGOGTTFLYSRS---EGLOSTLKFHKDNGYALSFSTL--VKGRLLSGSDDHTV
T 4psw B
                                                                                  185 (401)
 T ss dssp
                  EEEEEESSCEEEEEETTEEEEEEETTSCEEEEETT---TEEEEEECCCSCCCEEEECSS--STTEEEEECTTSCE
                  EEEEeCCCCcEEEEECCCCCCEEEEECC---CCCceECCCCCEEEEECC--CCCeEEECCCCEE
 T ss pred
                  EEEEccCC----eEEEEEEecc-cCccEEEEEECC-ccCCcEEEEEECCCcchhhhhhhhcccceeEEE
Q ss pred
O Fri Mar 04 23:
               80 LIWKEENG----RWSQIAVHAV-HSASVNSVQWAP-HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASW
                                                                                  153 (297)
O Consensus
               80 ~iwd~~~~v~~~v~~~
                                                ----l----d--i-i---
                                                                                  153 (297)
                  T Consensus
               259 (401)
               186 ALWEYGSGGDPTK--PVRTWNDLHSDIINDNKWHNFN--KDLFGTVSEDSLLKINDVRANNTTIDT--VKCPOPENTLAF
T 4psw_B
                                                                                  259 (401)
                  EEEECSSSSCCSS--CSEEESSSCSSCEEEEEECSSC--TTEEEEEETTSBEEEEETTCSSCEEEE--EECSSCEEEEE
T ss_dssp
T ss pred
                  EEEECCCCCccc--cceEecCCCCCeEeEEEECCC--CCEEEEEECCCcEEEE--eccCCCccEEE
Q ss_pred
                  CCCcccccccCCccce=EEEEeCCceEEEEEECCCCceeEEEEEecCCCCCEEEEEECCCCCCCEEEEEECCCCEEE
Q Fri_Mar_04_23: 154 APATIEEDGEHNGTKESRK-FVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCI
                                                                                  232 (297)
Q Consensus
               154 ------l-tq--d--i--wd------h---v--l--s-----las-s-Dq-i-
                                                                                  232 (297)
                             260 ~
                                                                                  321 (401)
               260 SHHS-----SNLLAAAGMDSYVYLYDLRNMKE---PLHHMSGHEDAVNNLEFSTHV--DGVVVSSGSDNRLM
T 4psw B
                                                                                  321 (401)
T ss dssp
                  CSSC-----SSEEEEEETTSCEEEEETTCTTS---CSEEECCCSSCEEEEEECSSS--TTEEEEEETTSCEE
T ss pred
                  EEEccC-----CCCceeEEEecccCCceEEEEECCCCC-EEEEEECCCCCEEEEEEC
Q ss_pred
Q Fri_Mar_04_23: 233 IWTQDN------EQGPWKKTLLKEEKFPDVLWRASWSLSGN-VLALSGGDNKVTLWKEN
                                                                        284 (297)
               233 jw----d--i-jw---
 Q Consensus
                                                                        284 (297)
                  +||+.. ....+.. |...|.+++|+|+++ +|++++.||.|++|+..
               322 jwd------
                                         ----h---v---
                                                       ----l-s-s-dg-v-iw--
T Consensus
                                                                        383 (401)
               322 MWDLKQIGAEQTPDDAEDGVPE---LIMVHAG--HRSSVNDFDLNPQIPWLVASAEEENILQVWKCS
T 4psw_B
                                                                        383 (401)
                  EEEGGGTTCCCCHHHHTTCCTT---EEEEECC--CSSCEEEEEECSSSTTEEEEEETTSEEEEEEEC
T ss_dssp
                  EEECCCCcccCCcccCCCcc--eEEEeCC--cCCCceEEEECCCCCEEEEEECCC
T ss pred
                            PDB" S NCBI
No 39
                                             Pub Med
🗌 >3jam_g RACK1; eukaryotic translation initiation, small ribosome subun 43S, translation; 3.46A {Kluyveromyces
lactis PDB: 3j81 g 3j80 g
Probab=100.00 E-value=3.9e-36 Score=252.56 Aligned cols=247 Identities=21% Similarity=0.301 Sum probs=0.0
Q ss_pred
                  ceEecCCcCeeeEEEccC-CCCEEEEEecCCCc---cceeEEeccCCcCEEEEEecCCCCCEEEEEEcCCC
                2 VVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGET---HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDG
                                                                                   77 (297)
Q Fri Mar 04 23:
O Consensus
                77 (297)
                 T Consensus
                   --l--h---v-----s-d--g--l-sgs-D--i-i\----------h---v----s-d--g--l-s-s-D-
                                                                                   88 (326)
T 3jam_g
               11 RGTLEGHNGWVTSLSTSAAQPNLLVSGSRDKTLISWRLTENEQQFGVPVRSYKGHSHIVQDVVVSAD--GNYAVSASWDK
                                                                                   88 (326)
                  EEEECCCSSCCCEEECCSSCSSEEEEECTTSCEEEEEECCSSSCSEEEEEEECCCSSCEEEEEECSS--SSEEEEEETTS
T ss_dssp
                  EEEecccCcceEEEEccCCCcEEEEecCcCccceehhhhccCccceEEEEccCc--CCEEEEEcCCC
T ss_pred
Q ss_pred
                  Q Fri Mar 04 23:
               78 KVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPAT
                                                                                  157 (297)
O Consensus
               157 (297)
                 89 ~v~iwd~~~~~h~~~v~~~~~~l~s~s~d~i~iwd~~~~~~~v~~~~v~~~
T Consensus
                                                                                  161 (326)
T 3jam_g
               89 TLRLWNLATGN--SEARFVGHTGDVLSVAIDAN--SSKIISASRDKTIRVWNTVGD---CAYVLLGHTDWVTKVRVAPKN
                                                                                  161 (326)
 T ss dssp
                  CEEEEETTTE--EEEEECCCSSCEEEEEECTT--SCEEEEEETTSCEEEEESSSC---EEEEECCCSSCEEEEEECCCC
T ss_pred
                  CEEEEECCCC--cceEEeccCCcEEEEECCC--CCEEEEECCCC---eeEEeeccCccEEEEEecCCc
Q ss pred
                  cccccccCccce-----EEEEEeCCceEEEEEEcCCcceeEEEEEeccCCccEEEEEeC
Q Fri_Mar_04_23: 158 IEEDGEHNGTKESR-----KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQ
                                                                                  227 (297)
               158
                      -----l-tg--d--i--wd-------h---v--l--s-----las-s-
                                                                                  227 (297)
Q Consensus
               T Consensus
                                                                                  223 (326)
T 3jam_g
               162 -----LEDGEVDDGRITFVSAGMDKIVRSWSLNEDSYR--IEADFIGHNNYINVVOPSPDG---SLAASAGK 223 (326)
```

```
T ss_dssp
                  -----CCCSCEEEEEESSSEEEEEEC-CCS-EEEEEECCSSCEEEEECSSS--SEEEEET
T ss_pred
                  -----cccceecCCceEEEEecCCCcEEEEecCCCcc--ceeeecCCCcceEEEECCCC---CEEEEecC
                  CCeEEEEccCCCceeEEEecccCCceEEEEE
Q ss_pred
 Q Fri_Mar_04_23: 228 DRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
               228 Dg-i-iw-----d--i-iw-
|+.|++||++... ++...++++|+|++.+++++ .++.|++|+
 O Consensus
                                                               282 (297)
               224 dg~i~vwd~~~~~i~iwd 271 (326)
T Consensus
               224 DGQIYVWNLKHKS----AFMNFDAKDEVFALAFSPSRFWLTAA-TASGIKIYD
T 3jam q
                                                               271 (326)
                  TSEEEEETTTTB-----CCCEEECSSCCCEEEECSSSEEEEE-CSSSEEEEE
 T ss_dssp
                  CCEEEEECCCCc-----EEEEeecCCCEEEEEcCCccEEEE
T ss pred
                           PDB STOCK PROTEIN DATA BANK PROTEIN DATA BANK PROTEIN DATA BANK
No 40
        GIB2, G protein beta subunit GIB2; signaling protein, scaffold protein, ribosome binding; 2.20A
{Cryptococcus neoformans var} PDB: 4aow A 5flx g 4d61 g 4d51 g 4kzx g 4kzz g 4kzy g 5a2q g Probab=100.00 E-value=6e-36 Score=250.08 Aligned_cols=249 Identities=21% Similarity=0.289 Sum_probs=0.0
                  ceEecCCcCeeeEEEccC-CCCEEEEEecCCCc=--cceeEEeccCCcCEEEEEccCCC
Q ss pred
Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGET---HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDG
                                                                                    77 (297)
                O Consensus
                                                                                    77 (297)
T Consensus
                                                                                    85 (314)
T 4d6v A
                8 KGNLAGHNGWVTAIATSSENPDMILTASRDKTVIAWQLTREDNLYGFPKKILHGHNHFVSDVAISSD--GQFALSSSWDH
                                                                                    85 (314)
 T ss_dssp
                  EEEECCCSSCEEEEECCSSCTTEEEEEETTSCEEEEEECCCSSCEEEEEECCTT--SSEEEEEETTS
                  T ss_pred
0 ss pred
                  eEEEEEccCCeEEEEEecccCccEEEEEEcCCccCcEEEEEECCCcchhhhhhhhcccceeEEEECCCc
Q Fri_Mar_04_23:
               78 KVLIWKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPAT
                                                                                   157 (297)
                T Consensus
                160 (314)
                86 TLRLWDLNTGL--TTKKFVGHTGDVLSVSFSAD--NRQIVSASRDRSIKLWNTLGE-CKFDIVEDGHTEWVSCVRFSPNP
T 4d6v A
                                                                                   160 (314)
T ss dssp
                  CEEEEETTTE--EEEEECCCSSCEEEEEECTT-SSCEEEEETTSCEEEECTTSC-EEEEECTTCCSSCEEEEECCCS
                  eEEEEECCCc--eeEEEEcCCCCEEEEEECCC--CCEEEEEeCCC-ceEeeeecCCcCcEEEEECCCCC
 T ss pred
Q ss_pred
                  Q Fri Mar 04 23: 158 IEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQD
                                                                                   237 (297)
               158 -----l-tg--d--i--wd-------h--v--l--s----las-s-Dg-i-iw---
....++++.|+.|++||++.....++||...++||++ ...++++.||...++||+...|
Q Consensus
                                                                                   237 (297)
               161 -----l-s-~-d--i--wd------v----v---s--g----i-s---dg-v-iwd--
T Consensus
                                                                                   222 (314)
               161 -----ALPVITSAGWDKTVKVWELSNC----KLKTTHHGHTGYLNTLAVSPDG---SLAASGGKDGITMLWDLN
T 4d6v A
                                                                                   222 (314)
                  -----SSCEEEEETTSCEEEEETTTT---EEEEEECCCSSCEEEEECTTS---SEEEEEESSSEEEEEESS
T ss dssp
                  -----ceeeeeeecccceeeeeccccceeeeecccc
T ss_pred
Q ss_pred
                 CCCCceeEEEecccCCceEEEEECCCCCEEEEE
Q Fri_Mar_04_23: 238 NEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Consensus
               238 ----d-i-iw-
                                                       282 (297)
                  ... .+.....+.++|+|++.+|+++ .++.|++|+
               223 ----i-iwd 260 (314)
T Consensus
               223 EGK-----HLYSLDAGDVINALVFSPNRYWLCAA-TASSIKIFD
T 4d6v A
                                                       260 (314)
T ss_dssp
                  SSS----EEEEEECSSCEEEEEECSSSSEEEEE-ESSCEEEEE
T ss_pred
                  CCc----EEEEecCCCeEEEEecCCceEEEEE
                    SCOPe PODE NCBI
                                                            Pub Med
>4ggc_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; HET:
MRD; 1.35A {Homo sapiens} SCOP: b.69.4.0 PDB: 4n14 A*
Probab=100.00 E-value=7.1e-36 Score=250.36 Aligned_cols=247 Identities=25% Similarity=0.394 Sum_probs=0.0
                  \tt ceEecCCcCeeeEEEecCCCcEeEEEeccCCcceeEEeccCCcceeEEeccCCcCCEEEEEeccCccCEEEEE
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                    81 (297)
                2 ~~~~~h~~~v~~~~~~g~~l~t~s~d~~v~lwd~~~~~~h~~~v~~~~~~l~s~s~b~~i~i
Q Consensus
                                                                                    81 (297)
                T Consensus
                                                                  ------------d---i--
                60 LLQMEQPGEYISSVAWIKEGNYLAVGTSSAEVQLWDV--QQQKRLRNMTSHSARVGSLSWN----SYILSSGSRSGHIHH
T 4ggc A
                                                                                   133 (318)
T ss_dssp
                  EEECCSTTCCEEEEECTTSSEEEEEETTSEEEEET--TTTEEEEEEECCSSCEEEEEE----TTEEEEEETTSEEEE
                  eeeecCCccEEEEECCCCCEEEEEcC-CCcceeeeccccCcEEEEecc----CCEEEEEcCCCCEEE
T ss_pred
Q ss_pred
                  EECCCCeEEEEEecccCccEEEEEECCCcCCeEEEEEECCCC--cchhhhhhhhcccceeEEEECCCcc
Q Fri_Mar_04_23:
               82 WKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENG--TTSPIIIDAHAIGVNSASWAPATIE 159 (297)
O Consensus
                159 (297)
               T Consensus
                                                                                   209 (318)
               134 HDVRVAE-HHVATLSGHSQEVCGLRWAPD--GRHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQS-
T 4ggc A
                                                                                   209 (318)
T ss dssp
                  EETTSSS-CEEEEECCSSCEEEEECTT--SSEEEEEETTSCEEEEESSCBTTBSCCSEEECCCSCEEEEECTTST-
T ss_pred
                  Eecccc-cceeeecCCCCEeEEEECCC--CCEEEEEeCCCeEEEecCCCccccceeeecCCCceEEEEEccCCC-
                  \verb|cccccCCccceEEEEe--CCceEEEEEccCCcceeEEEEEccCCcceeEEEEeccCCcceEEEEe--CCCeEEEEE|
Q ss pred
Q Fri_Mar_04_23:
               160 EDGEHNGTKESRKFVTGG--ADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS--QDRTCIIWT 235 (297)
               Q Consensus
T Consensus
```

```
210 -----NVLATGGGTSDRHIRIWNVCSGA----CLSAVDAHSQ-VCSILWSPHY---KELISGHGFAQNQLVIWK 270 (318)
  T 4ggc A
  T ss_dssp
                                            -----TEREFERECTTTCEREREFTTTCC----ERREFECSSC-FERERETTT---TEREFERECTTTCCRFFER
  T ss_pred
                                            -----CEEEEeccCCCCcEEEEECCCCc---EeEEeccCCc-eeEEEECCCC---CeEEEEE
                                           \verb|cccccceeEEEecccccceeEEEEEccccceeEEEE| \\
  Q ss_pred
  Q Fri_Mar_04_23: 236 QDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
  Q Consensus
                                    236 ----d--j-iw-
                                                                                                                                        282 (297)
                                           +.... |...|.+++|+|+|+++++.|++|+|+
                                           312 (318)
  T Consensus
                                    271 YPTMA---KVAELKG--HTSRVLSLTMSPDGATVASAAADETLRLWR
  T 4ggc_A
                                                                                                                                      312 (318)
                                            TTTCC---EEEEECC--CSSCEEEEECTTSSCEEEEETTTEEEEEC
  T ss_dssp
  T ss_pred
                                           CccCc---eeEEEec--cccceEEEEECCCCCeEEEecCCccEEEEE
  No 42
                                                                   PDB"
                                                                                        NCBI
                                                                                                                            Pub Med
🗌 >41g8_A PRE-mRNA-processing factor 19; structural genomics consortium, SGC, WD40 repeat, DNA bindin; 1.89A {Homo
  sapiens}
  Probab=100.00 E-value=5.3e-36 Score=254.85 Aligned cols=241 Identities=22% Similarity=0.333 Sum probs=0.0
                                           CcCe---eeEEEEcC-CCCEEEEEEcCCCcEEEEEEccCCcceeEEeccCCccCEEEEEEccCCceEEEEE
  Q Fri_Mar_04_23:
                                       8 HNEL---IHDAVLDY-YGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWK
                                                                                                                                                                                                         83 (297)
                                                                                                                                                                                                         83 (297)
  Q Consensus
                                       8 h-----v-----g--l-t-s-d--v-lwd-----h---v-----l-s-s-D--i-iwd
                                                        T Consensus
                                                                                                                                                                                                       142 (354)
  T 41g8_A
                                      67 HSASIPGILALDLCPSDTNKILTGGADKNVVVVFDK--SSEQILATLKGHTKKVTSVVFHPS--QDLVFSASPDATIRIWS
                                                                                                                                                                                                       142 (354)
                                           SCSSSCCEEEEETTEEEEEEEETTSCEEEET--TTTEEEEEECCCSSCCCEEEECTT--SSEEEEECTTSCEEEEE
  T ss dssp
  T ss_pred
                                           CCCCCCCERRERACCCCCCRERRERCCCCCERREREC--CCCARRERECCCCCCRERRERCCCC--CCRERRECCCCCCRERA
  Q ss pred
                                           ccCceEEEEEecccCccEEEEEeCCccCcEEEEEECCCCEEEEEEEcCCCcchhhhhhhhcccceeEEEECCCccccc
  Q Fri Mar 04 23:
                                      84 EENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGE
                                                                                                                                                                                                       163 (297)
  O Consensus
                                      84 -----v----v
                                                                                                                                                                                                       163 (297)
                                    212 (354)
  T Consensus
  T 41q8 A
                                    143 VPNAS--CVQVVRAHESAVTGLSLHAT--GDYLLSSSDDQYWAFSDIQTGRVLTKVTDETSGCSLTCAQFHPDG-----
                                                                                                                                                                                                       212 (354)
                                            TTTTE--EEEEECCCSSCEEEEECTT--SSEEEEEETTSEEEEEETTTCCEEEEEECTTTCCCEEEEECTTS-----
  T ss_dssp
  T ss_pred
                                            CCCCe--eeEEEecCCCCEEEEEEcCC--CCEEEEEECCCCEEEEEECCCCCCEEEEEECCCC-----
  Q ss pred
                                           ccCccceEEEEecCcceEEEEEccCCcceEEEEEEccCCccEEEEEEccCCccc
  Q Fri_Mar_04_23:
                                    164 HNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPW 243 (297)
                                    243 (297)
                                                         .++++|+.|+.|++||++..
                                                                                                      .+...+.|...|.+++|+|++ .+|+++.|+.|++|++.|
  T Consensus
                                    213 -----1~g~dg~i~iwd~~~-----h~~v~v~v~s~~----l~s~s~d~~v~lwd~~~--
                                                                                                                                                                                                       275 (354)
                                    213 -----LIFGTGTMDSOIKIWDLKER----TNVANFPGHSGPITSIAFSENG---YYLATAADDSSVKLWDLRKLK---
  T 41a8 A
                                                                                                                                                                                                       275 (354)
  T ss_dssp
                                          -----SEEEEEETTSCEEEEETTTT---EEEEEECCCCSCEEEEEECTTS---SEEEEEETTTEEEE
  T ss_pred
                                            -----CEEEEEcCCCeEEEEECCCC---ceEEEECCCcceEEEEECCCC---CEEEEEeCCCCeEEEEECCCC---
                                           eeeecccccceeeeeeccccceeee
  Q ss_pred
  Q Fri_Mar_04_23: 244 KKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                                    244 ~~~~i~~~i~~~~i~~~~l~~~~d~~i~iw~ 282 (297)
  Q Consensus
                                             .....+..+.++|+|+|+++++.| ++|+
                                    276 ----v---v---s--g--1----d----v
  T Consensus
                                                                                                                         311 (354)
                                    276 -NFKTLQLDNNFEVKSLIFDQSGTYLALGGTD--VQIYI
  T 41g8_A
                                                                                                                         311 (354)
  T ss_dssp
                                           -EEREEECCTTCCEEEEEECTTSSEEEEEESS--EEREE
                                            -eeEEEecCCCCeEEEEECCCCCEEEEEecC--eEEEE
  T ss pred
                                                                                                                              Pub Med
>5ams_A SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}
  Probab=100.00 E-value=5.6e-36 Score=261.09 Aligned_cols=254 Identities=16% Similarity=0.197 Sum_probs=0.0
                                           Q Fri_Mar_04_23:
                                       1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                                                                                                         80 (297)
  Q Consensus
                                       1 -----h---v-------l-s-s-b--i-
                                                                                                                                                                                                         80 (297)
                                            T Consensus
                                      57 \quad \text{$\sim\sim\sim\sim\sim-h} \\ \sim \text{$v\sim\sim\sim\sim-h} \\ \sim \text{$v\sim\sim\sim-s} \\ \sim -\text{$g\sim\sim1$} \\ \sim \text{$s\sim\sim-dg\sim\text{$i\sim$}} \\ \sim \text{$i\sim>-dg\sim\text{$i\sim$}} \\ \sim \text{$i\sim$} \\ \sim \text{$i\sim>-dg\sim\text{$i\sim$}} \\ \sim \text{$i\sim>-dg\sim
                                      57 \ \text{SLTYFD} \\ \textbf{KHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSHSQPPK} \\ \textbf{FAGTLTGYGESVISCSFTSE} - - \textbf{GGFLVTADMSGKVL} \\ \textbf{SLTYFDKHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSHSQPPKFAGTLTGYGESVISCSFTSE} \\ \textbf{SLTYFDKHTDSVFAIGHTGYGNLAHLWTSHSQPPKFAGTLTGYGGSVISCSFTSE} \\ \textbf{SLTYFDKHTDSVFAIGHTGYGNLAHLWTSHSQPPKFAGTLTGYGGSVISCSFTSE} \\ \textbf{SLTYFDKHTGYGNLAHLWTSHSMAGTLTGYGGSVISCSFTSE} \\ \textbf{SLTYFDKHTGYGNLAHLWTSHSMAGTLTGYGGSVISCSFTSE} \\ \textbf{SLTYFDKHTGYGNLAHLWTSHSMAGTLTGYGNLAHLWTSHSMAGTLTGYGGSVISCSFTSE \\ \textbf{SLTYFDKHTGYGNLAHLWTSHSMAGTLTGYGNLAHLWTSHSMAGTLTGYGNLAHLWTSH \\ \textbf{SLTYFUL MAGTLTGYGNLAHLWTSHMAGTLTGYGNLAHLWTSH \\ \textbf{SLTYFUL MAGTLTGYGNLAHLWTSHMAGTLTGYGNLAHLWTSH \\ \textbf{SLTYFUL MAGTLTGYGNLAHLWTSHMAGTLTGYGNLAHLWTSH \\ \textbf{SLTYFUL MAGTLTGYGNLAHLWTSH \\ \textbf{SLTYFUL M
  T 5ams A
                                                                                                                                                                                                       134 (431)
  T ss_dssp
                                           CSEEECCCSSCCCCEEECSSSSEEECCTTSCEEEEESSSSSCCEEEEECCCSSCEEEEECTT--SSEEEEETTSCEE
  T ss_pred
                                           Q ss pred
                                           EEEccCCe-EEEEEecccCccEEEEEEcCccCcEEEEEEcCCcchhhhhhhh--cccceeEEEEc---
  Q Fri_Mar_04_23:
                                     81 IWKEENGR-WSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA--HAIGVNSASWA--- 154 (297)
  O Consensus
                                      81 iwd-----v----v------154 (297)
                                    T Consensus
                                                                                                                                                                                                       213 (431)
  T 5ams A
                                    135 VHMGQKGGAQWKLASQMQEVEEIVWLKTHPTI-ARTFAFGATDGSVWCYQINEQDGSLEQLMSGFVHQQDCSMGEFINTD
  T ss dssp
                                           EEEEEGGGTEEEEEECCSSCEEEEEECSSS-TTEEEEEETTCCEEEEEEECCTTTCCEEEEEEECCSSCEEEEEESCS
  T ss_pred
                                           EEECCCCceeEEEeeccCcCcEEEEEecCCC-CCEEEEEecCCceEEEEeeccCCcceEEEEEeccCCCceEEEEEeccc
                                           --CCcccccccCCccceEEEEEcCcceEEEEEccCcceeEEEEec-----cCCCcEeEEEECC------CCCCCCE
  Q ss pred
  Q Fri_Mar_04_23:
                                    155 --PATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE----GHSDWVRDVAWSP-----TVLLRSY 221 (297)
                                    Q Consensus
                                                                                                                                                                                                     221 (297)
                                                                                                                                                 +|...|.+++|+|
                                               ++
                                                                              .+|++|+.|+.|++||++.+.
  T Consensus
                                    214 ~
                                                   -----l~s~~~dg~i~~wd~~~~~
                                                                                                                                                       ---i----p
                                                                                                                                                                                                       273 (431)
```

```
T 5ams A
               214 KGENT-----LELVTCSLDSTIVAWNCFTGQ---QLFKITQAEIKGLEAPWISLSLAPETLTKGNS--GV 273 (431)
T ss dssp
                  SCSSC-----CEEEEEETTSCEEEEETTTCC---EEEEECGGGTTTCCCCEEEEEEECTTTTTTSCT---TE
T ss_pred
                  EEEEeCCCeEEEEEccC-CCCceeEEEec------cccCCceEEEEECCCCCEEEEE
Q ss pred
 Q Fri_Mar_04_23: 222 LASVSQDRTCIIWTQDN-EQGPWKKTLLK------EEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Consensus
               222 las~s~Dg~i~iw~~~~d~i~iw~
                                                                              282 (297)
               T Consensus
               274 VACGSNNGLLAVINCNNGGA---ILHLSTVIELKPEQDE--LDASIESISWSSKFSLMAIGLVCGEILLYD
T 5ams A
                                                                             339 (431)
                  EEEEETTSEEEEEGGGTSE---EEEEEESCCCCSSSCG--GGGCEEEEEETTTTEEEEEETTSEEEEEE
T ss_dssp
T ss_pred
                   EEEECCCCeEEEEECCCCc---EEEEEeeeecccccc--cCCcEEEEEEcCCCCEEEEE
No 44
                                     PDB"
PROTEIN DATA BANK
                                               NCBI
                           SCOPe
                                                               Pub Med
->4gga_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; 2.04A
{Homo sapiens} SCOP: b.69.4.0 PDB: 4ggd _A
Probab=100.00 E-value=1e-35 Score=258.74 Aliqned cols=247 Identities=24% Similarity=0.386 Sum probs=0.0
                  Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                      81 (297)
                                                                                      81 (297)
Q Consensus
                 2 -----h---v-----g--l-t-s-d--v-lwd-----h---v----h---v-----l-s-s-D--i-i
                  +.+|++++.|+.|++
               140 -----l-sgs-dg-i-iwd-------h-v-v-l----l-sgs-dg-i-i
T Consensus
                                                                                      213 (420)
 T 4gga_A
               140 LLQMEQPGEYISSVAWIKEGNYLAVGTSSAEVQLWDV--QQQKRLRNMTSHSARVGSLSWN----SYILSSGSRSGHIHH
                                                                                      213 (420)
T ss dssp
                  EEECCSTTCCEEEEECTTSSEEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEE----TTEEEEEETTSEEEE
T ss_pred
                  ERECCCCCCERRERECCCCCCRERERECCCCCCREREREC--CCCRERERECCCCCCRERERECC----CCRERERECCCCCCRERE
Q ss pred
                  EECCCCeEEEEEecccCcceEEEEEcCcccCcEEEEEECCCC--cchhhhhhhhccceeEEEECCCcc
Q Fri Mar 04 23:
                82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENG--TTSPIIIDAHAIGVNSASWAPATIE
                                                                                     159 (297)
O Consensus
                159 (297)
               T Consensus
                                                                                      289 (420)
               214 HDVRVAE-HHVATLSGHSQEVCGLRWAPD--GRHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQS-
T 4qqa A
                                                                                      289 (420)
                   EETTSSS-CEEEEECCSSCEEEEECTT--SSEEEEEETTSCEEEEESSCCSSCSCSEEECCCSSCEEEECTTCT-
 T ss_dssp
T ss_pred
                   EECCCCC-ccEEEEcCCCccEEEEEECCC--CCEEEEEECCCCeEEEEECCCCccceEEEEeCCCCcc
                  cccccCCccceEEEEe--CCceEEEEEcCCCceeEEEEEeccCCcceEEEEEcCCCCCCEEEEEe--CCCeEEEE
Q ss pred
Q Fri_Mar_04_23:
               160 EDGEHNGTKESRKFVTGG--ADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS--QDRTCIIWT
                                                                                      235 (297)
               160 -----l-tg----d--i--wd------h---v--l--s-----las-s---Dg-i-iw-
                           ++++|+ .|+.|++|+... .|..+..|..|..|++|+|++ .|+|+++.
               290 ------v--lasg-gs-d--i-iwd------v--l--s-----l----g--d--i-iwd
T Consensus
                                                                                      350 (420)
               290 -----NVLATGGGTSDRHIRIWNVCSG---ACLSAVDAHS-QVCSILWSPHY---KELISGHGFAQNQLVIWK
T 4gga A
                                                                                      350 (420)
T ss_dssp
                  -------TEEEEEECTTTCEEEEEETTTT---EEEEEEECSS-CEEEEEEETTT---TEEEEEECTTTCCEEEEE
T ss_pred
                   -----CEEEEeCCCCCEEEEEECCCC---CEeEEecCCC-ceEEEEECCCC---CEEEEEeccCCCeEEEEE
                  ccCCCceeEEEecccCCceEEEEECCCCCEEEEE
Q ss_pred
Q Fri_Mar_04_23: 236 QDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
               236 ----d-i-iw- 282 (297)
Q Consensus
                  +.... |...|.+++|+|+|+++++|++++|++
               351 \quad \text{-----spdg--l-s-s-D---} v-i \mathbb{W}-
T Consensus
                                                          392 (420)
               351 YPTMA---KVAELKG--HTSRVLSLTMSPDGATVASAAADETLRLWR 392 (420)
T 4gga A
                  TTTCC---EEEEECC--CSSCEEEEECTTSSCEEEEETTTEEEEEC
T ss_dssp
                  CCCcC---EEEEEcC--cCccEEEEECCCCCEEEEE
T ss pred
                                               Pub Med
No 45
□ >3ei3_B DNA damage-binding protein 2; UV-damage, DDB, nucleotide excision repair, xeroderma pigmentosum,
cytoplasm, DNA repair; HET: DNA PG4; 2.30A {Danio rerio} PDB: 3ei1 B* 3ei2 B* 4a08 B* 4a09 B* 4a0a B* 4a0b B*
Probab=100.00 E-value=1e-35 Score=255.55 Aligned_cols=258 Identities=14% Similarity=0.162 Sum_probs=0.0
                  ceEecCCcCeeeEEEccCC-CEEEEEecCCcceeEEEccCCccceeEEeccCCccEEEEEccCCceE
Q ss pred
Q Fri Mar 04 23:
                 2 VVIANAHNELIHDAVLDYYG-KRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAH-PKFGTILASCSYDGKV
                                                                                      79 (297)
                     ----h---v------g---l-t-s-d--v-lwd-------h---v------l-s-s-D--i
                                                                                      79 (297)
Q Consensus
                T Consensus
                                                                                      143 (383)
                66 HRTASPFDRRVTSLEWHPTHPTTVAVGSKGGDIILWDYDVQNKTSFIQGMGPGDAITGMKFNQFN--TNQLFVSSIRGAT
                                                                                      143 (383)
T 3ei3 B
T ss dssp
                  EEEECCCSSCEEEEECSSCTTEEEEEEBTSCEEEEETTSTTCEEEECCCSTTCBEEEEEETTE--EEEEEEETTTEE
T ss pred
                   eeccCCCCCEEEEEcCCCCCEEEEEeCCCCEEEEEECCCccceeEecCCCCCEEEEEeCCCC--CCEEEEEeCCCeE
Q ss_pred
                  EEEEccCCeEEEEEecccCccEEEEEeCCccCcEEEEEECCCCEEEEEEecCCCcchhhhhhhhcccceeEEEECCCccc
Q Fri Mar 04 23:
                80 LIWKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIE 159 (297)
                O Consensus
                                                                                      159 (297)
               T Consensus
                                                                                      216 (383)
               144 TLRDFSGSVIQVFAKTDSWDYWYCCVDVSVS--RQMLATGDSTGRLLLLGLDGH---EIFKEKLHKAKVTHAEFNPRC--
T 3ei3 B
                                                                                     216 (383)
T ss_dssp
                  EEEETTSCEEEEECCCCSSCCEEEEEETT--TTEEEEEETTSEEEEETTSC---EEEEECSSSCEEEEECSSC--
T ss pred
                   EEEECCCceEEEecCCCccceeEEEECCC--CCEEEEEeCCCceEEEEecCCc---eeEEeeccCCceEEEEECCCC--
 Q ss pred
                  \verb|cccccCCcce+EEEEeCCceeEEEEEcccCCceeEEEEEcccCCceeEEEEEcc||
 Q Fri_mar_04_23: 160 EDGEHNGTKESR-KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSP-TVLLRSYLASVSQDRTCIIWTQD 237 (297)
 O Consensus
               160
                  ------h---v--l-tg--d--i--wd-------h---v--l--s-----las-s-Dg-i-iw---
                                                                                     237 (297)
```

```
. ++++|+.|+.|++||++...+....+ +|...|.+++|+| ++ ..+|++++.|+.|++||++
              217 -----s---l-s---d--i-iwd--------v----sp--g----l-s---d--i-vwd--
T Consensus
                                                                                281 (383)
              217 -----DWLMATSSVDATVKLWDLRNIKDKNSYIAEM-PHEKPVNAAYFNPTDS--TKLLTTDORNEIRVYSSY
T 3ei3 B
                                                                               281 (383)
                 -----TTEEEEEETTSEEEEEEGGGCCSTTCEEEEE-ECSSCEEEEEECTTTS---CEEEEEEESSSEEEEEETT
T ss dssp
 T ss_pred
                 -----CCEEEEECCCCEEEEecCCCCCCCEEECCCCCCCCEEEEECCCCCC---CEEEEECCCCCEEEEECC
                 CCCCceeEE------EeggcCCceEEEEEEC
Q ss pred
Q Fri Mar 04 23: 238 NEQGPWKKT------LLKEEKFPDVLWRASWS
                                                                               263 (297)
              238
Q Consensus
                                                                     ~~~~i~~
                                                                                263 (297)
                        T Consensus
              282
              282 DWSKPDOTTTHPHROFOHTTPIKATWHPMYDTTVAGRYPDDOLLINDKRTTDTYDANSGGTVHOLRDPNAAGTISLNKFS
T 3ei3 B
                                                                                361 (383)
                 BTTSCSEEEECCBCCCTTSCCCCCEECSSSSEEEEECBCCTTTCTTCCCCEEEEETTTCCEEEEECBTTBCSCCCEEEEC
T ss dssp
T ss pred
                 Q ss pred
                 CCCCEEEECCCCCEEEEEC
Q Fri Mar 04 23: 264 LSGNVLALSGGDNKVTLWKEN 284 (297)
              264 ~~~~l~~~~d~~i~iw~~~ 284 (297)
Q Consensus
                 |+|++|++++ |+.|++|+..
              362 pdg~~l~s~s-d~~i~iW~~~
T Consensus
                                  381 (383)
              362 PTGDVLASGM-GFNILIWNRE 381 (383)
T 3ei3 B
T ss_dssp
                 TTSSEEEEE-TTEEEEECC
T ss_pred
                 CCCCeEEEec-CCeEEEEecC
                           PDB"
                                   NCBI
                                            Pub Med
>4wjs A RSA4; ribosome assembly, ribosome biogenesis, biosynthetic protein; 1.80A {Chaetomium thermophilum}
Probab=100.00 E-value=6.4e-36 Score=264.69 Aligned cols=253 Identities=24% Similarity=0.414 Sum probs=0.0
Q ss_pred
                 CceEccCccCeeeEEEcc-CCCEEEEEccCCcceeEEeccCCccceeEEeccCCccCeEEEEEccCCceE
Q Fri_Mar_04_23:
               1 MVVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                79 (297)
O Consensus
               79 (297)
              106 ----l-gh---v----fsp-----lasgs-D--v-iwd----t-----l-gh----V--v-spd--g--las-s-D--i
T Consensus
                                                                                181 (485)
T 4wjs_A
              106 LAHRIPGHGQPILSCQFSPVSSSRLATGSGDNTARIWDT--DSGTPKFTLKGHTGWVLGVSWSPD--GKYLATCSMDTTV
                                                                                181 (485)
T ss_dssp
                 EEEEECCCSSCEEEEEECSSCTTEEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEECTT--SSCEEEEETTSCE
T ss pred
                 cceeccCcCCEEEEEccCCCCEEEEEeCC--CCCcceEeCCCCCEEEEECCC--CCEEEEECCC
                 EEEEccCCeEEEEEeccCccEEEEEEcC----ccCccEEEEEECCCcchhhhhhhhccceeEEEECCC
Q ss pred
               80 LIWKEENGRWSQIAVHAVHSASVNSVQWAP----HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAP
 Q Fri Mar 04 23:
                                                                                155 (297)
 O Consensus
               155 (297)
              T Consensus
                                                                                258 (485)
              182 RVWDPESGK-QVNQEFRGHAKWVLALAWQPYHLWRDGTARLASASKDCTVRIWLVNTG--RTEHVLSGHKGSVSCVKWGG
T 4wis A
                                                                                258 (485)
                 EEEETTTTE-ECSSCBCCCSSCEEEEECCGGGCBTTBCEEEEEETTSCEEEEETTTT--EEEEEECCCSSCEEEEEECT
T ss dssp
T ss_pred
                 EEEECCCCc-cccccCCCccEEEEEecccCCCCCCEEEEEECCCc--ceeEeccCCCCCceEEEEECC
                 CcccccccCCcceEEEEEeCCceEEEEEEcCCCceeEE------
Q ss pred
Q Fri Mar 04 23:
              156 ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVL-----
                                                                                196 (297)
                 -----l-tg--d--i--wd-----
                                                                                196 (297)
 Q Consensus
                            ..+++|+.|+.|++||...+....+
T Consensus
              259 ~--
                     324 (485)
              259 T-----DT.TYTGSHDRSVRVWDAVKGTT.VHNFTAHGHWVNHTAT.SSDHVLRTAYHDHTKEVPGTEEERRAK
T 4wjs_A
                                                                               324 (485)
                 T-----SEEEEEETTSCEEEEETTTTEEEEEECCCSSCEEEEEETTHHHHHTTTCCTTCCCCSSHHHHHHH
T ss dssp
                   T ss pred
Q ss_pred
                 -----EEEeccCCCcEeEEEECCCCCCEEEEEE
Q Fri Mar 04 23: 197 -----ESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQ
                                                                               236 (297)
              197 -----h---v--l--s----las-s-Dq-i-iw--
O Consensus
                                                                                236 (297)
              T Consensus
                                                                                401 (485)
T 4wjs_A
              325 AKERFEKAAKIKGKVAERLVSASDDFTMYLWDPTNNGSKPVARLLGHONKVNHVOFSPDG---TLIASAGWDNSTKLWNA
                                                                                401 (485)
                 HHHHHHHHEETTEECCCEEEEETTSCEEEECHHHHTTSCSEEECCCSSCEEEEECTTS---SEEEEEETTSCEEEEET
T ss_dssp
                 HhhhhhhhhccCCcccEEEEEeCCCEEEEecCCCCCcceEecCCCCCCEEEEEECCCC---CEEEEEECCCcEEEEEC
T ss pred
                 ccccceeeeeecccccceeeeeeccccceeeee
Q ss pred
Q Fri_Mar_04_23: 237 DNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
                                                      282 (297)
              237 ----d-i-iw-
O Consensus
                                                      282 (297)
              T Consensus
              402 RDGK---FIKNLRG--HVAPVYQCAWSADSRLVVTGSKDCTLKVWN
T 4wjs_A
                                                      442 (485)
T ss_dssp
                 TTCC---EEEEECC--CSSCEEEEEECTTSSEEEEEETTSCEEEEE
T ss_pred
                 CCCc---EEEEEeC--CCCCEEEEEECCCCCEEEEE
                         PDB NCBI Pub Med
->4xyh_A Kinetochore protein MIS16; centromere, CENP-A, MIS18 complex, histone; 2.30A {Schizosaccharomyces
 japonicus}
 Probab=100.00 E-value=1.9e-36 Score=264.20 Aligned cols=257 Identities=23% Similarity=0.340 Sum probs=0.0
                 ceEecCCcCeeeEEEcC-CCCEEEEEecCCc-----ccceeEEeccCCCCEEEEEecCCccC-EEEEE
               2 VVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGE-----THKLIDTLTGHEGPVWRVDWAHPKFGT-ILASC
 Q Fri Mar 04 23:
                                                                                73 (297)
               O Consensus
                                                                                73 (297)
```

```
+....+|...|++++|+| ++++||+++.||.|++||++... .....+.+|...|++++|+++ +...+|++|
124 -----h---v-1--p----lat---dg-v-iwd---------h---v-1--sg
T Consensus
                                                                               201 (430)
              124 IVQKIHHEGDVNKARFMPQNPDIIATLGLNGNGYIFDLNLYREQPIVQTGHQACLRHHTSEGFGLGWNFI--QEGTLATG
T 4xyh_A
                                                                               201 (430)
                 EEEEEEESSCCCEEEEETTEEEEEEECGGGCEEEEEGGGCSSCSEETTCCSEEECCCSSCCCEEEECSS--STTEEEEE
T ss dssp
 T ss_pred
                 EEEEeCCCCceEEEEecCCCCCEEEEECCCCccEEEEECCCCccccccCCCCCEEEEecCCC--CCCEEEEE
                 cCCCeEEEEEccCCeE-----EEEEEeccCCcCEEEEEECCCCCEEEEEECCCCcC-hhhhhhh
Q ss pred
Q Fri_Mar_04_23:
               74 SYDGKVLIWKEENGRW-----SQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTT-SPIIIDAH
                                                                               144 (297)
               Q Consensus
                                                                               144 (297)
              T Consensus
              202 TEDTSICVWDIKGKSLSLEKSIDVAPVSVYHRHTAVVNDLOFHLOH-EALLTSVSDDCTLOTHDTRLPSSSSASOCVKAH
T 4xyh_A
                                                                               280 (430)
                 CTTSCEEEECTTCCCBTTBCEEECCSEEECCCSSCEEEEECTTC-TTEEEEEEETTSEEEEEETTSCTTSCCSEEEECC
T ss dssp
T ss pred
                 Q ss pred
                 ccceeEEEECCCccccccCCccceE-EEEEeCCcceEEEEEEcCCCceeEEEEEeccCCccEeEEEECCCCCCCEEE
Q Fri Mar 04 23: 145 AIGVNSASWAPATIEEDGEHNGTKESRK-FVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLA
                                                                               223 (297)
                         Q Consensus
              145 ~~~v~~~
                                                                               223 (297)
                 ...+.+++|+|++
                                    .. |++|+.|+.|++||++.... ++..+.+|...|.+++|+|++ ..+|+
              281 ~~~v~~l~~~p~~---
                                   ----ll-tg--dg-v-vwd------l-
T Consensus
              281 EQPVNGVAFNPFN------DYLLATASADHTVALWDLRRLNQ---RLHTLEGHEDEVYNVQWSPHD--EPILV
T 4xyh A
                                                                               342 (430)
T ss_dssp
                 SSCEEEEECSSC-----TEEEEEETTSCEEEEETTCTTS--CSEEECCCSSCEEEEECSSC--TTEEE
T ss_pred
                 CCCeEEEEecCCC------CGEEEEECCCCeEEEEECCCCC--CGeeecCCCCCEEEEEECCCC--CCEEE
                 EEeCCCeEEEEEccC-----CCCceeEEEeccccCCceEEEEECCCCC-EEEEEECC
Q ss pred
Q Fri_Mar_04_23: 224 SVSQDRTCIIWTQDN------EQGPWKKTLLKEEKFPDVLWRASWSLSGN-VLALSGGDNKVTLWKEN
                                                                            284 (297)
O Consensus
              224 s~s~Dg~i~iw~~~~d~i~iw~~~d~i~iw~~~
                                                                            284 (297)
                 +++.||.|++||+..
                                .. ..... |...|.+++|+|+++ +|++++.||.|+||+..
              343 s-s-Dg-i-iwd------
                                        T Consensus
                                                                             413 (430)
T 4xyh_A
              343 TSSTDRRVCVWDLSKIGEEOTVEDSEDGAPE---LMFMHGG--HTNRVSDLSWNPNNKWVLASLADDNILOIWSPS
                                                                             413 (430)
                 EEETTSCEEEEEGGGTTCCCCHHHHTSCCTT---EEEEECC--CSSCEEEEEECSSSTTCEEEEETTSEEEEEECC
T ss dssp
T ss_pred
                 PDB<sup>™</sup>
PROTEIN DATA BANK
No 48
                                   NCBI Pub Med
->4j0w_A U3 small nucleolar RNA-interacting protein 2; beta-propeller, WD domain, RNA binding protein,
preribosome; 1.70A {Homo sapiens} PDB: 4jxm _A
Probab=100.00 E-value=5.6e-36 Score=253.65 Aligned cols=259 Identities=17% Similarity=0.196 Sum probs=0.0
Q ss pred
                 84 (297)
Q Fri_Mar_04_23:
               5 ANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKE
O Consensus
               5 ---h---v------q--l-t-s-d--v-lwd-------h---v-----l-s-s-D--i-iwd-
                                                                                84 (297)
               T Consensus
                                                                               138 (343)
               63 PPGHSSHVLCMAISSDGKYLASGDRSKLILIWEA--QSCQHLYTFTGHRDAVSGLAFRRG--THQLYSTSHDRSVKVWNV
                                                                               138 (343)
T 4j0w A
                 {\tt CSCCSSCEEEEECTTSCEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEECTT--SSEEEEEETTSEEEEEEG}
T ss_dssp
                 T ss pred
                 Q ss pred
Q Fri_Mar_04_23:
               85 ENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEH
                       Q Consensus
               85 ~~~~
                                                                               164 (297)
                 ++++ .+..+..|...+.++.|+|+ +...++++.|+.|++|++... ....+..+|...+..+|..+.
              T Consensus
                                                                               203 (343)
              139 AENS-YVETLFGHQDAVAALDALSR-ECCVTAGGRDGTVRVWKIPEE--SQLVFYGHQGSIDCIHLINE-----
T 4j0w A
                                                                               203 (343)
 T ss dssp
                 GGTE--EEEEEECCSSCCCEEECSS--SEEEEECBTTCEEEEEETTTT---EEEEEECSSSCEEEEEEET-----
                 CCCc--ceEEEeCCCCccEEEEecCC--CCEEEEEcCCCeEEEEEcCCC---ccEEEecCCCcEEEEEEcCC------
T ss_pred
                 Q ss pred
O Fri Mar 04 23: 165 NGTKESRKFVTGGADNLVKIWKYNSDAOTYVLESTLEGHSDW------VRDVAWSPTVLLRSYLASVSODRTCII
                                                                               233 (297)
                    ----l-tg--d--i--wd------h-----h---------v--l--s----las-s-Dg-i-i
O Consensus
                                                                               233 (297)
                      ..+++|+.|+.|++||++...
                                                         |.+++|+|++
                                                                   .+||+++.|++|+|
T Consensus
                 -----v---s-s-d--v-lwd-------lasgs-d--v-l
                                                                               270 (343)
              204 ----EHMVSGADDGSVALWGLSKKR---PLALOREAHGLRGEPGLEOPFWISSVAALLNT---DLVATGSHSSCVRL
T 4j0w A
                                                                               270 (343)
                 -----TEEEEEETTSCEEEEESSCSS---CSEETTTTCEESSTTCCEECCCEEEECTTS---SEEEEECSSSEEEE
T ss dssp
                 -----CEEEEEeCCCeEEEEECCCCC----cceeehhhhcCCCCccccccceEEeeeCCCC---CEEEEeCCCCeEEE
T ss pred
Q ss_pred
                 EECCCCCCeeEEEeccccCCceEEEEEECCCCCEEEEEc--CCCCEEEEEECCCCCEEEEeeeccC
Q Fri Mar 04 23: 234 WTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSG--GDNKVTLWKENLEGKWEPAGEVHO 297 (297)
                                           --1----d--i-iw-----
Q Consensus
              234 w~
                     ~~~~~i~~
                                                                     297 (297)
                 271 WQCGEGFRQLDLLCDIP--LVGFINSLKFSSSGDFLVAGVGQEHRLGRWWRIKEARNSVCIIPLRR 334 (343)
T 4j0w A
T ss dssp
                 EEECGGGCCEEEEEEE--CCSEEEEEECSSSSEEEEEEESSCTTCSSCCCTTSCCEEEEEC--
                 T ss pred
No 49
                          PDB<sup>IN</sup>
PROTEIN DATA BANK
                                   NCBI
                                            Pub Med
>3jam g RACK1; eukaryotic translation initiation, small ribosome subun 43S, translation; 3.46A (Kluyveromyces
 lactis} PDB: 3j81 _g 3j80 _g
 Probab=100.00 E-value=5.9e-35
                        Score=245.37 Aligned_cols=247 Identities=21% Similarity=0.290 Sum_probs=0.0
Q ss pred
                 Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                81 (297)
```

```
Q Consensus
                                                                                  81 (297)
                 T Consensus
                                                                                 134 (326)
               59 VRSYKGHSHIVQDVVVSADGNYAVSASWDKTLRLWNL--ATGNSEARFVGHTGDVLSVAIDAN--SSKIISASRDKTIRV
T 3iam q
                                                                                 134 (326)
                  EEECCCCSSCEEEEEECSSSSEEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEECTT--SCEEEEETTSCEEE
T ss dssp
                 hhhhcCccceEEEECCCCCEEEEEcC-CCCCcceEEeccCCcEEEEEcCC-CCEEEEEcCCCcEEE
T ss pred
                 EEccCCeEEEEEeccCccEEEEEeCCccCc-----EEEEEECCCEEEEEEecCCCcchhhhhhhhhcccceeEE
Q ss pred
Q Fri_Mar_04_23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGP------LLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSA
                                                                                 151 (297)
Q Consensus
                                           -----l~~~~d~~i~i~~~
                                                                                 151 (297)
                                                 .+++++.|+.+++|++.....+.+|...+.++
               T Consensus
                                                                                 209 (326)
               135 WNTVGD---CAYVLLGHTDWVTKVRVAPK--NLEDGEVDDGRITFVSAGMDKIVRSWSLNEDSYRIEADFIGHNNYINVV
T 3jam g
                                                                                 209 (326)
T ss_dssp
                 EESSSC---EEEEECCCSSCEEEEECCC--CC----CCCSCEEEEEEESSSEEEEEEC--CCSEEEEEECCSSCEEEE
T ss_pred
                  EeCCCC---eeEEeeccCcEEEEEecCC--cccceecCCceEEEEecCCCcEEEEeccCCCcceeeecCCCCceEEE
Q ss_pred
                 EECCCccccccccCCccceEEEEEeCCcceEEEEEcCCCceeEEEEEccCCCcEeEEEECCCCCCCEEEEEE
Q Fri_Mar_04_23: 152 SWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTC
                                                                                 231 (297)
Q Consensus
               152
                               ----l-tg--d--i--wd-------h---v--l--s-----las-s-Dg-i
                                                                                 231 (297)
                                .++++|+.|+.|++||++.....+.
                                                      +...|.+++|+|+
                               ----l-s---dg-i-vwd--------v-----s-----s
T Consensus
               210 ~
               210 OPSPDG-----SLAASAGKDGOIYVWNLKHKSAFMNFD----AKDEVFALAFSPS----RFWLTAATASGI
T 3jam_g
                                                                                 267 (326)
                  EECSSS-----SEEEEEETTSEEEEEETTTBCCCEEE----CSSCCCEEECSS---SSEEEECSSSE
T ss_dssp
                  EECCCC-----CEEEEecCCCEEEEEECCCCcEEEEee----cCCCEEEEEecCC---ccEEEEecCCCE
T ss pred
Q ss_pred
                 EEEEccCCCceeEEEec-----cccCcceEEEEECCCCCEEEEE
Q Fri Mar 04 23: 232 IIWTQDNEQGPWKKTLLK-----EEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
              232 ~iw~~~~d~i~iw~
O Consensus
               T Consensus
               268 KIYDLENEV---LIDELKPEFAGYTKAQDPHAVSLAWSADGQTLFAGYTDNVIRVWQ 321 (326)
T 3jam_g
T ss_dssp
                  EEEESSSCC---EEEEECCCCSSCCSSCCCCEEEEEECTTSCEEEEE
                  EEEECCCch---hhhhhchhcccchhhccCceEEEEECCCCEEEEEE
T ss_pred
No 50
                           PDB<sup>IN</sup>
PROTEIN DATA BANK

NCBI
                                             Pub Med
3jb9_L PRE-mRNA-splicing factor CWF17; spliceosome, U2/U5/U6, lariat, RNA binding protein-RNA compl; HET: GDP
ADP; 3.60A {Schizosaccharomyces pombe 972h-}
Probab=100.00 E-value=2e-37 Score=262.21 Aligned cols=253 Identities=22% Similarity=0.292 Sum probs=0.0
Q ss pred
                 CceEccCcCeeeEEEccCCcEEEEEccCCcceEEEEccCCccceEEEccCCccCEEEEEccCCccCEEEEEccCCccEE
Q Fri Mar 04 23:
               1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                  80 (297)
O Consensus
               80 (297)
                 T Consensus
               42 PNLQMFGHTAEVLVARFDPSGSYFASGGMDRQILLWNVF-GDVKNYGVLNGCKGAITDLQWSRD--SRVVYCSSSDTHLM
T 3jb9 L
T ss_dssp
                 CCCCEECCSSCCCEEECSSSSEEEEESTTSEEEEEECC--CCCEEEEEECCSSCCCCCEECTT--SSEEECCCSSSCCE
                 T ss_pred
Q ss_pred
                 EEEccCCeEEEEEeccCCccEEEEEECCCccCcEEEEEECCCCcchhhhhhhhcccceeEEEECCCccc
 Q Fri Mar 04 23:
               81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                 160 (297)
               Q Consensus
                 +||+.+++ .+..+..|...|.+++|.|.+ +.+++++.|+..++||+...
                                       ----l~s~s~d~~i~iwd~~~---
T Consensus
               119 ~wd~~~~~h~~~v~~~~
                                                                                 189 (340)
               119 SWDAVSGQ--KIRKHKGHAGVVNALDVLKVG-SELLTSVSDDCTMKVWDSRSK---DCIKTIEEKYPLTAVAIAQQG--- 189 (340)
T 3jb9_L
                 EEETTTCC--EEEECCCCSSCCCEEEECCC--CCEEEEECSSSEEEEEETTTS---SEEEEEECSSCCCEEEECSSS---
T ss_dssp
T ss pred
                 EEECCCCc--EEEEecCCCCeEEEEEEcCC-CcEEEEeCCCCC---ceEEeeccccceeEEEEcCCC---
                 0 ss pred
Q Fri_Mar_04_23:
               161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNE-
                                                                                 239 (297)
                 ~~~~~~~~~las~s~Dg~i~iw~~~~
                                                                                 239 (297)
                         190 -----l~g~dg~i~iwd~~~~h~~v~l~sp~g--~l~s-sd~v~iwd~~~~
T Consensus
                                                                                 252 (340)
               190 -----TQVFIGGIDGAIKIWDLRNNH----CSHVLKGHKDIITSLAISKDG---SSLLSNSMDNTVRIFDVKPFA
T 3jb9 L
                                                                                 252 (340)
                 -----CEEEEECSSSCCEEEETTTCS---CCEECCCCSCEEEECCCSS--SEEEEEETTSBCCEEECC---
T ss dssp
                  -----CEEEEEcCCCcEEEEECCCc---cceeeEccCCCEEEEEECCCc---CEEEEEECCceEEEEECchhc
 T ss pred
                 --CCceeEEEecccCCceEEEEECCCCCEEEEE
Q ss pred
Q Fri Mar 04 23: 240 --QGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                 -----d--i-iw- 282 (297)
                   T Consensus
              253 ----v-v-v-s----l-sgs-d--v-iw- 297 (340)
T 3jb9 L
               253 SAQRQLQIFEGAIHGQEHNLLGVAWSRNSRFVGAGSSDKNVYVWS 297 (340)
                  -CCCBCCCCBCCCCTTCCCCCCCBCTTSSCBEEECTTSCEEEEC
T ss dssp
                  CCcceeEEeeecCccCCEEEEEECCCCCeEEEEE
T ss pred
                                                  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=100.00 E-value=8.5e-36 Score=250.70 Aligned_cols=243 Identities=14% Similarity=0.255 Sum_probs=0.0
Q ss_pred
                 eeEEEEcCCCCEEEEEecCCCcceeEEeccCCcceeEEeccCCccCEEEEEccCCceEEE
```

```
Q Fri_Mar_04_23: 12 IHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEENGRWSQ
                                                                       91 (297)
             O Consensus
                                                                       91 (297)
              3 -s----d---l-s-s-D--v--Wd------
T Consensus
                                                                       77 (326)
             3 TSPGTVGSDPVILATAGYDHTVRFWQA--HSGICTRTVQHQDSQVNALEVTPD--RSMIAAAGYQ-HIRMYDLNSNNPNP
T 4jsn_D
                                                                       77 (326)
               ----CCSSSEEEEEETTSEEEEECT--TTCCEEEEEECTTSCCCEEEECTT--SSEEEEECBS-CEEEEESSSCSCCC
T ss_dssp
               CCCCacCCCceeeeeccCcaeeeecc--ccceeeeecccccceeeeeccc--cceeeeccc--aeeeeeccccaa
T ss pred
               Q ss pred
Q Fri_Mar_04_23:
             92 IAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESR
                                                                      171 (297)
             141 (326)
T Consensus
             78 IISYDGVNKNIASVGFHED--GRWMYTGGEDCTARIWDLRSR-NLQCQRIFQVNAPINCVCLHPNQ------A
T 4jsn D
                                                                      141 (326)
               SEEECCCCSBEEEEECTT--SSEEEEEETTSEEEEEETTSC-CSSCSEEEECSSCEEEEECTTS------S
T ss dssp
T ss_pred
               EEEEEECCCceEEEEEccCCceeEEEEeccCCcceEEEEeccCCcccEEEEEeccCc---CcceeEEEe
Q ss pred
Q Fri Mar 04 23: 172 KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNE---QGPWKKTLL
                                                                      248 (297)
             172 ~l~tq~~d~i~wd~~~~~~h~~v~~l~~s~~~~~las~s~Dq~i~iw~~~~~
                                                                      248 (297)
Q Consensus
               .+++|+.|+.|++||++...
             T Consensus
                                                                      214 (326)
             142 ELIVGDQSGAIHIWDLKTDH----NEQLIPEPEVSITSAHIDPDA---SYMAAVNSTGNCYVWNLTGGIGDEVTQLIPKT
T 4jsn D
                                                                      214 (326)
               EEEEEETTSCEEEEETTTCC----EEEECSSTTSCEEEEEECTTS---SEEEEEETTSCEEEEEECCCGGGSCCCEEEEE
T ss_dssp
               T ss_pred
               CCCCCCCEEEEECCCCCCEEEE
Q ss_pred
Q Fri Mar 04 23: 249 KEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
             249 -----1-----1-----d--i-iw- 282 (297)
Q Consensus
               ....+...+.++|+|+++++|++++.|++|++|+
             215 ~~~h~~~v~~~~sp~~~l~s~s~D~~i~iwd 248 (326)
T 4jsn D
             215 KIPAHTRYALQCRFSPDSTLLATCSADQTCKIWR 248 (326)
               EECCCSSCEEEEECTTSSEEEEEETTTEEEEEE
T ss_dssp
               CCCCCCCEEEEECCCCCEEEEE
T ss pred
No 52
                                            Pub Med
>4j0x A Ribosomal RNA-processing protein 9; beta-propeller, WD domain, RNA binding protein, preribosome; 2.50A
 {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.5e-35 Score=259.30 Aligned cols=266 Identities=15% Similarity=0.131 Sum probs=0.0
Q ss_pred
               Q Fri Mar 04 23:
             43 (297)
              O Consensus
                                                                       43 (297)
                                      +++|++|+.|++|++||+....
                           T 4j0x A
             25 QSFTRVGENNLTCISCFQPVLNKYTFEESSNGDKNKGRLFAYTVSKDLQLTKYDITDFSKRPKKLKYAKGGAKYIPTSKH
                                                                      104 (451)
T ss_dssp
               EEEEECSSSCEEEEEECC-----CCEEEEEETTSEEEEECCCTTSCCEEEEEECCGGGCC---
T ss pred
               ceeEEccCCCCEEEEEecCCccCEEEEEEcCCCeEEEEEccCCeEEEEEEcc
Q ss pred
Q Fri_Mar_04_23:
             44 KLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEENGRWSQIAVHA--VHSASVNSVQWAPHEYGPLLLVASS 121 (297)
O Consensus
             121 (297)
               T Consensus
             105 EYENTTEGHYDEILTVAASPD--GKYVVTGGRDRKLIVWSTESLS--PVKVIPTKDRRGEVLSLAFRKN--SDQLYASCA
T 4j0x A
                                                                      178 (451)
T ss_dssp
               ---CCCSSCCSCEEEEECTT--SSEEEEEETTSEEEEETTTTE--EEEEECCCTTCCEEEEEECTT--SSEEEEEET
T ss_pred
               eeeEEeccCCccEEEEECCC--CCEEEEecCCCceEEEEECCCCc--EEEEEecCCCCccEEEEEecC--CCEEEEEEC
               Q ss_pred
Q Fri_Mar_04_23: 122 DGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLEST--
                                                                      199 (297)
             122 d--i-i-----v-----v------v------l-tg--d--i--wd--------
                                                                      199 (297)
O Consensus
               |+.|++|++... ....+..+..+++|+|++
                                               .+|++++.|+.|++||++.....
                                      ~~---d~i~iwd~~~
            179 d-~i~vwd~~~--
T Consensus
                               -~~v~~~
                                                                      243 (451)
             179 DFKIRTYSINQF--SQLEILYGHHDIVEDISALAME------RCVTVGARDRTAMLWKIPDETRLTFRGGDEP
T 4j0x A
                                                                      243 (451)
T ss_dssp
               TSEEEEEETTTT--EEEEEEECCSSCCCEEECCSSS-----EEEEECBTTCEEEEEEGGGTEEEEEECCCCH
               CCEEEEEECCCC--cEEEEECCCCCeEEEEEeCCCC-------CEEEEECCCCeEEEEECCCCceeeeeCCCCc
T ss_pred
               ----eccCCceeEEEEccCCccceeEEEeccCCccceeEEEecc
Q ss pred
Q Fri_Mar_04_23: 200 -----LEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKE 250 (297)
               -----las-s-Dg-i-iw-------
Q Consensus
             200
                                                                      250 (297)
                                  ...|...|.+++|+|+
                                     ...|.++++|+ .+++++.|+.|++|++... ...+..
T Consensus
                                                                      316 (451)
             244 OKLLRRWMKENAKEGEDGEVKYPDESEAPLFFCEGSIDVVSMVDD----FHFITGSDNGNICLWSLAKKK---PIFTERI
T 4j0x A
                                                                      316 (451)
               HHHHHHHTTC------CCCCCCEEEEEEET---TEEEEEETTSCEEEEETTCSS---CSEEETT
T ss dssp
T ss_pred
               cceccCCceeEEecCCccEEEecCccccCCCCcEEEEEeCCC----CEEEEEeCCCEEEEEECCCC---eeeEEec
Q ss pred
                     Q Fri_Mar_04_23: 251 -----EKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENL-EGKWEPAGEV 295 (297)
            251 -----d--i-iw-----
Q Consensus
                                                                   295 (297)
            T Consensus
                                                                  ~ 392 (451)
T 4j0x_A
            317 AHGILPEPSFNDISGETDEELRKROLOGKKLLOPFWITSLYAIPYSNVFISGSWSGSLKVWKISDNLRSFELLGEL 392 (451)
```

```
T ss_dssp
                   TTCBC------CCCBCCCCEEEECTTBSEEEEECSSSCEEEEEECTTSSCEEEEEE
T ss_pred
                   CCCeeccCCcceEEEcCCCCEEEEEECCCcccCCCceEEEEEecCCCEEEEEeCCCCeEEEEEE
                                                Pub Med
No 53
                             PDB"
                                      NCBI
>5gan H U4/U6 small nuclear ribonucleoprotein PRP4; snRNP, GTPase, U5 snRNA, PRP8, spliceosom snRNP, BRR2,
transcription; HET: GTP; 3.60A {Saccharomyces cerevisiae} PDB: 5gap _H
Probab=100.00 E-value=3.3e-36 Score=265.19 Aligned_cols=246 Identities=20% Similarity=0.361 Sum_probs=0.0
                   Q Fri_Mar_04_23:
                 \mathbf{6} \quad \text{NAHNELIHDAVLDYY-GKRLATCSSDKTIKIFEVEGETH--KLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW}
                                                                                        82 (297)
O Consensus
                 6 ~~h~~v~~~~~q~~l~t~s~d~~v~lwd~~~~~~h~~v~~~~~l~s~s~D~~i~iw
                                                                                        82 (297)
                  T Consensus
                                                                                       292 (465)
                {\tt 215~DSHVGKIGAIDWHPDSNNQMISCAEDGLIKNFQYSNEEGGLRLLGDLVGHERRISDVKYHPS--GKFIGSASHDMTWRLW}
T 5gan H
T ss dssp
                   TSCSSCEEEECCSSSSCEEEEETTSCEEEEECSSSCSEEEEEEECCCSSCEEEEEETT--TTEEEEEESSSCEEEE
T ss_pred
                   Q ss_pred
                   {\tt EccCCeEEEEEecccCccEEEEEecCCccCcEEEEEEecCCccehhhhhhhhccceeeEEEECCcccccc}
 Q Fri Mar 04 23:
                83 KEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDG
                                                                                       162 (297)
                O Consensus
                                                                                       162 (297)
               T Consensus
                                                                                       361 (465)
T 5gan H
                293 DASTHQ--ELLLQEGHDKGVFSLSFQCD--GSLVCSGGMDSLSMLWDIRSG--SKVMTLAGHSKPIYTVAWSPNG----
                                                                                       361 (465)
 T ss_dssp
                   ETTTTE--ECCCCCCSSCEEECCBCTT--SSEEEEEETTSCBEEEETTTT--EECCBCSSCSSCCCEEEEETTT----
                   ECCCCe--EEEEecCCCCCEEEEEEcCC--CCEEEEECCCC--ceeEEeccCCCcEEEEEECCCC-----
T ss_pred
0 ss pred
                   cccCccceEEEEEcCCceEEEEEccCCCceeEEEEEccCCCceEEEEEccCCC
Q Fri_Mar_04_23: 163 EHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT--VLLRSYLASVSQDRTCIIWTQDNEQ
                                                                                       240 (297)
                163 ~~~~~~latg~~d~~i~~wd~~~~~~h~~~v~~l~~s~~-~~~las~s~Dg~i~iw~~~
                         .+|++|+.|+.|++||++.... ....+..|...|.+++|+|+ + .+||++++.||.|++|++....
                362 ------YQVATGGGDGIINVWDIRKRDEG--QLNQILAHRNIVTQVRFSKEDGG--KKLVSCGYDNLINVYSSDTWL
T Consensus
                                                                                       428 (465)
T 5gan H
                                                                                       428 (465)
 T ss dssp
                   -----TEEEEECSSSEEEECCSCTTCC--CSEEEECCSSCEEEECCTTTSC---CEEEEEESSSEEEEETTTCC
 T ss pred
                   -----CEEEEEcCCCeEEEEECCCCcc--cceeccCCCcEEEEEEccCCCC---CEEEEEeCCCeEEEEeCCCCe
Q ss pred
                   CceeEEEecccCCceEEEEECCCCCEEEEE
Q Fri Mar 04 23: 241 GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
                                                      282 (297)
                241 ----d-i-iw-
                                                       282 (297)
Q Consensus
                     ...+.. |...|.+++|+|+++++|++++.||+|++|+
T Consensus
                429 ---~v~~v~~s~d~~~l~s~s~dg~i~iWd 465 (465)
                429 --- KMGST.AG--HTDKTTST.DTSNNSHFT.VSGGWDRSTKT.WN
T 5gan H
                                                       465 (465)
T ss dssp
                   ---EEEEEEC--CSSCEEEEECCSSSSCEEEEETTSEEEEEC
                   ---EeeeecC--CCCceEEEEEcCCCCEEEEEcCCCeEEeCC
T ss pred
                             SCOPe PROTEIN DATA BANK
No 54
                                                NCBI
                                                                Pub Med
>1gxr A ESG1, transducin-like enhancer protein 1; transcriptional CO-repressor, WD40, transcription repressor, WD
repeat; 1.65A (Homo sapiens) SCOP: b.69.4.1 PDB: 2ce8 A
Probab=100.00 E-value=8.3e-35 Score=244.76 Aligned_cols=241 Identities=16% Similarity=0.251 Sum_probs=0.0
                   CCCCeeeEEEEcCCCCEEEEEecCCCccceeEEeccCCccceeEEeccCCccCEEEEEccCCccEEEEEccCCcc
Q ss_pred
Q Fri Mar 04 23:
                 7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEEN
                                                                                        86 (297)
                 7 ~h~~~v~~~~~q~~l~t~s~d~~v~lwd~~~~~h~~~v~~~~~l~s~s~D~~i~iwd~~
Q Consensus
                                                                                        86 (297)
                   -----dg-i---d-----
                                                                                       172 (337)
T Consensus
                                                                ----l----dg-i---d---
T 1gxr_A
                95 NRDNYIRSCKLLPDGCTLIVGGEASTLSIWDLAAPTPRIKAELTSSAPACYALAISPD--SKVCFSCCSDGNIAVWDLHN
                                                                                       172 (337)
                   CTTSBEEEEECTTSSEEEEEESSSEEEEECCCC-EEEEEEECSSSCEEEEEECTT-SSEEEEEETTSCEEEEETTT
T ss dssp
                   CCCCeEEEEECCCCcEEEEEcCCCeEEEEecCCCccceeeeecccccEEEEEECCC--CCEEEEEcCCCeEEEEeCCC
T ss_pred
                   CeEEEEEeccCCccEEEEEeCCccCcEEEEEEECCCCcchhhhhhhhcccceeEEEECCCcccccccCC
Q ss pred
                87 GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNG
 Q Fri Mar 04 23:
                                                                                       166 (297)
Q Consensus
                87 -----v----v----v-----v-----v-----
                                                                                       166 (297)
                   T Consensus
                                      ~--~~l~~~~d~~i~i~d~~~-
                                                                                       236 (337)
                173 QT--LVRQFQGHTDGASCIDISND--GTKLWTGGLDNTVRSWDLREG---RQLQQHDFTSQIFSLGYCPTG-----
T 1gxr A
                                                                                       236 (337)
T ss_dssp
                   TE--EEREECCCSSCEEEEECTT--SSEEEEEETTSEEEEETTTT---EEEEEEECSSCEEEEECTTS-----
                   Cc--eeEEEcCcCCCeEEEEEcCC--CCEEEEEeCCCC---ccccccCCCccEEEEECCCC-----
T ss_pred
Q ss pred
                   Q Fri_Mar_04_23: 167 TKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKT 246 (297)
O Consensus
                167 -----l-tg--d--i--wd---------h---v--l--s-----las-s-Dg-i-iw------
                                                                                       246 (297)
                                         .+++++.++.|++||++.+
                T Consensus
                                                                                       298 (337)
T 1gxr A
                237 ----EWLAVGMESSNVEVLHVNKP-----DKYQLHLHESCVLSLKFAYCG---KWFVSTGKDNLLNAWRTPYGA-----
                                                                                       298 (337)
T ss_dssp
                   ----SEEEEEETTSCEEEEETTSS----CEEEECCCSSCEEEEECTTS---SEEEEEETTSEEEEEETTTCC----
                   ----CEEEEEeCCCceEEEEeCCCC----cceEeecCCCCEEEEEECCCC---CEEEEECCCCeEEEEECCCCc-----
T ss pred
                   EecccCCceEEEEECCCCCEEEEE
Q ss pred
               247 LLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE 283 (297)
 Q Fri_Mar_04_23:
 Q Consensus
               247 ----i----i------l-----d--i-iw-- 283 (297)
                  .....+...+.++|+|++++|++++.||.|++|+.
T Consensus
               299 -----v---s----l----dg-i--w-l 335 (337)
```

```
T 1gxr A
                      299 SIFOSKESSSVLSCDISVDDKYIVTGSGDKKATVYEV 335 (337)
 T ss_dssp
                           EFFERCSSCEEFFERCTTSCEFFFFFTTSCEFFFF
 T ss pred
                           ceeecCCCceeEEEECCCCCeEEEEec
                                                        NCBI
                                                                               Pub Med
>3jb9 L PRE-mRNA-splicing factor CWF17; spliceosome, U2/U5/U6, lariat, RNA binding protein-RNA compl; HET: GDP
 ADP; 3.60A {Schizosaccharomyces pombe 972h-}
 Probab=100.00 E-value=5.1e-37 Score=259.66
                                                       Aligned cols=251 Identities=17% Similarity=0.294 Sum probs=0.0
                           Q Fri_Mar_04_23:
                         2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                                                              81 (297)
                                              ----q--1-t-s-d--v-lwd-----h---v--
                         2 ~~~~h~~~v~~~
                                                                                                  -----l-s-s-D--i-i
 Q Consensus
                                                                                                                              81 (297)
                            ~~~v~~l~~s~d~~l~~~~d~~i~~wd~~~~~~~h~~~v~~~~~~~l~s~s~d~~i~i
                                                                                                                             162 (340)
 T 3jb9_L
                        86 YGVLNGCKGAITDLOWSRDSRVVYCSSSDTHLMSWDA--VSGOKIRKHKGHAGVVNALDVLKVG-SELLTSVSDDCTMKV
                                                                                                                             162 (340)
 T ss dssp
                           ERRERCCSSCCCCCERCTTSSERECCCSSSCCERET--TTCCERERCCCCSSCCCERECCC--CCERERCCSSSERE
 T ss_pred
                           eEEEecCCCCEeEEEcCCCCEEEEEcC--CCCcEEEEecCCCCCeEEEEcCC-CcEEEEecCCCCEEEE
                           EEccCCeEEEEEeccCcccEEEEEECCCccCcEEEEEECCCccchhhhhhhhcccceeEEEECCCcccc
 Q ss pred
 Q Fri_Mar_04_23:
                        82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                                                                             161 (297)
 Q Consensus
                        82 wd-----v----v------l-----d--i-i------v-----v----
                                                                                                                             161 (297)
                            ||+++++ .....+..+.++|+|+ +...++++.|+.|+.|++||+.... ....+.+|...|.+++|+|++
 T Consensus
                       163 wd~~~~
                                                             -----h---v--l--sp-g----
                                                                                                                             231 (340)
 T 3jb9 L
                       163 WDSRSKD---CIKTIEEKYPLTAVAIAQQ--GTQVFIGGIDGAIKIWDLRNNH--CSHVLKGHKDIITSLAISKDG----
                                                                                                                             231 (340)
 T ss dssp
                           EETTTSS---EEEEEECSSCCCEEEECSS--SCEEEEECSSSCCEEEETTTCS--CCEECCCCSCEEEECCCSSS----
 T ss_pred
                           ECCCCC---EEEEcccccceEEEEccC--CCEEEEEcCCCcEEEEECCCCc--cceeeEccCCCEEEEEECCCC----
 Q ss pred
                           Q Fri Mar 04 23:
                       162 \ \ \mathsf{GEHNGTKESRKFVTGGADNLVKIWKYNS----DAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQD
                                                                                                                             237 (297)
 O Consensus
                       237 (297)
                                      .+|++++.|+.|++||++.
                                                               232 -----l~s~s~d~~v~iwd~~~
                                                                                   ~~~v~~v~~s~~~----l~sqs~d~~v~iw~~
                                                                                                                             299 (340)
 T Consensus
 T 3jb9 L
                       232 -----SSLLSNSMDNTVRIFDVKPFASAQRQLQIFEGAIHGQEHNLLGVAWSRNS---RFVGAGSSDKNVYVWSAT
                                                                                                                             299 (340)
                            -----SEEEEEETTSBCCEEECC---CCCBCCCCBCCCCCTTCCCCCCBCTTS---SCBEEECTTSCEEEECSS
 T ss_dssp
 T ss_pred
                            -----CEEEEEECCCeEEEEECchhcCCcceeEEeeecCccCEEEEEECCC---CeEEEECCCCeEEEEECC
                           CCCCceeEEEecccCCceEEEEECCCCCEEEEECC
 Q ss pred
 Q Fri_Mar_04_23: 238 NEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
                       238 ~~
                                               ---i-----l----d--i-iw---
                                                                                      284 (297)
                                    ...+.. |...|++++|+|++++.||+|++|+.+
                       T Consensus
                                                                                     340 (340)
                       300 GDL----RYVLPG--HEGSVNHVDFHPHQDIILSCSSDRTIFLGELN
 T 3ib9 L
                                                                                     340 (340)
 T ss_dssp
                           SCE----EEEECC--CSSCEEEECCCSSSCEEEEETTTEEEEEECC
 T ss_pred
                           Cce---eEEEec--CCCCeeEEEEcCCCCEEEEEcCCC
                                        SCOPe POB<sup>™</sup> PROTEIN DATA BANK
 No 56
                                                                                           Pub Med
3frx_A Guanine nucleotide-binding protein subunit beta- like protein; RACK1, WD40, beta propeller, ribosome,
 translation, acetylation; 2.13A {Saccharomyces cerevisiae} SCOP: b.69.4.0 PDB: lvwv_h lvxv_s lvxy_s lvwy_h 3izb
3o2z_T 3o30_T 3u5c_g 3u5g_g 4byl_6 4byt_6 4ujp_h 4uer_R 4uji_G* 4ujf_h 4ujn_G* 4ujk_h 4ujs_G*
 Probab=100.00 E-value=1.3e-34 Score=242.67 Aligned_cols=246 Identities=21% Similarity=0.316 Sum_probs=0.0
 Q ss pred
                           ceEecCCcCeeeEEEccCCcEEEEEccCCcceEEEeccCccceeEEeccCCccCeEEEE
 O Fri Mar 04 23:
                         2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                                                              81 (297)
 O Consensus
                         2 -----h---v------q--l-t-s-d--v-lwd------h---v------l-s-s-D--i-i
                                                                                                                              81 (297)
                           T Consensus
                        133 (319)
 T 3frx_A
                        58 VRSFKGHSHIVQDCTLTADGAYALSASWDKTLRLWDV--ATGETYQRFVGHKSDVMSVDIDKK--ASMIISGSRDKTIKV
                                                                                                                             133 (319)
                           EEEEECCSSCEEEEECTTSSEEEEEETTSEEEEET--TTTEEEEEEECCSSCEEEEEECTT--SCEEEEETTSCEEE
 T ss dssp
                           T ss pred
                           EECCCCeEEEEEecccCccEEEEEEcCccCc-----EEEEEECCCEEEEEEecCCCchhhhhhhhcccceeEEEECC
 Q ss pred
 Q Fri_Mar_04_23:
                        82 \ \ \text{WKEENGRWSQIAV} \\ \text{HAVHSASVNSVQWAPHEYGP-----LLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAP} \\ \text{WKEENGRWSQIAV} \\ \text{WASDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAP} \\ \text{WKEENGRWSQIAV} \\ \text{WASDGKVSVVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WKEENGRWSQIAV} \\ \text{WASDGKVSVVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WKEENGRWSQIAV} \\ \text{WASDGKVSVVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WASDGKVSVVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WASDGKVSVVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WASDGKVSVEFKENGTSPIIIDAHAIGVNSASWAP} \\ \text{WASDGKVSVEF
                                                                                                                             155 (297)
                        155 (297)
                           ||++..
                                      .+..+..|...+..+..|.|+ +.
                                                                         .++++.|+.++|++...
 T Consensus
                       134 wd~~~~--
                                               -~~~v~~~~
                                                             -_-~v~v~v~d~~v~d~~~v~~h~~~v~~~h~~~v~~~
                                                                                                                             206 (319)
 T 3frx A
                       134 WTIKGQ---CLATLLGHNDWVSQVRVVPN--EKADDDSVTIISAGNDKMVKAWNLNQF--QIEADFIGHNSNINTLTASP
                                                                                                                             206 (319)
 T ss_dssp
                           EETTSC---EEEEECCCSSCEEEEECCC------CCEEEEEETTSCEEEEETTTT--EEEEEECCCSCEEEEEECT
 T ss_pred
                           EECCCc---cEEEEEecCCceeeEEEecC--CCcCcCccEEEEEECCCc--eeeEEecCCCcceEEEEECC
 Q ss pred
                           O Fri Mar 04 23: 156 ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAOTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSODRTCIIWT
                                                                                                                             235 (297)
 O Consensus
                       156 ~
                                   -----las-s-Dg-i-iw-
                                                                                                                             235 (297)
                                                                        ..+..+.. ...|.+++|+|++
                                             .+|++|+.|+.|++||+...
                                                                                                       .+++++ .++.+++|+
                      207 ~g-
 T Consensus
                                          -----l-s---dg-i-iwd-----i-v--
                                                                                                                             264 (319)
                       207 DG------TLIASAGKDGEIMLWNLAAK---KAMYTLSA-QDEVFSLAFSPNR---YWLAAA-TATGIKVFS
 T 3frx A
                                                                                                                             264 (319)
                           TS-----SEEEEEETTCEEEEEETTTT---EEEEEEEC-CSCEEEEEECSSS--SEEEEE-ETTEEEEE
 T ss dssp
                           CC-----hhheeccC-CCEEEEECCCC---hhheeccC-CCEEEEECCCC---CEEEEE
 T ss pred
 Q ss_pred
                           CCCCCCeeEEEec----CCCCCCeEEEEECCCCCEEEEE
 Q Fri Mar 04 23: 236 QDNEQGPWKKTLLK-----EEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE 283 (297)
```

```
Q Consensus
               236 ----d-i-iw-- 283 (297)
               ++... ...+. ...+..+..+|+|+|+++++..||.|++|+.
265 -----s-dg-l-sg-dg-i-vw-
T Consensus
                                                                 315 (319)
               265 LDPQY---LVDDLRPEFAGYSKAAEPHAVSLAWSADGQTLFAGYTDNVIRVWQV 315 (319)
T 3frx A
                   ETTEE---EEEEECCCCTTCCGGGCCCEEEEEECTTSSEEEEEETTSCEEEEE
T ss dssp
                   cccc---cccCCccccccCCCCceEEEEECCCCcEEEEEE
T ss pred
                             PDB<sup>™</sup>
No 57
                                               Pub Med
->4d6v_A GIB2, G protein beta subunit GIB2; signaling protein, scaffold protein, ribosome binding; 2.20A
{Cryptococcus neoformans var} PDB: 4aow A 5flx g 4d61 g 4d51 g 4kzx g 4kzz g 4kzz g 5a2q g Probab=100.00 E-value=1.3e-34 Score=242.03 Aligned_cols=250 Identities=21% Similarity=0.344 Sum_probs=0.0
                   Q ss_pred
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                        81 (297)
O Consensus
                 2 -----h---v-----g--l-t-s-d--v-lwd------h---h---v------l-s-s-b--i-i
                                                                                        81 (297)
                T Consensus
                                                                                       131 (314)
T 4d6v A
                56 KKILHGHNHFVSDVAISSDGQFALSSSWDHTLRLWDL--NTGLTTKKFVGHTGDVLSVSFSAD--NRQIVSASRDRSIKL
                                                                                       131 (314)
 T ss_dssp
                   EEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEET--TTTEEEEEECCCSSCEEEEEECTT--SSCEEEEETTSCEEE
                   cccccCCCeEEEEEcCCCCEEEEEcCCCeEEEECCCCeEEEECCCCeEEEE
T ss_pred
                   {\tt EEccCCeEEEEEecccCccEEEEEecCCccCcEEEEEECCCcceEEEEEecCCCcchhhhhhhhccceeeEEEECCCcccc}
Q ss pred
Q Fri_Mar_04_23:
                82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED 161 (297)
                Q Consensus
                132 wd-----v-----v------l-s---d-i--wd------v-----v----s--q----
T Consensus
                                                                                       204 (314)
                132 WNTLGEC-KFDIVEDGHTEWVSCVRFSPNPALPVIISAGWDKTVKVWELSNC--KLKTTHHGHTGYLNTLAVSPDG----
T 4d6v A
                                                                                       204 (314)
T ss dssp
                   ECTTSCE-EEEECTTCCSSCEEEEEECCCSSSCEEEEEETTSCEEEEETTTT--EEEEEECCCSSCEEEEEECTTS----
T ss_pred
                   eccccc-eeeeecccccceeeeecccccceeeeeeecccc--cceeeeeccccceeeeeccc---
Q ss_pred
                   CCCCCCcceEEEEeCCcceEEEEEccCCcceEEEEEccCCCceEEEEECCCCCCEEEEEE
Q Fri_Mar_04_23: 162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG 241 (297)
Q Consensus
                162 -----lass-Dg-i-iw-
                                                                                       241 (297)
                T Consensus
                                                                                       265 (314)
T 4d6v_A
                205 -----SLAASGGKDGITMLWDLNEGKHLYSLD----AGDVINALVFSPN----RYWLCAATASSIKIFDLESKS-
                   -----SEEEEEESSSEEEEEESSSSEEEEEE----CSSCEEEEEECSS----SSEEEEEESSCEEEEETTTTE-
T ss_dssp
T ss pred
                   -----CEEEEECCCCEEEEECCCCEEEEec----CCCeEEEEecCC----ceEEEEecCCcEEEEEcccCc-
Q ss_pred
                   ceeEEEecc-----ccCCceEEEEEECCCCCEEEEEE
Q Fri_Mar_04_23: 242 PWKKTLLKE-----EKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE 283 (297)
O Consensus
               242 ----d-i-iw-- 283 (297)
               ...+.. ..+..+|+|+|+|+++++.||.|++|+.
266 -----v--l--s-dg--l-sg--dg-v-vw--
T Consensus
               266 -- LVDDLQPDFDGLSDKARKPECTSLAWSADGQTLFAGFSDNLVRVWAV 312 (314)
T 4d6v A
T ss_dssp
                --EEEEECCCCSSCCSSCCCCCEEEEEECTTSSEEEEEETTSCEEEEEE
T ss_pred
                   --eehhhccCccccccccccccccccccccEEEEccCCCCEEEEEec
                            PDB<sup>™</sup>
PROTEIN DATA BANK
No 58
                                                Pub Med
🗌 >4yvd_A Pleiotropic regulator 1; WD40 repeat, mRNA processing, mRNA splicing, structural GENO structural genomics
consortium, SGC, RNA binding protein; 1.70A {Homo sapiens}
Probab=100.00 E-value=1.6e-34 Score=246.87 Aligned cols=244 Identities=23% Similarity=0.317 Sum probs=0.0
Q ss pred
                   CeEecCCcCeeeEEEccCCcEEEEEccCCcceeEEeccCCcceeEEeccCccCEEEEEccCCccEEEE
Q Fri Mar 04 23:
                 2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                        81 (297)
                 2 \  \  \, \text{------}h - - \cdot v - v - - - - - q - \cdot 1 - t - s - d - - v - 1wd - - - - - - - - h - - \cdot v - v - - - - - - 1 - s - s - D - i - i
                                                                                        81 (297)
O Consensus
                ----l-s---d--i-i
T Consensus
                57 YRVISGHLGWVRCIAVEPGNQWFVTGSADRTIKIWDL--ASGKLKLSLTGHISTVRGVIVSTR--SPYLFSCGEDKQVKC
T 4yvd A
                   EEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEET--TTCCEEEEECCCSSCEEEEEECSS--SSEEEEEETTSCEEE
T ss dssp
T ss_pred
                   eEEEcCCCCCEEEEEcCCCCEEEEEcCCCceEEEECCCCceEEEECCCCceEEEECCCCceEEE
                   EECCCCeEEEEEeccCcccEEEEEECCCccccc
Q ss pred
                82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
 Q Fri Mar 04 23:
                                                                                       161 (297)
                Q Consensus
                                                                                       161 (297)
                   133 wd------v----v----
T Consensus
                                                                                       202 (374)
                133 WDLEYNK--VIRHYHGHLSAVYGLDLHPT--IDVLVTCSRDSTARIWDVRTKA--SVHTLSGHTNAVATVRCQAAE----
T 4yvd A
                                                                                       202 (374)
T ss dssp
                   EETTTTE--EEEECCCCSSCEEEEEECSS--SSEEEEEETTSEEEEEETTTCC--EEEEEECCSSCEEEEEECSSS----
T ss pred
                   EECCCCc--eEEEEccccccEEEEECCC--CCEEEEEeCCCcEEEEECCCc--eeEEeCCCCccEEEEEECCCC---
0 ss pred
                   Q Fri_Mar_04_23:
                162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                                       241 (297)
                T Consensus
                                                                                       264 (374)
                203 -----POIITGSHDTTIRLWDLVAG---KTRVTLTNHKKSVRAVVLHPRH---YTFASGSPDN-IKOWKFPDGS-
T 4yvd A
                                                                                       264 (374)
                   -----SEEEEETTSCEEEEETTTT---EEEEEECCCSSCCCEEECTTS---SEEEEECSSC-EEEETTTTE-
 T ss dssp
 T ss pred
                   -----CEEEEECCCeEEEEECCCC---eEEEEecCCCccEEEEEECCCC--CEEEEECCCCc-
Q ss_pred
                   ceeEEEecccCCceEEEEE
```

```
Q Fri_Mar_04_23: 242 PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
O Consensus
              242 ----d--i-iw- 282 (297)
                  ....+.. +...+.++|+|++ +|++++.||.|++|+
T Consensus
              265 -----v---v------l----dg-i-iwd 300 (374)
               265 --FIQNLSG--HNAIINTLTVNSDG-VLVSGADNGTMHLWD
T 4yvd_A
               --EEEEECC--CCSCEEEEEECTTC-EEEEEETTSCEEEEE
T ss_dssp
                  --EEeeccc--CcceeEEEEECCCC-EEEEccCCCeEEEEE
T ss pred
                            PDB"
No 59
                                                    Pub Med
>2hes_X YDR267CP; beta-propeller, WD40 repeat, biosynthetic protein; 1.70A {Saccharomyces cerevisiae}
Probab=100.00 E-value=4.9e-34 Score=238.86 Aligned cols=270 Identities=26% Similarity=0.441 Sum probs=0.0
                  ceEecCCcCeeeEEEEcCCCCEEEEEecCCccEEEEEccCCccceeEEe--ccCCCCEEEEEEcCCCcEEEEEcCCCeE
Q ss_pred
Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTL--TGHEGPVWRVDWAHPKFGTILASCSYDGKV
                                                                                   79 (297)
O Consensus
                2 \  \  \, \hbox{$\sim\sim\sim\sim-h\sim\sim v\sim\sim\sim\sim-l^-s-s-b\sim i$}
                                                                                   79 (297)
                T Consensus
                                                                                   82 (330)
T 2hes X
                7 IKSLKLYKEKIWSFDFSQG--ILATGSTDRKIKLVSVKYDDFTLIDVLDETAHKKAIRSVAWRPH--TSLLAAGSFDSTV
                                                                                   82 (330)
 T ss dssp
                  EEEEECCSSCEEEEEETT--EEEEEESSSCEEEEECSSSCCEEEEECTT--SSEEEEEETTSCE
                  EeeecCCCccEEEEeccCC--eEEEEecCCcEEEEEecCCCeeEeeeeecccCCeEEEEEcCC--CCEEEEecCCCEE
T ss_pred
                  EEEEccCCeE----EEEEEecccCccEEEEEECCccCcEEEEEEccCCc-chhhhhhhhcccceeEEE
Q ss pred
Q Fri_Mar_04_23:
               80 LIWKEENGRW-----SQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGT--TSPIIIDAHAIGVNSAS
                                                                                  152 (297)
               152 (297)
Q Consensus
                     T Consensus
               83 ~~w
                                                                                  160 (330)
               83 SIWAKEESADRTFEMDLLAIIEGHENEVKGVAWSND--GYYLATCSRDKSVWIWETDESGEEYECISVLQEHSQDVKHVI
T 2hes X
                                                                                  160 (330)
T ss dssp
                  EEEEC-----CCCEEEEEC----CEEEEEECTT--SCEEEEEETTSCEEEEEECCTTCCCCEEEEEECCCSSCEEEEE
T ss_pred
                  Q ss_pred
                  Q Fri_Mar_04_23: 153 WAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRS--YLASVSQDRT 230 (297)
Q Consensus
               153 ~~
                    -----h---v--l-tg--d--i--wd------h---v--l--s------las-s-Dg-
                                                                                  230 (297)
                       T Consensus
               161 ~~
                                                          ---v---d--
                                                                                  222 (330)
               161 WHPSE----ALLASSSYDDTVRIWKDYDD--DWECVAVLNGHEGTVWSSDFDKTE---GVFRLCSGSDDST
T 2hes X
T ss_dssp
                  ECSSS-----SEEEEEETTSCEEEEEETT--EEEEEEECCCSSCEEEEECCSS---SSCEEEEETTSC
T ss pred
                  ECCCC------CEEEEEeCCCCEEEEecCCC--CceeeEEeccCCC--CceEEEEEcCCC---CceEEEE
Q ss_pred
                  EEEEEccC----CCCceeEEEecccCCceEEEEECCCCCEEEEEECCCCCEEEeeeccC
Q Fri_Mar_04_23: 231 CIIWTQDN----EQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (297)
O Consensus
              231 i~iw~~~~d~~i~iw~~~~~~~ 297 (297)
              291 (330)
T Consensus
              223 VRVWKYMGDDEDDQQEWVCEAILPDVHKRQVYNVAWGFNG-LIASVGADGVLAVYEEV-DGEWKVFAKRAL 291 (330)
T 2hes X
                  EEEEEEEECTTSCEEEEEEECCSCCSSCEEEEEECTTS-CEEEEEETTSCEEEEEE-TTEEEEEEEESC
T ss dssp
T ss_pred
                  EEEEEecCCccccccceeeeeecCcCCCceEEEEECCCC-eEEEECCCCEEEEEEcc-CCceeeeeeccc
                          PDB<sup>N</sup>
PROTEIN DATA BANK
NCBI
No 60
                                                  Pub Med
>2xyi_A Probable histone-binding protein CAF1; transcription, repressor, phosphoprotein, WD-repeat; HET: PG4;
1.75A (Drosophila melanogaster) PDB: 3c99 A 3c9c A 2yb8 B 2yba A 4r7a B 3gfc A 4pby A 4pbz A 4pc0 A 2xu7
Probab=100.00 E-value=1.5e-35 Score=258.43 Aligned_cols=263 Identities=21% Similarity=0.329 Sum_probs=0.0
Q ss_pred
                  Q Fri Mar 04 23:
                2 VVIANAHNELIHDAVLDY-YGKRLATCSSDKTIKIFEVE-----GETHKLIDTLTGHEGPVWRVDWAHPKFGTILAS
                                                                                   72 (297)
                O Consensus
                                                                                   72 (297)
               121 IEIKINHEGEVNRARYMPQNACVIATKTPSSDVLVFDYTKHPSKPEPSGECQPDLRLRGHQKEGYGLSWNPNL-NGYLLS
T 2xyi A
                                                                                  199 (430)
T ss_dssp
                  EEEEEEESSCCSEEEEETTEEEEEEECSSSCEEEEEGGGSCSSCCTTCCCCCSEEEECCSSCCCCEEECTTS-TTEEEE
T ss pred
                  EEEEecCCCceEEEEecCCCCCEEEEEcCCCccCCcccCCcccCCCccEEEecCCC-CCeEEE
                  ECCCCEEEEEEccC----CeEEEEEEeccCccEEEEEeCCccCcEEEEEEcCCC-cchhhhhhhhccc
Q ss pred
 Q Fri_Mar_04_23:
               73 CSYDGKVLIWKEEN----GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENG-TTSPIIIDAHAI
                                                                                  146 (297)
               73 ~s-D--i-iwd-------v-----v------1----d--i-i-------
                                                                                  146 (297)
Q Consensus
                  |+.|++|++||++|
                   ...dg-i-lwd------h---v--v--v------l-s---dg-i-iwd-------
T Consensus
T 2xyi A
               200 ASDDHTICLWDINATPKEHRVIDAKNIFTGHTAVVEDVAWHLLH-ESLFGSVADDQKLMIWDTRNNNTSKPSHTVDAHTA
                                                                                  278 (430)
T ss_dssp
                  ECTTSCEEEEETTSCCBGGGEEECSEECCCSSCEEEEECSSC-TTEEEEEETTSEEEEEETTCSCSSSCSEEEECCSS
T ss_pred
                  ECCCCCEEEEeCccCCCCceeccceeecCCCCcEeeeEecCCC-CCeEEEecCCCcEEEEECCCCCCCCCEEeeccCC
Q ss_pred
                  ceeEEEECCCcccccccCCccce-EEEEEeCCceEEEEEEcCCCceeEEEEEeccCCcceeEEEE
 Q Fri_Mar_04_23: 147 GVNSASWAPATIEEDGEHNGTKESR-KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASV
                                                                                  225 (297)
Q Consensus
               147 ~v~~~~~h~~v~l~s~~~~las~
                                                                                  225 (297)
               .+.++|+|++ .+|+|+|+...+|+|+|++...+|++|+|++...+|++|
279 -v-l---p-------latg-dg-i-iwd-------h---v-l-sp-----l-s-
T Consensus
                                                                                  340 (430)
               279 EVNCLSFNPYS-----EFILATGSADKTVALWDLRNLKL--KLHSFESHKDEIFQVQWSPHN-ETILASS
T 2xyi A
                                                                                  340 (430)
 T ss_dssp
                  CEEEEECSSC-----TTEEEEEETTSEEEEEETTCTTS---CSEEEECCSSCEEEEECSSC-TTEEEEE
 T ss_pred
                  CeeEEEeCCCC----------------CCEEEEEECCCCCC---CceEEeCCCCCCEEEEEE
```

```
Q ss pred
                  eCCCeEEEEccCCCCee-----EEEecccCCCceEEEEECCCCC-EEEEEcCCCCEEEEEE
Q Fri Mar 04 23: 226 SQDRTCIIWTQDNEQGPWK------KTLLKEEKFPDVLWRASWSLSGN-VLALSGGDNKVTLWKEN
                                                                         284 (297)
O Consensus
              226 s-Dg-i-iw----d--i-iw---
                                                                          284 (297)
               341\ \mathtt{GTD}{RRLHVWDLSKIGEEQSTEDAEDGPPELLFIHGGHTAKISDFSWNPNEPWIICSVSEDNIMQVWQMA}
T 2xyi A
                                                                          409 (430)
T ss_dssp
                  ETTSCCEEEEGGGTTCCCCHHHHHHCCTTEEEECCCCSSCEEEEEECSSSTTEEEEEETTSEEEEEEC
T ss_pred
                  PROTEIN DATA BANK
                                                  Pub Med
>5ams A SOT1, ribosome assembly protein SOT1; chaperone, UL16; 3.35A (Saccharomyces cerevisiae)
Probab=100.00 E-value=9.2e-35 Score=253.41 Aligned cols=247 Identities=13% Similarity=0.132 Sum probs=0.0
Q ss_pred
                  ceEecCCcCeeeEEEEcCCCCEEEEEecCCc-----
Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGET------
                                                                                   42 (297)
O Consensus
                2 ~~~~~h~~~v~~~~~~g~~l~t~s~d~~v~lwd~~~~~
                                                                                   42 (297)
                  +..+.|...|++++|+|+|++++.|+.|++|+++...
-----h---v-----s--g--1-s---dg-i-vwd--------
T Consensus
                                                                           ~dg~i~i 181 (431)
T 5ams A
               102 AGTLTGYGESVISCSFTSEGGFLVTADMSGKVLVHMGQKGGAQWKLASQMQEVEEIVWLKTHPTIARTFAFGATDGSVWC 181 (431)
                  EEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEEEGGGTEEEEEEECCSSCEEEEECSSSTTEEEEEETTCCEEE
T ss_dssp
                  eEEecCcCCCEEEEEccCCCCEEEEEecCCCcEEEEEeccCCCceeEEEeeccCcCcEEEEEecCCCCCEEEEE
T ss pred
                  -----cceeEeecc--CCCCEEEEEec-----CCcCCEEEEEEcCCCeEEEEEec-----ccCccEE
Q ss pred
Q Fri_Mar_04_23:
               43 -----HKLIDTLTG--HEGPVWRVDWA-----HPKFGTILASCSYDGKVLIWKEENGRWSQIAVHA-----VHSASVN
               182 wd-----h---V-------l-s---dg-i--wd------
T Consensus
                                                                                  257 (431)
T 5ams A
               182 YQINEQDGSLEQLMSGFVHQQDCSMGEFINTDKGEN--TLELVTCSLDSTIVAWNCFTGQ--QLFKITQAEIKGLEAPWI
                                                                                  257 (431)
T ss dssp
                  EEECTTTCCEEEEEEECCCSSCEEEEEEESCSSCSS--CCEEEEEETTSCEEEEETTTCC--EEEEECGGGTTTCCCCEE
T ss_pred
                  EEeeCCCCceEEEEeccCCCCceEEEEEecccCCC--CCEEEEEeCCCceEEEEECCCcc--EEEEECCcccCCCCCEE
                  EEEeCC------hcccceeEEEECCCccccccCC
Q ss pred
               104 SVQWAP-----HEYGPLLLVASSDGKVSVVEFKE-NGTTSPIIID------AHAIGVNSASWAPATIEEDGEHNGT
Q Fri Mar 04 23:
                                                                                  167 (297)
 Q Consensus
               104 -----l-----l-----d--i-i------
                           + +.+++++.|+.|++|+++. . ....+.
               T Consensus
                                                                                  323 (431)
               258 SISIAPETITKGN-SGVVACGSNNGLIAVINCNNGG-AILHISTVIELKPEODELDASIESISWSSKF-----
T 5ams A
                                                                                  323 (431)
                  EEEEECTTTTTSC--TTEEEEEETTSEEEEEEGGGTS--EEEEEEESCCCCSSSCGGGCEEEEEETTT-----
T ss dssp
                  EEEECCccccCCC--CCEEEEECCCCeEEEEECCCC--cEEEEEeeeeccccccCCCEEEEEEEcCCC------
T ss_pred
                  Q ss_pred
Q Fri Mar 04 23: 168 KESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSODRTCIIWTODNEOGPWKKTL
                                                                                  247 (297)
               168 -----l-tg--d--i--wd-------h---v--l--s-----las-s-Dg-i-iw-------
O Consensus
                                                                                  247 (297)
                    .+|++|+.|+.|++||+... .+...+ +|...|.+++|+|
                                                          .+|++++.||.|++|++....
               324 ----v----v------
                                                       -----1~~~~dg~i~vwd~~~~~
               324 ---SLMAIGLVCGEILLYDTSAW----RVRHKF-VLEDSVTKLMFDN-----DDLFASCINGKVYOFNARTGO---EKFV
T 5ams A
                                                                                  387 (431)
T ss_dssp
                  ---TEEEEEETTSEEEEETTTT----EEEEEE-ECSSCEEEEEET----TEEEEEETTSCEEEEETTTCC---EEEE
                  ---CEEEEEeCCCcEEEEECCCc----eEEEE-cCCCCEEEEEec-----CEEEEEeCCCc---EeEE
T ss pred
                  ecccCCceEEEEEC-----CCCCEEEEECCCCCEEEEEC
Q ss pred
 Q Fri_Mar_04_23: 248 LKEEKFPDVLWRASWS-----LSGNVLALSGGDNKVTLWKEN 284 (297)
Q Consensus
               248 ~~~~d~i~iw~~~
                                                       284 (297)
                  +.. |...|.+++|+ |++++|++++.||.|++|+..
                                      ----l-s---dg-i-vw---
T Consensus
               388 CVG--HNMGVLDFILLHPVANTGTEQKRKVITAGDEGVSLVFEVP 430 (431)
T 5ams A
T ss_dssp
                  ECC--CSSCEEEEEECCCCCSSCCCCEEEEEETTSCEEEEEC
T ss_pred
                  EeC--CCCccEEEEEeccccccCCCCCEEEEEeCCCeEEEEeCC
                          PDB NCBI Pub Med
>3w15_A Peroxisomal targeting signal 2 receptor; beta-propeller, targeting signal recognition, cytosol; 1.80A
 {Saccharomyces cerevisiae}
Probab=100.00 E-value=5e-35 Score=250.12 Aligned cols=254 Identities=12% Similarity=0.155 Sum probs=0.0
                  CceEecCCcCeeeEEEcc--CCCEEEEEec------CCcEEEEEEccCCccceeEEeccCCcCCEEEE
Q ss pred
Q Fri_Mar_04_23:
                1 MVVIANAHNELIHDAVLDY--YGKRLATCSS-----DKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILAS
                                                                                   72 (297)
Q Consensus
                72 (297)
                  ----v--sp-----
T Consensus
                                                                 ---v--v-sp----las
                                                                                   80 (368)
                {\tt 2~SMLRYHMQGFSGYGVQYSPFFDNRLAVAAGSNFGLVGNGKLFILEIDRSGRIVEVNSFLTQDCLFDLAWNESH-ENQVLV}
                                                                                   80 (368)
T ss_dssp
                  -CEEEECTTEEEEEEECSSCTTEEEEEEEEGGGTSSCEEEEEEECTTCCEEEEEEEESSCEEEEECTTC-TTEEEE
T ss_pred
                  ccceccCCcceEEEECCCCCceEEEEchhcccccCCEEEEEEeCCCCceEEEeeeccCCcceEEEeCCCC-CCEEEE
Q ss_pred
                  ECCCCeEEEEEccCC-eEEEEEeccCccEEEEEeCC-ccCCcEEEEEECCCcchhhhhhhhc-----
 Q Fri_Mar_04_23:
               73 CSYDGKVLIWKEENG-RWSQIAVHAVHSASVNSVQWAP-HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAH-----
                                                                                  144 (297)
Q Consensus
               144 (297)
               T Consensus
                                                                                  154 (368)
               81 AQGDGTLRLFDTTFKEF--PIAIFKEHEREVFSCNWNLVN--RQNFLSSSWDGSIKIWSPLRKQ--SLMTLTPRPLEITK 154 (368)
T 3w15 A
 T ss_dssp
                  EETTSEEEEETTSCSS--CSEEEECCSSCEEEEEECSSS--SSCEEEEETTSCEEEECTTCSS--CSEEECCCCHHHHHH
 T ss_pred
                  EccCcceEEEEccccc--cceeehhccccEEEEEccccc--cceEEEeccccc--ceeeecccccee
```

```
Q ss pred
                          -----ccceeEEEECCCccccccCCccceEEEEEeCCceEEEEEEcCCCceeEEEEEecc-
Q Fri Mar 04 23: 145 -----AIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEG-
                                                                                 202 (297)
O Consensus
               145 -----l-tq~d~i~wd~~~~~~~
                                                                                 202 (297)
                                                    .+|++|+.|+.|++||++.+... ....+.+
-----las-s-D--i-lWd-------
                                  ...|.+++|+|++.
                                    v~~v~fsp~~~-
               155\ \texttt{MVDPLNAIILKKKSFTGISKNRNCVYQAQFSPHDQ-------NLVLSCSGNSYASLFDIRLPSGK--NQNNFLVH}
T 3w15 A
                                                                                 220 (368)
T ss_dssp
                 HSCTTGGGSCC------CCEEEEEECSSCT-----TEEEEEETTSEEEEETTSCTTS-SEEEEECS
T ss_pred
                  Q ss_pred
                 CCCceeEEEECCCCCCCEEEEEECC----CCCCcee-----EEEe-cccCCceEEEEEECC-CCEEE
 Q Fri Mar 04 23:
              203 HSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQD----NEQGPWK-----KTLL-KEEKFPDVLWRASWSLS-GNVLA
                                                                                 270 (297)
O Consensus
              203 h---v-l--s----las-s-Dg-i-iw-----l-
                                                                                 270 (297)
              ----l----h----V---v-fsp--
T Consensus
                                                                            ~~~la 293 (368)
               221 SGLEALTCDFNKYR--PYVVATGGVDNAIRIWDIRMLNKNPG---QLHNSSCINEIPNA--HGLAIRKVTWSPHHSNILM
T 3w15 A
                                                                                 293 (368)
                  TTSCEEEEEECSSC--TTEEEEEETTSCEEEEETTC------CEEEEETTS-SSSCEEEEEECSSCTTEEE
T ss dssp
T ss pred
                 CCcceEEEecCCCC--CCEEEEecCCCcEEEEECCcccCcC---cccccchhhhccCc--cccccceEECCCCCCEEE
Q ss pred
                 EECCCCCEEEE
Q Fri_Mar_04_23: 271 LSGGDNKVTLWK 282 (297)
               271 ~~~~d~~i~iw~
                            282 (297)
                 +++.|++|+|+
              294 s~s~D~~vrlWd 305 (368)
T Consensus
              294 SASYDMTCRIWR
T 3w15 A
                            305 (368)
                 EEETTSCEEEEE
T ss_dssp
T ss_pred
                  EEeCCCEEEEe
                           PDB DATA BANK
No 63
                                    NCBI
                                                  Pub Med
>4zox_A Ribosome assembly protein SQT1; chaperone, ribosomal biogenesis, WD40 - repeat; 1.60A {Saccharomyces
 cerevisiae PDB: 4zov A
Probab=100.00 E-value=1.5e-34 Score=247.03 Aligned cols=258 Identities=15% Similarity=0.181 Sum probs=0.0
Q ss pred
                 \texttt{CceEecCCcCeeeEEEecCCCcEEEEEecCCcceeEEeccCCccceeEEeccCCccCEEEEEecCCccCEEEEEccCCceEE}
Q Fri_Mar_04_23:
                1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                  80 (297)
 Q Consensus
                80 (297)
                 T Consensus
                                                                                  84 (381)
                7 SLTYFDKHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSHSQPPKFAGTLTGYGESVISCSFTSE--GGFLVTADMSGKVL
T 4zox A
                                                                                  84 (381)
                 CSEEECCCSSCEEEEEECSSSSEEEEEETTSCEEEEESSSSSCCEEEEECCCSSCEEEEEECTT--SSEEEEEETTSEEE
 T ss_dssp
 T ss_pred
                  eEEEEecCCCCEEEEEecCCCCeEEEEecCCCceeeeeecccCCceEEEEecCC--CCEEEEEecCCCCEE
Q ss pred
                 EEEccCCeEE-EEEEcccCccEEEEEeCCccCc-EEEEEECCCEEEEEEccCcchhhhhhhh--cccceeEEEECC-
               81 IWKEENGRWS-QIAVHAVHSASVNSVQWAPHEYGP-LLLVASSDGKVSVVEFKENGTTSPIIIDA--HAIGVNSASWAP-
O Fri Mar 04 23:
                                                                                 155 (297)
                                       ----d--i-i-----
O Consensus
                                                                                 155 (297)
                  ------1----g-i-i-----
T Consensus
                                                                                 162 (381)
               55 V.M.GOKGGAOWKLASOMOEVEEIVWLKTHPT--IARTFAFGATDGSVWCYOINEODGSLEOLMSGFVHOODCSMGEFINT
T 4zox A
                                                                                 162 (381)
                 EEEEEGGGTEEEEEECSSCEEEEEECSS--STTEEEEEETTSCEEEEEECTTTCCEEEEEEECCCSSCEEEEEECT
T ss_dssp
                 EEECCCCCcceeccccCCCCeEEEEECCC--CCeEEEEEcCCCcEEEEEecCCCchhhhcccccCCCeEEEEEecc
T ss pred
Q ss_pred
                 Q Fri_Mar_04_23: 156 ----ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE----GHSDWVRDVAWSPTVLLR-----S
                                                                                 220 (297)
                        Q Consensus
              156 ----~
                                                                                 220 (297)
                                .+++++.|+.|++||++.+
                               ----l----d--i---d-----
T 4zox A
               163 DKGENT-----LELVTCSLDSTIVAWNCFTG---OOLFKITOAEIKGLEAPWISLSLAPE--TLTKGNSG
                                                                                 222 (381)
T ss dssp
                 TSCTTC-----CEEEEETTSCEEEETTTT---EEEEEECGGGTTTCCCCEEEEEECCG---GGTTTCTT
T ss_pred
                 EEEEEeCCCeEEEEEccC-CCCceeEEEeccccCC----ceEEEEEECCCCCEEEEE
Q ss pred
Q Fri_Mar_04_23: 221 YLASVSQDRTCIIWTQDN-EQGPWKKTLLKEEKFP----DVLWRASWSLSGNVLALSGGDNKVTLWK
                                                                       282 (297)
               Q Consensus
                                                                       282 (297)
                 223 ~1~~~~dg~i~i~d~~~~~
                                            ----v----s----i----d--i-i-d
                                                                       289 (381)
T Consensus
T 4zox_A
               223 VVACGSNNGLLAVINCNNGGAILHLSTVIELKPEQDELDASIESISWSSKFSLMAIGLVCGEILLYD
                                                                       289 (381)
                  EEEEETTSEEEEEETTTTEEEEEEECCCCCTTSCGGGGCEEEEEETTTTEEEEEETTSEEEEE
 T ss dssp
T ss pred
                  PDB"
                                    NCBI
No 64
                                                   Pub Med
>5a31_R The anaphase-promoting complex chain R; ubiquitination, cell cycle, APC/C; 4.30A {Homo sapiens}
Probab=100.00 E-value=5.6e-35 Score=251.43 Aligned_cols=244 Identities=23% Similarity=0.368 Sum_probs=0.0
                 \tt ceEecCCcCeeeEEEecCCCcEeEEEeccCCcceeEEeccCCcceeEEeccCCcCCEEEEEeccCccCEEEEE
Q ss_pred
                                                                                  81 (297)
 Q Fri Mar 04 23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
Q Consensus
                2 ~~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~~h~~~v~~~~~~~l~s~s~D~~i~i
                                                                                  81 (297)
                 T Consensus
                                                                                 197 (386)
               124 VVHLCDTENEYTSLSWIGAGSHLAVGQANGLVEIYDV--MKRKCIRTLSGHIDRVACLSWN----NHVLTSGSRDHRILH
T 5a31 R
                                                                                 197 (386)
 T ss_dssp
                  EEEEEECSSCEEEEECTTSSEEEEEETTSCEEEET--TTTEEEEEECCCSSCEEEEEE----TTEEEEEESSSCEEE
 T ss_pred
                  EEEEcCCCCCEEEEEccCCCEEEEEecCCCceEEEEcc----CCeeEEEeccCCCceEEEE
```

```
Q ss pred
                                EECCCCEEEEEEecccCccEEEEEECCCccCcEEEEEECCCCcchhhhhhhhcccceeEEEECCCcccc
 Q Fri Mar 04 23:
                            82 WKEENGRWSOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                                                                                                   161 (297)
 O Consensus
                            82 wd-----v----v----v------l-----d-i-i------v------v----
                                                                                                                                                   161 (297)
                           268 (386)
                           198 RDVRMPD-PFFETIESHTQEVCGLKWNVA--DNKLASGGNDNVVHVYEGTSKS--PILTFDEHKAAVKAMAWSPHK----
 T 5a31 R
                                                                                                                                                   268 (386)
 T ss_dssp
                                EETTSSS-SCSEEECCCSSCEEEEECSS-SSEEEEETTSCEEEEETTCSS-CSEEECCCSSCEEEEECSSS----
                                EECCCCc-ceeEEEcCcCCCEEEEEECCC--CCEEEEEeCCCCEEEEEECCCC--EeEEEcccccccEEEEECCCC----
 T ss_pred
                                ccccCccce=EEEEEe--CcceEEEEEEcCCCceeEEEEEeccCCccEEEE--EeCCCeEEEEc
 Q ss_pred
  Q Fri_Mar_04_23:
                           162 GEHNGTKESR-KFVTGG--ADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLAS--VSQDRTCIIWTQ
                                                                                                                                                   236 (297)
 O Consensus
                           236 (297)
                                           . ++++|+ .|+.|++||++.+ .+...+. +...|.+++|+|++ .++++ |+.|+.|++|++
                           269 ------'s-----l1-sq-q-d--i-iwd--------v-----'y-----'s------l----q-d--i-iwd-
 T Consensus
                                                                                                                                                   331 (386)
                           269 -----RGVLATGGGTADRRLKIWNVNTS---IKMSDID-SGSQICNMVWSKNT---NELVTSHGYSKYNLTLWDC
 T 5a31 R
                                                                                                                                                   331 (386)
                                -----TTEEEEEECTTTCEEEEEETTTT----EEEEEEE-CSSCEEEEEECSSS---SCEEEEECTTCCCEEEECS
 T ss dssp
 T ss pred
                                -----CCEEEEeCCCCCEEEEECCCC---CEEEEC-CCCCEEEEEECCCC---CEEEEECCCCCEEEEEC
 Q ss pred
                                ccccceeeeeecccccceeeeeeccccceeeee
                           237 DNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
 Q Fri_Mar_04_23:
                                                                                                   282 (297)
                                      -----i-iw-
 Q Consensus
                           237 ~~~
                                                                                                   282 (297)
                                       ...+.. |...|.+++|+|+|++++.|++|++|+
                           .... ....+.. |...|.++|+|+|++++.|++|++|+
332 ------h---v--l--spdg--l-s---d--i-iw-
 T Consensus
                                                                                                   372 (386)
                           332 NSMD---PIAILKG--HSFRVLHLTLSNDGTTVVSGAGDETLRYWK
 T 5a31 R
                                                                                                   372 (386)
                                SSCC---EEEEECC--CSSCEEEEEECTTSSEEEEEETTTEEEEEE
 T ss_dssp
                                CCCC---EEEEEcC--CCCcEEEEEECCCCCEEEEE
 T ss_pred
                                                 PDB<sup>IM</sup>
PROTEIN DATA BANK
                                                                 NCBI
 No 65
                                                                                            Pub Med
              WD repeat-containing protein 48; UAF1, USP, deubiquitinase, DUB, protein BI; 3.00A {Homo sapiens} PDB:
 Probab=100.00 E-value=3.6e-35 Score=266.00 Aligned_cols=248 Identities=18% Similarity=0.243 Sum_probs=0.0
 Q ss pred
                                EccCcceeeEEEccCccEEEEEccCcccEEEEEccCcc-cceeEEeccCccCEEEEEEccCccCEEEEE
 Q Fri_Mar_04_23:
                              4 IANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGET-HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW
                                                                                                                                                     82 (297)
 Q Consensus
                              \  \, 4 \  \, \sim \sim \sim h \sim \sim v \sim v \sim \sim -q \sim 1 \sim t \sim s \sim d \sim v \sim 1 w d \sim \sim \sim \sim -h \sim \sim v \sim v \sim \sim \sim -1 \sim s \sim s \sim D \sim i \sim i w \sim 1 \sim v \sim 1 \sim v \sim \sim -1 \sim v \sim \sim -1 \sim r \sim 1 \sim s \sim 1 \sim v 
                                                                                                                                                     82 (297)
                                T Consensus
                            40 ----H---V--l--spdg--latg--dg-I-iwd-------h---V--l--s-d--g--l-sgs-Dg-I-vw
                                                                                                                                                   117 (598)
                            40 VEKYNRNGVNALQLDPALNRLFTAGRDSIIRIWSVNOHKODPYIASMEHHTDWVNDIVLCCN--GKTLISASSDTTVKVW
 T 5cvl A
                                                                                                                                                   117 (598)
                                CCCSBSSCEEEEEETTTTEEEEEETTSCEEEEECSSCCSCEEEEECCSSCEEEEEEGG--GTEEEEEETTSCEEEE
 T ss_dssp
                                T ss_pred
 Q ss pred
                                EccCCeEEEEEecccCccEEEEEeCCccCcEEEEEECCCEEEEEEccCcc-----hhhhhhhccceeeEEEECC
                            83 KEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTT-----SPIIIDAHAIGVNSASWAP
 O Fri Mar 04 23:
                                                                                                                                                   155 (297)
                            83 d-----v---
                                                                   -----l----d--i-i------
 O Consensus
                                                                                                                                                   155 (297)
                           T Consensus
                                                                                                                                                   193 (598)
                           118 NAHKGF--CMSTLRTHKDYVKALAYAKD--KELVASAGLDROIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNO
 T 5cvl A
                                                                                                                                                   193 (598)
                                ETTTTE--EEEEECCCSSCEEEEEETT--TTEEEEEETTSCEEEEEHHHHHSCSSSCCCCCEEECCCCSCEEEEECT
 T ss dssp
                                ECCCC--eeeEecCCCceEEEEEcCC--CCEEEEEeCCCeEEEEECCCcccccCCCccceeccCCCCCEEEEEECC
 T ss pred
 Q ss_pred
                                Q Fri_Mar_04_23: 156 ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWT
                                                                                                                                                   235 (297)
                                         -----l-tq--d-i--wd------h---v-l-s----las-s-Dq-i-iw-
 Q Consensus
                           156
                                                                                                                                                   235 (297)
                                                    .++++|+.|+.|++||++... ...+|+||+||++ .+||+|+||+|
                                                   ----l~sg~-dg~l~vwd~~~~---h~~~v~-l~~spdg---~l~sgs~dg~V~lwd
 T 5cvl A
                           194 LG-----TIIVSGSTEKVLRVWDPRTCA---KLMKLKGHTDNVKALLLNRDG--TOCLSGSSDGTIRLWS
                                                                                                                                                   253 (598)
 T ss dssp
                                TS-----SCEEEEETTSSEEEECTTTCC---EEEEECCCSSCEEEEECTTS---SEEEEEETTSEEEEE
 T ss_pred
                                CC-----CEEEEECCCCEEEEecCCCC---eeEEEeCCCCCEEEEEE
                                Q ss pred
 Q Fri_Mar_04_23: 236 QDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
 Q Consensus
                           236 ----d-i-iw- 282 (297)
                                +.... +...|++++|+|+++++|+|++++|
                                    ----h---v--l--s-dg--l-sg--dg-v-vwd 295 (598)
 T Consensus
                           254 LGQQR---CIATYRV--HDEGVWALQVNDAFTHVYSGGRDRKIYCTD
 T 5cvl A
                                                                                                     295 (598)
                                TTTTE---EEEEEC--CSSCEEEEECTTSCEEEEEETTCEEEEEE
 T ss dssp
 T ss pred
                                CCCCc---eeeeec--cccceeeeeccccceeeee
                                                  PDB"
 No 66
                                                                                            Pub Med
🗌 >4gqb_B Methylosome protein 50; TIM barrel, beta-propeller, methyltransferase, methylation, transferase-protein
 binding complex; HET: 0XU; 2.06A {Homo sapiens} PDB: 4x60 B* 4x61 B* 4x63 B*
Probab=100.00 E-value=8.1e-35 Score=246.00 Aligned cols=253 Identities=21% Similarity=0.259 Sum probs=0.0
 Q ss pred
                                Q Fri_Mar_04_23:
                             {\tt 2~VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTL--TGHEGPVWRVDWAHPKFGTILASCSYDGKV}
                                                                                                                                                    79 (297)
                             2 -----h---v------l-s-d--v-lwd-------h---v------l-s-s-D--i
 O Consensus
                                                                                                                                                    79 (297)
                                ~~~v~~~~~-~~l~~~~dg~i
 T Consensus
                                                                                                                                                   151 (344)
 T 4gqb_B
                            75 CSAGVQTEAGVADLTWVGERGILV-ASDSGAVELWELDENETLIVSKFCKYEHDDIVSTVSVLSS--GTQAVSGSKDICI
                                                                                                                                                   151 (344)
 T ss dssp
                                T ss_pred
```

```
Q ss_pred
                  ERRECCCCERREREE.cccCccrrrrerCcccCcc-rrrrrerccccerreree.ccccchhhhhhhhcccceerrerccc-c
Q Fri Mar 04 23:
                                                                                  157 (297)
               80 LIWKEENGRWSOIAVHAVHSASVNSVOWAPHEYGP-LLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPA-T
                        -----d--i-i-----v-----v-----v--
O Consensus
               80 ~iwd~~~
                                                                                  157 (297)
                  ------i----i----i
T Consensus
               152 KVWDLAQOV--VLSSYRAHAAQVTCVAASPH--KDSVFLSCSEDNRILLWDTRCPKPASQIGCSAPGYLPTSLAWHPOOS
T 4gqb_B
                                                                                  227 (344)
                  EEEETTTTE--EEEEECCCSSCEEEEECSS--CTTEEEEEETTSCEEEEETTSSSCEEECC----CCCEEEEEECSSCT
T ss_dssp
                  EEEECCCCe--eeeEecCCCCCEEEEEEecC--CCCEEEEEeCCCcceeEEeeccCCCceeeEEccCCCC
T ss pred
                  Q ss_pred
Q Fri Mar 04 23: 158 IEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQD
                                                                                  237 (297)
               158 -----l-tg--d-i-wd------h--y--l-s-----las-s-Dg-i-iw---
                                                                                  237 (297)
O Consensus
                   .++++++.|+.|++||++......++||...|.+++|+|++...+|+++...||...+|+++...|+|+...+|++...|
T Consensus
                                                                                  288 (344)
               228 -----EVFVFGDENGTVSLVDTKST---SCVLSSAVHSQCVTGLVFSPHS--VPFLASLSEDCSLAVLDSS
T 4gqb_B
                                                                                  288 (344)
T ss_dssp
                  -----TEEEEETTSEEEEESCC-----CCEEEECCSSCEEEEECSSS--SCCEEEETTSCEEECTT
T ss_pred
                  CCCCceeEEEecccCCceEEEEEECCC
Q ss_pred
 Q Fri_Mar_04_23:
               238 NEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLA-LSGGDNKVTLWKENLE 286 (297)
               238 ----d--i-jw----
 Q Consensus
                                                          286 (297)
                  ... ....+...|.+++|+|++++||.|++|+...+
                  ~~~~l~~s~~~dg~i~iw~~~~
T Consensus
                                                           332 (344)
               289 LSE-----LFRSQAHRDFVRDATWSPLNHSLLTTVGWDHQVVHHVVPTE 332 (344)
T 4qqb B
                  CCE----EEEECCCSSCEEEEECSSSTTEEEEEETTSCEEEEECCC-
T ss dssp
                  Ccc----ceEecCCcccEEEEEccCCCCEEEEEeccCC
T ss pred
                          PDB NCBI Pub Med
No 67
>3dwl_C Actin-related protein 2/3 complex subunit 1; propellor, actin-binding, ATP-binding, cytoskeleton, nucleot
binding, WD repeat; HET: ATP; 3.78A {Schizosaccharomyces pombe}
Probab=100.00 E-value=1.1e-36 Score=260.49 Aligned_cols=268 Identities=18% Similarity=0.290 Sum_probs=0.0
Q ss pred
                  CceEecCCcCeeeEEEccCCCEEEEEecCCCcEEEEEccCCccceeEEeccCCCCEEEEEecCCCcCEEEEEccCCCeEE
Q Fri Mar 04 23:
                1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                   80 (297)
                O Consensus
                                                                                   80 (297)
T Consensus
                                                                                   80 (377)
                3 TSQVLHILPKPSYEHAFNSQRTEFVTTTATNQVELYEQDGNGWKHARTFSDHDKIVTCVDWAPK--SNRIVTCSQDRNAY
T 3dwl C
                                                                                   80 (377)
                  CEEEEEECSSCCSCCEECSSSSEEECCCSSSCBCEEEETTEEEECCCBCCCSSCEEEEEECTT--TCCEEEEETTSSEE
T ss_dssp
T ss pred
                  ccecccCCcceEEEEEccccceEEEEeccCcceEEEEeccccccceEEEeccccccceEEEEeccc--cceEEEEeccceEE
                  0 ss pred
Q Fri_Mar_04_23:
               81\ {\tt IWKEENGR-WSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENG-TTSPIIIDA-HAIGVNSASWAPAT}
                                                                                  157 (297)
                81 iwd-----d--i-i------
               158 (377)
T Consensus
                81 VYEKRPDGTWKQTLVLLRLNRAATFVRWSPN--EDKFAVGSGARVISVCYFEQENDWWVSKHLKRPLRSTILSLDWHPNN
T 3dwl C
                                                                                  158 (377)
                  EC-----CCCCEEECCCCSSCEEEEECCTT--SSCCEEEESSSCEEECCC----CCCCEEECSSCCSCEEEEEECTTS
 T ss dssp
                  EEEccCCCcceeeEEeccCCccEEEEECCC--CCEEEEEECCCeEEEEecccCcchhhhhhhcccccCCceEEEEECCCC
 T ss_pred
                  GCCCCCCCCCEEEEEECCCCEEEEEEC.------CCCCeeEEEEEEccCCCCCEEEEEECCCCCCC
Q ss_pred
Q Fri Mar 04 23: 158 IEEDGEHNGTKESRKFVTGGADNLVKIWKYN-----SDAQTYVLESTLEGHSDWVRDVAWSPTVLLR
                                                                                  219 (297)
                  219 (297)
               T Consensus
                                                                                  217 (377)
T 3dwl C
               159 -----TVCAEY-PSGGWVHAVGFSPSG--
                                                                                  217 (377)
                  -----SEEEEEESSCEEEEECCSCC-CCCSCSCCCCE---EEEECC-CCSSEEEEEECTTS---
T ss dssp
                  T ss_pred
Q ss_pred
                  CERERECCCCERERECCCCCC-eerreccccCccererecccCCCERERECCCCCERERECCCCCREREceeccC
Q Fri_Mar_04_23: 220 SYLASVSQDRTCIIWTQDNEQGP-WKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (297)
               Q Consensus
                                                                                 297 (297)
                 .+|++++.|+.|++|++....+ .....+ ....+.. +...|.+++|+|++++|+++ .|+.++|+....+ |....+..
               218 --1----d--i-iwd-----v----v----
T Consensus
               {\tt 218~NALAYAGHDSSVTIAYPSAPEQPPRALITVKL--SQLPLRSLLWANESAIVAAG-YNYSPILLQGNESG-WAHTROLDA}
T 3dwl C
                                                                                 292 (377)
T ss dssp
                  SCREEEETTEEC-CEECSTTSCEEECCCEEC--SSSCEEEEEEETTEEEEEE-SSSSEEEECCCC----CCSBCCCS
                  CEEEEECCCceEEEECCCCcchhhheeecC--CCCceEEEEEcCCCcEEEEE-cCCeEEEEEecCCC-eEEEEEecc
T ss pred
                          PDB NCBI Pub Med
>2j04_B YDR362CP, TAU91; beta propeller, type 2 promoters, transcription, hypothetica protein, preinitiation
complex, yeast RNA polymerase III: 3.2A (Saccharomyces cerevisiae)
Probab=100.00 E-value=4.7e-36 Score=267.98 Aligned_cols=258 Identities=15% Similarity=0.089 Sum_probs=0.0
Q ss pred
                  ceEecCCcCeeeEEEcC-----CCCEEEEEEcCCcceEEEEccCCcc------ceeEeccCCCCEEEEEecCCcc
                2 VVIANAHNELIHDAVLDY-----YGKRLATCSSDKTIKIFEVEGETH-----KLIDTLTGHEGPVWRVDWAHPKF
Q Fri_Mar_04_23:
                                                                                   66 (297)
Q Consensus
                2 -----h---v------h---v-----h---v---
                                                                                   66 (297)
                  +..+.+|...|++++|+|
                                  ++++|++++.|++|++||+.....
                                                              +.+..+.+|...|++++|++
               200 ---1--h---V--1---p------1-s-s-dg-v-iwd------
T Consensus
                                                                  ----h---v---
 T 2j04 B
               200 VQTIVHSFGEVWDLKWHEGCHAPHLVGCLSFVSQEGTINFLEIIDNATDVHVFKMCEKPSLTLSLADSLITTFDFLS---
T ss dssp
                  ERRERECCCSEREERECSSCCCSSSSCEERERETTSCERERECCCCSSSSSERECCCSCSERECCTTTCREERERSS---
T ss_pred
                  EEEEEecCCceeeeEECcCCCCCCCEEEEEecCCcEEEEEecCCcccceeEeccceEEEECCCcceEEEEecC---
```

```
CCEEEEECCCCeEEEEEccCCeEEEEE-EeccCcccEEEEEECCcc-CcEEEEEECCCCEEEEEE
Q ss pred
               67 GTILASCSYDGKVLIWKEENGRWSQIA-VHAVHSASVNSVQWAPHEY-GPLLLVASSDGKVSVVEFKENGTTSPIIIDAH
                                                                                144 (297)
O Fri Mar 04 23:
               144 (297)
                 277 ---l-sg--dg-i-iwd------h---v------l-s-s-d--i--wd------
T Consensus
                                                                                352 (524)
              277 PTTVVCGFKNGFVAEFDLTDPE--VPSFYDQVHDSYILSVSTAYSDFEDTVVSTVAVDGYFYIFNPKDI--ATTKTTVSR
T 2j04 B
                                                                                352 (524)
                 SSEEEEETTSEEEEETTBCS--SCSEEEECSSSCEEEEEECCTTSCCEEEEEETTSEEEECGGGH--HHHCEEEEE
T ss dssp
                 T ss pred
                 Q ss_pred
O Fri Mar 04 23: 145 AI--GVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAOTYVLESTLEGHSDWVRDVAWSPTVLLRSYL
                                                                                222 (297)
              Q Consensus
                                                                                222 (297)
                               .+|++|+.|+.|++||++.+. +...+.+|...|.+++|+|++
              353 ----v-v-sp-g-----1-s---d-v-iwd------h---v--v-sp------1
                                                                                412 (524)
T Consensus
T 2j04 B
              353 FRGSNLVPVVYCPOI------YSYIYSDGASSLRAVPSRAAF---AVHPLVSRETTITAIGVSRLH---PMV
                                                                                412 (524)
T ss_dssp
                 CSCCSCCCEEEETTT----TEEEEECSSSEEEEETTCTT----CCEEEEECSSCEEEEECCSSC---CBC
                 ecccccceEEcccc----ceeEeccccc---cceeEeccccc---ccee
T ss pred
                 EEEeCCCeEEEEEccCCCCceeEEEeccc-----
Q ss pred
                                                                    --cCCceEEEEEC
Q Fri_Mar_04_23: 223 ASVSQDRTCIIWTQDNEQGPWKKTLLKEE-----KFPDVLWRASWS
                                                                                263 (297)
              223 as~s~Dg~i~iw~~~~~~~~~~~~
Q Consensus
                                                                      ~~~~ i ~~~~~
                                                                                263 (297)
                 ++|+.||.|++|++........
                                                                     . | . . . | ++++ | +
              492 (524)
T Consensus
                                                                      -h---V--v--s
              413 LAGSADGSLIITNAARRLLHGIKNSSATQKSLRLWKWDYSIKDDKYRIDSSYEVYPLTVNDVSKAKIDAHGINITCTKWN
T 2j04 B
                                                                                492 (524)
T ss_dssp
                 EEEETTTEEECCBSCSSTTTCC-----CCCCEEEECBCCSSSCEEEECCCCCCC------CCCSCCCEEEC
T ss_pred
                 EEEeCCCEEEEEecchhhhccccCCcccceEEEEEEEcCCCCcceEeccCccccCCCCcceeEcCccceEEEEEeC
Q ss_pred
                 CC---CCEEEEEcCCCCEEEEECCC
Q Fri_Mar_04_23: 264 LS---GNVLALSGGDNKVTLWKENLE 286 (297)
              264 ~~----d~~i~iw~~~~
Q Consensus
                                       286 (297)
                 |+ |++|++|+.||.|+||+...+
              493 p---g--lasg--dg-vrl-----
                                       518 (524)
T Consensus
T 2j04 B
              493 ETSAGGKCYAFSNSAGLLTLEYLSLE 518 (524)
                 CSTTTTTEEEEECTTSEEEEECSCC
T ss_dssp
                 CCCCCceEEEecCCcc
T ss pred
                   SCOPe PROTEIN DATA BANK
No 69
                                                          Pub Med
>1k8k_C P40, ARP2/3 complex 41 kDa subunit, P41-ARC; beta-propeller, structural protein; 2.00A {Bos taurus} SCOP:
b.69.4.1 PDB: 1tyq C* 1u2v C* 2p9i C* 2p9k C* 2p9l C 2p9n C* 2p9p C* 2p9s C* 2p9u C* 3ukr C* 3dxm C*
3rse C* 3uku C* 3ule C* 4jd2 C*
Probab=100.00 E-value=6.8e-35 Score=248.53 Aligned cols=256 Identities=16% Similarity=0.137 Sum probs=0.0
Q ss_pred
                 \tt ceEecCCcCeeeEEEecCCCcEeEEEeccCCcceeEEeccCCccceeEEeccCCcCCEEEEEeccCCccCEEEEEccCCceEEE
Q Fri_Mar_04_23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                 81 (297)
                2 -----h---v----q--l-t-s-d--v-lwd------h---v-----l-s-s-D--i-i
Q Consensus
                                                                                 81 (297)
                 122 (372)
T Consensus
               45 VHELKEHNGQVTGVDWAPDSNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPN--EKKFAVGSGSRVISI
T 1k8k_C
                                                                                122 (372)
                 EEEEECCSSCEEEEEETTTEEEEEETTSCEEEEEEETTEEEEEECCCCSSCEEEEEECTT--SSEEEEEETTSSEEE
T ss_dssp
                 T ss pred
Q ss_pred
                 EECCCCeE--EEEEEecccCccEEEEEECCccCcEEEEEECC------CCcchhhhhhhh
               82 WKEENGRW--SQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKE-----NGTTSPIIIDA
Q Fri Mar 04 23:
                                                                                143 (297)
 O Consensus
               143 (297)
                 ||++....|...|...|.+++|+|+ +..++++.|+.+++||+..
              123
                  T Consensus
                                                                                200 (372)
              123 CYFEQENDWWVCKHIKKPIRSTVLSLDWHPN--SVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMFESSS
T 1k8k C
                                                                                200 (372)
                 EEEETTTEEEEEEECTTCCSCEEEEEECTT--SSEEEEEETTSCEEEEECCCTTTSCCCCCBTTBSCCCTTCEEEECCC
T ss dssp
                 T ss pred
                 Q ss pred
Q Fri Mar 04 23:
              144 HAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLA
                                                                                223 (297)
                 {\scriptstyle \text{----}} v {\scriptstyle \text{----}} v {\scriptstyle \text{----}} v {\scriptstyle \text{----}} v {\scriptstyle \text{-----}} v {\scriptstyle \text{------}} v {\scriptstyle \text{------}} v {\scriptstyle \text{-------}} u {\scriptstyle \text{-------}} u
                                                                                223 (297)
Q Consensus
                          T Consensus
              201
                  ~~~~~~~
                                                               260 (372)
              201 SCGWVHGVCFSANG-----SRVAWVSHDSTVCLADADKKM---AVATLASETLPLLAVTFITES---SLVA
T 1k8k C
                                                                                260 (372)
                 CSSCEEEEECSSS-----SEEEEEETTTEEEEEEGGGTT----EEEEEECSSCCEEEEEEETT---EEE
T ss dssp
                 CCCceEEEECCCC-----CEEEEEcCCceEEEECCCc---eEEEEecCCCCeeEEEECCCC---CEEE
T ss pred
Q ss_pred
                 Q Fri Mar 04 23: 224 SVSQDRTCIIWTQDNEQGPW--------KKTLLKEEKFPDVLWRASWSL-- 264 (297)
              224 s~s~Dg~i~iw~~~~~~
Q Consensus
                                                                                264 (297)
                 ++ . | + . | ++ | ++ . . . . . .
              261 ---d-i-i----g------h---v--
T 1k8k C
              261 AG-HDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERFQNLDKKASSEGSAAAGAGLDSLHKNSVSQISVLSGGK
                                                                                339 (372)
                 EE-TTSSCEEEEETTTTEEEECCCCCC-----CHHHHHHHHCCCCC------CCCSSSSSSCEEEEEEESTT
T ss_dssp
                 Ee-cCCeEEEEecCCCCeEEEeEecCccccccccCCCCccCceeEecCCcchhhhhhccccCCcceeEEecCcC
T ss pred
                 -CCCEEEEEcCCCCEEEEE
Q ss pred
 Q Fri_Mar_04_23: 265 -SGNVLALSGGDNKVTLWK 282 (297)
```

```
Q Consensus
              265 ----l----d--i-iw- 282 (297)
                 ++++|++++.||.|++|+
              340 ~~~~l~s~s~Dg~i~iW~ 358 (372)
T Consensus
              340 AKCSQFCTTGMDGGMSIWD 358 (372)
T 1k8k C
T ss dssp
                 TSCSEEEEETTSEEEEE
                 CceeEEEeecCCCcEEEEe
T ss pred
                           PDB'
                                                PubMed
No 70
                                           NCBI
                  processing protein 9; beta-propeller, WD domain, RNA binding protein, preribosome; 2.50-
>4j0x A Ribosomal RNA
 {Saccharomyces cerevisiae}
Probab=100.00 E-value=1.2e-35 Score=259.88 Aligned cols=265 Identities=14% Similarity=0.155 Sum probs=0.0
                 CceEccCccceeEEEEccCccEEEEEccCccceeEEec--ccccceEEEEccCccc
Q ss_pred
Q Fri Mar 04 23:
               1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLT--GHEGPVWRVDWAHPKFGTILASCSYDGK
                                                                               78 (297)
O Consensus
               78 (297)
              T Consensus
                                                                               181 (451)
              106 YENTTEGHYDEILTVAASPDGKYVVTGGRDRKLIVWST--ESLSPVKVIPTKDRRGEVLSLAFRKN--SDQLYASCADFK
T 4i0x A
                                                                               181 (451)
 T ss dssp
                 eeEEeccCCccEEEEECCCCCEEEEEcCCCceEEEEC--CCCeEEEEEecCCCCCccEEEEEEccC--CCEEEEEECCCE
T ss_pred
                 EEEEEccCCeEEEEEecccCccEEEEEecCccCcEEEEEEccCccchhhh------
Q ss pred
Q Fri_Mar_04_23:
               79 VLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPII------ 140 (297)
               Q Consensus
                 T Consensus
              182 i~ywd~~~~~d~~i~jwd~~~~~~
                                                                               257 (451)
              182 IRTYSINOFS--QLEILYGHHDIVEDISALAM--ERCVTVGARDRTAMLWKIPDETRLTFRGGDEPQKLLRRWMKENAKE 257 (451)
T 4i0x A
T ss_dssp
                 EEEEETTTTE--EEEEEECCSSCCEEECCSS-SEEEEECBTTCEEEEEEGGGTEEEEECCCCHHHHHHHHTTC----
T ss_pred
                 EEEEECCCCc--EEEEECCCCCeEEEEEeCC--CCEEEEECCCCeEEEEECCCCceeeeeCCCCcceeEEE
                 -----hhhccceeEEEECCCccccccCCCcceEEEEEECCCceeEEEEE
Q ss_pred
Q Fri_Mar_04_23: 141 ------IDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTL---- 200 (297)
Q Consensus
              141 -----v~~~v~~~~v
                                        -----l-tg--d--i--wd------
                                                                         ~---- 200 (297)
                                                .++++|+.|+.|++||++... ++.
----~l~~~~dg~i~iwd~~~~~
T Consensus
              258 -----
              258 GEDGEVKYPDESEAPLFFCEGSIDVVSMVDD------FHFITGSDNGNICLWSLAKKK---PIFTERIAHG 319 (451)
T 4j0x_A
T ss_dssp
                 -----TEEEEETTSCEEEEETTCSS---CSEETTTTC
T ss pred
                 cCCccEEEecCccccCCCCcEEEEEeCCC------CEEEEEeCCCEEEEEECCCC----eeeEEeccCc
Q ss_pred
                                -----cccccceeEEEccccccceEEEEeccceEEEEccccccc
Q Fri Mar 04 23: 201 -----EGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKF 253 (297)
O Consensus
              201 -----las-s-Dg-i-iw-----------
                                                                               253 (297)
                                     .+|...|.+++|+|++ .+|++++.||.|++|++.....+ ..+....|
                                        ---v---s----l-s---dg-v-iw--------
                                                                           ~~h 395 (451)
T Consensus
              320 ILPEPSFNDISGETDEELRKRQLQGKKLLQPFWITSLYAIPYS---NVFISGSWSGSLKVWKISDNLRSF-ELLGELSGA
T 4j0x A
                 BC-----CCCBCCCCEEECTTB--SEEEEECSSSCEEEEECTTSSCE-EEEEETTC
T ss dssp
                 eeccCcceEEEccCcEEEEEEccCccccCCcceEEEEEeccC---CEEEEEEeCCCeEEEEEECCC
T ss_pred
Q ss_pred
                 CceEEEEECCCC-----CEEEEECCCCCEEEEeecc
 Q Fri Mar 04 23: 254 PDVLWRASWSLSG-----NVLALSGGDNKVTLWKENLEGKWEPAGEV 295 (297)
              T Consensus
              396 ~~~v~~~
                                                       444 (451)
              396 KGVVTKIQVVESGKHGKEKFRILASIAKEHRLGRWIANVSGARNGIYSA 444 (451)
T 4j0x_A
                 CSEEEEEEEC-----CEEEEEEEESSCTTCCCCSCCTTCCCEEEEE
T ss_dssp
T ss pred
                 CCcEEEEECCCCcccccccEEEEecCCCEEEEE
                           PDB'
No 71
                                                 Pub Med
       \overline{
m U4/U6} small nuclear ribonucleoprotein PRP4; snRNP, GTPase, U5 snRNA, PRP8, spliceosom snRNP, BRR2,
transcription; HET: GTP; 3.60A {Saccharomyces cerevisiae} PDB: 5gap H
Probab=100.00 E-value=2.9e-35 Score=259.20 Aligned_cols=249 Identities=22% Similarity=0.314 Sum_probs=0.0
                 Q ss pred
 Q Fri Mar 04 23:
               2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLT-GHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                80 (297)
               Q Consensus
                                                                                80 (297)
                   T Consensus
              168
                                                                               244 (465)
              168 AGSQLVSTKPISAVSLSTDDMVVATGSWAGDLQVLNS--QTLQPLTQKLDSHVGKIGAIDWHPDS-NNQMISCAEDGLIK
T 5gan_H
                                                                               244 (465)
T ss dssp
                 EEEEECCSSCCCEEEECSSSSEEEEEETTTEEEEEET--TTCCBCCCCTTSCSSCEEEEECCSSS-SCEEEEETTSCEE
T ss pred
                 cccccCCCceeEEEECCCCceEEEEeCCCCEEEEEC--CcCceeeEEecCCCCeEEEEEecCC-CCEEEEEeCCCEEE
0 ss pred
                 EEEccCC----eEEEEEEeccCccEEEEEECCCcCEEEEEECCCcchhhhhhhhhcccceeEEEECCC
Q Fri_Mar_04_23:
               81 IWKEENG----RWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPA
                                                                               156 (297)
               +||+...+ . ....+..|..|.+++||+| +..+++++.|+.|++||+... .....+..|...+..+++||+||+
              T Consensus
                                                                               318 (465)
              245 NFQYSNEEGGLR--LLGDLVGHERRISDVKYHPS--GKFIGSASHDMTWRLWDASTH--OELLLOEGHDKGVFSLSFQCD
T 5gan H
                                                                               318 (465)
                 EEEECSSSCSEE--EEEEECCCSSCEEEEEETT--TTEEEEEESSSCEEEEETTTT--EECCCCCCSSCEEECCBCTT
 T ss dssp
 T ss pred
                 EEECCCCCcce--eeeeccCCCCeeEEEECCC--CCEEEEECCCCcEEEEECCCC--eEEEEecCCCCCEEEEEECCC
Q ss_pred
```

```
Q Fri_Mar_04_23: 157 TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQ 236 (297)
 O Consensus
                     157 -----h---v--l--tg--d--i--wd------h---v--l--s-----las-s-Dg-i-iw--
                                                                                                                     236 (297)
                     ~~v~~~~sp~q---~l~t~s~dg~v~iwd~
 T Consensus
                                                                                                                     378 (465)
                     319 G-----SLVCSGGMDSLSMLWDIRSG---SKVMTLAGHSKPIYTVAWSPNG---YQVATGGGDGIINVWDI
 T 5gan_H
                                                                                                                     378 (465)
                         S-----SEEEEEETTSCBEEEETTTT----EECCBCSSCSSCCCEEEEETTT---TEEEEECSSSEEEEECC
 T ss_dssp
                         C-----CEEEEECCCCCEEEEECCCC---ceeEEeccCCCcEEEEEECCCC---CEEEEECCCCeEEEEEC
 T ss pred
                         ccccceeEEEeccccccceEEEEEccc--cceEEEE
 Q ss pred
 Q Fri_Mar_04_23:
                     237 DNEQGPWKKTLLKEEKFPDVLWRASWSLS--GNVLALSGGDNKVTLWK
                     237 ----d-i-iw-
                         +..... +... | .+++ | + | + +++ | ++++ . | | . | ++ | ++
                     379 -----q--1-s-s-dq-v-vwd
                                                                                 423 (465)
 T Consensus
 T 5gan H
                     379 RKRDEGQLNQILA---HRNIVTQVRFSKEDGGKKLVSCGYDNLINVYS
                                                                                 423 (465)
 T ss_dssp
                         SCTTCCCSEEEC---CSSCEEEECCTTTSCCEEEEEESSSEEEEE
 T ss_pred
                          CCCCccceeccC---CCCcEEEEEEccCCCCCEEEEEe
                                        PDB"
                                                                Pub Med
 No 72
               damage-binding protein 2; beta barrel, double helix, DDB1:WD40 beta-barrel fold, DNA D DNA repair,
 HOST-virus interactions; HET: DNA 3DR; 2.85A {Homo sapiens} PDB: 4e5z _B* 3ei4 _B*
 Probab=100.00 E-value=5.5e-36 Score=261.37 Aligned_cols=254 Identities=13% Similarity=0.157 Sum_probs=0.0
                         Q ss pred
 Q Fri_Mar_04_23:
                       1 MVVIANAHNELIHDAVLDYYG-KRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKV
                       79 (297)
                          111 \ -----h--v--s-q--1-sq-dq-v-vwd------h--v--s-d----1-s--d--v
 T Consensus
                                                                                                                     189 (435)
                     111 ILQKAAPFDRRATSLAWHPTHPSTVAVGSKGGDIMLWNFGIKDKPTFIKGIGAGGSITGLKFNPLN-TNQFYASSMEGTT
 T 4e54 B
                                                                                                                     189 (435)
 T ss dssp
                         SCCEEECSSCEEEEECSSCTTCEEEEETTSCEEEECSSCCSCCEEECCSSSCCCCEEECSSC-TTEEEEECSSSCE
 T ss_pred
                          {\tt EEEEccCCeEEEEEecccCccEEEEEecCcccCeEEEEEecCCcceEEEEEecCCccchhhhhhhhhccceeeEEEECCCccc}
 Q ss pred
 Q Fri Mar 04 23:
                      80 LIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIE
                                                                                                                     159 (297)
 Q Consensus
                      80 -iwd-----d--i-i------
                                                                                                                     159 (297)
                         ++||++++...+....+....+...+.++|+|+ +.++++++.|+.|++|++...
 T Consensus
                     262 (435)
 T 4e54 B
                     190 RLODFKGNILRVFASSDTINTWFCSLDVSAS--SRMVVTGDNVGNVILLNMDGK---ELWNLRMHKKKVTHVALNPCC--
                                                                                                                     262 (435)
 T ss dssp
                         EEEETTSCEEEEECCSSCSCCCCCEEEETT--TTEEEEECSSSBEEEEESSSC---BCCCSBCCSSCEEEEECTTC--
                          EEEECCCCceeeeccCCcccceEEEEEcCC--CCEEEEEcCCCeEEEEeCCCc---eEEEeecCCCCEEEEEEcCCC-
 T ss pred
 Q ss_pred
                         Q Fri Mar 04 23: 160 EDGEHNGTKESR-KFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSODRTCIIWTODN
                                                                                                                     238 (297)
                     160 ------latq-d-i-wd------h--v-l-s---las-s-Dq-i-iw----
 O Consensus
                                                                                                                     238 (297)
                                     . +|++|+.|+.|++||++......+. |...|.+++|+|++ .+|++++.|+.|++||+..
                                  -----l~s~~~d~~i~iwd~~~~~~
                                                                                     -s--g----l----d--i-iwd---
                     263 -----DWFLATASVDOTVKIWDLROVRGKASFLYSLP-HRHPVNAACFSPDG--ARIJTTDOKSETRVYSASO
 T 4e54 B
                                                                                                                     327 (435)
 T ss_dssp
                         -----SEEEEEETTSBCCEEETTTCCSSSCCSBCCB-CSSCEEECCBCTTS---SEEEEEESSSCEEEEESSS
 T ss pred
                          -----CCEEEEEeCCCcEEEEEccCCCCCceeEecc-CCCcEEEEECCCC---CEEEEEeCCCCEEEEECCC
                         CCCceeEEEecccCCceEE-----EEEECCCCCEEEEEc-----CCCCEEEEE
 Q ss pred
 Q Fri_Mar_04_23: 239 EQGPWKKTLLKEEKFPDVLW-----RASWSLSGNVLALSG------GDNKVTLWK 282 (297)
 Q Consensus
                     239 ----d-i-iw-
                                                                                                282 (297)
                                                   +++|+|++++|++++
                                                                                    .||.|+||+
                          .. ....+.. +...+.
                                                          -sp----1------t---d--i-iwd 384 (435)
 T Consensus
                     328 WD---CPLGLIP--HPHRHFQHLTPIKAAWHPRYNLIVVGRYPDPNFKSCTPYELRTIDVFD
 T 4e54 B
                                                                                                384 (435)
 T ss_dssp
                         SS---SEEECC--CCCCCSSSCCCBCEECSSSSCEEECCCCTTSCCSSTTCCCCEEEC
 T ss_pred
                         CC---Cccccc--CCcccccccccccccCCCCCEEEEeccCCcccccccCCCCCC
                                       PROTEIN DATA BANK
PROTEIN DATA BANK
PROTEIN DATA BANK
🗌 >3mkq_A Coatomer beta'-subunit; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
 cerevisiae PDB: 2ynp A
 Probab=100.00 E-value=5.8e-35 Score=273.81 Aligned cols=248 Identities=17% Similarity=0.253 Sum probs=0.0
                          Q ss pred
 Q Fri_Mar_04_23:
                       1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                      80 (297)
 O Consensus
                       1 ~~~~~h~~~v~~~~~g~l~t~s~d~~v~lwd~~~~~~h~~~v~~~~h~~~v~~~~l~s~s~b~~i~
                                                                                                                      80 (297)
                         T Consensus
 T 3mkq A
                       5 IKKTFSNRSDRVKGIDFHPTEPWVLTTLYSGRVEIWNY--ETQVEVRSIQVTETPVRAGKFIAR--KNWIIVGSDDFRIR
                                                                                                                      80 (814)
 T ss dssp
                         CEEEEEECSCEEEEECSSSSEEEEETTSEEEEET-TTTEEEEEEECCSSCEEEEEEGG-GTEEEEEETTSEEE
 T ss_pred
                         CCREE-CCCCCREERERCCCCCREERER-CCCCREERERC--CCCC--REFERCCCCCREERER-CC--CCREERERCCCCCREE
 Q ss_pred
                         \tt EEEccCCeEEEEEeccCcccEEEEEecCCccCcEEEEEECCCCcehhhhhhhhccceeEEEECC-Ccccentrate to the contract of the contra
 Q Fri_Mar_04_23:
                      81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAP-ATIE
                                                                                                                     159 (297)
 Q Consensus
                      159 (297)
                      T Consensus
                                                                                                                     153 (814)
                      81 VFNYNTGE--KVVDFEAHPDYIRSIAVHPT--KPYVLSGSDDLTVKLWNWENN-WALEQTFEGHEHFVMCVAFNPKDP--
 T 3mkg A
                                                                                                                     153 (814)
 T ss_dssp
                          EEETTTCC--EEEEEECCSSCEEEEECSS--SSEEEEEETTSEEEEEEGGGT-SEEEEEEECCSSCEEEEEETTEE--
 T ss_pred
                          EEECCCCc-EEEEEeCCCCCEEEEEEeCC-CCEEEEEECCCC-cEEEEEEcCCCccEEEEEEeCCCC-
```

```
Q ss pred
                  CCCCCCCCCEEEEEECCCCeEEEEEEcCCCCeeEEEEEccCC-CCEEEEEECC--CCCCCCEEEEEE
Q Fri_Mar_04_23: 160 EDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHS-DWVRDVAWSP--TVLLRSYLASVSODRTCIIWTO
                                                                                  236 (297)
               160 -----l-tq--d-i-wd------h---v-l-s-s--pq-i-iw--
O Consensus
                                                                                  236 (297)
               154 -----STFASGCLDRTVKVWSLGQST----PNFTLTTGQERGVNYVDYYPLPDK---PYMITASDDLTIKIWDY
T 3mkq A
                                                                                  215 (814)
T ss_dssp
                  -----EEEEEEETTSEEEEETTCSS----CSEEEECCCTTCCCEEEECCSTTC---CEEEEECTTSEEEEEET
                  -----CEEEEECCCEEEEECCCC----cceEEeCCCCCEEEEEECCCC---CEEEEECCCCEEEEEC
T ss_pred
                  ccccceeeeeecccccceeeeeeccccceeeee
Q ss_pred
                                                       282 (297)
 Q Fri_Mar_04_23: 237 DNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
O Consensus
               237 ----d-i-iw-
                                                       282 (297)
                  .... +...|.+++|+|+|+++++.||.|++|+
T Consensus
               216 QTKS---CVATLEG--HMSNVSFAVFHPTLPIIISGSEDGTLKIWN
T 3mkq_A
                  TTTE---EEEEEEC--CSSCEEEEEECSSSSEEEEEETTSCEEEEE
T ss dssp
T ss pred
                  CCCe---EEEEEeC--CCCCeEEEEEeCCCCEEEEEE
                            PDB"
                                    NCBI Pub Med
>4aez_A CDC20, WD repeat-containing protein SLP1; cell cycle, KEN-BOX, D-BOX, APC/C; 2.30A {Schizosaccharomyces
pombel
Probab=100.00 E-value=1.2e-34 Score=250.60 Aligned cols=246 Identities=19% Similarity=0.346 Sum probs=0.0
                  eEecCCcCeeeEEEccCCccEEEEEccCCccceeEEeccCCccceeEEeccCCccCEEEEE
Q ss pred
 Q Fri Mar 04 23:
                {\tt 3~VIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW}
                                                                                   82 (297)
O Consensus
                3 ----h---v-----q--l-t-s-d--v-lwd------h---v-----l-s-s-D--i-iw
                                                                                   82 (297)
                  T Consensus
               128 LAETDESTYVASVKWSHDGSFLSVGLGNGLVDIYDV--ESQTKLRTMAGHQARVGCLSWN----RHVLSSGSRSGAIHHH
T 4aez A
                                                                                  201 (401)
T ss dssp
                  EEECCTTCCEEEEEECTTSSEEEEEETTSCEEEEET--TTCCEEEEEECCCSSCEEEEEE----TTEEEEEETTSEEEEE
T ss pred
                  EEecCCCCcEEEEEcCCCCEEEEEcCCCCEEEEEC--CCCeEeeEccCCCCEEEEEC----CCEEEEEcCCCCEEEE
Q ss pred
                  {\tt EccCCeEEEEEeccCccEEEEEECCCccEEEEEEECCCcceeEEEEEECCCccchhhhhhhhhcccceeEEEECCCcccccc}
               83 KEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDG
Q Fri_Mar_04_23:
                                                                                  162 (297)
 Q Consensus
               162 (297)
               T Consensus
                                                                                  272 (401)
T 4aez A
                                                                                  272 (401)
                  ETTSSS-CEEEEECCSSCEEEEECTT--SSEEEEEETTSCEEEEETTCSS--EEEEECCCSSCCCEEECTTST----
 T ss_dssp
                  ECCCCC-ccEEEECCCCCCEEEEEECCC--CCEEEEEECCCCeEEEEECCCCc--eeEEecCCccceEEEEECCCCC----
 T ss_pred
Q ss pred
                  CCCCCCCEEEE--EeCCCeEEEEEcCCCCceeEEEEEccCCCceEEEE--EeCCCEEEE--EeCCCeEEEEccC
               163 EHNGTKESRKFVT--GGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLAS--VSQDRTCIIWTQDN
O Fri Mar 04 23:
                                                                                  238 (297)
                     -----l-t--g--d--i--wd-------h----v--l--s-----las---s-Dg-i-iw--
                                                                                  238 (297)
O Consensus
                        -----ll-s--gs-d--i-iwd-------v--l--s----l----g--d--i-vw----
T Consensus
                                                                                  336 (401)
               273 ------NLLATGGGTMDKOIHFWNAATGA----RVNTVD-AGSQVTSLIWSPHS---KEIMSTHGFPDNNLSIWSYSS
T 4aez A
                                                                                  336 (401)
                  -----TEEEEECCTTTCEEEEEETTTCC---EEEEEE-CSSCEEEEEECSSS--SEEEEEECTTTCEEEEEEEET
T ss dssp
                  -----CEEEEeccCCCCeEEEEECCCCC---EeEEEe-CCCCEEEEEECCCC---CEEEEEecCCCCeEEEEECCCC
T ss pred
Q ss_pred
                  CCCceeEEEecccCCceEEEEECCCCCEEEEE
Q Fri_Mar_04_23: 239 EQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK
                                                      282 (297)
                                        ~~~l~~~~d~~i~iw~
                                                      282 (297)
Q Consensus
                  ~~~~i~~~~i
                  337 SG---LTKQVDIPAHDTRVLYSALSPDGRILSTAASDENLKFWR 377 (401)
T 4aez A
T ss dssp
                  TE---EEEEEEECCSSCCCEEEECTTSSEEEEECTTSEEEEE
                  CC---ceeeeecCCCcceeeee
T ss pred
                           PDB<sup>IN</sup>
PROTEIN DATA BANK
No 75
                                    NCBI
                                                   Pub Med
                                             >2hes X YDR267CP; beta-propeller, WD40 repeat, biosynthetic protein; 1.70A (Saccharomyces cerevisiae)
Probab=100.00 E-value=3.6e-34 Score=239.70 Aligned cols=258 Identities=27% Similarity=0.415 Sum probs=0.0
                  ceEe--cCCcCeeeEEEccCCcEEEEEccCCcceEEEEccCCcc----ceeEEeccCCcCEEEEEc
Q ss pred
Q Fri_Mar_04_23:
                2 VVIA--NAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETH-----KLIDTLTGHEGPVWRVDWAHPKFGTILASCS
                                                                                   74 (297)
Q Consensus
                2 -----h---v------g--l-t-s-d--v-lwd------h---v--h---v------l-s-s
                                                                                   74 (297)
                  -----l----dg-i--w-------
T Consensus
T 2hes X
                49 IDVLDETAHKKAIRSVAWRPHTSLLAAGSFDSTVSIWAKEESADRTFEMDLLAIIEGHENEVKGVAWSND--GYYLATCS
                                                                                  126 (330)
T ss_dssp
                  EEEECTTCCCSCEEEEECTTSSEEEEEETTSCEEEEEC-----CCCEEEEEC----CEEEEEECTT-SCEEEEE
T ss_pred
                  Q ss_pred
                  CCCeEEEEccCC----eEEEEEecccCccEEEEEeCCCCCEEEEEECCCCcchhhhhhhhhcccceeE
 Q Fri_Mar_04_23:
               75 YDGKVLIWKEENG----RWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNS
                                                                                  150 (297)
               Q Consensus
                                                                                  150 (297)
               T Consensus
                                                                                  202 (330)
               127 RDKSVWIWETDESGEEYE--CISVLQEHSQDVKHVIWHPS--EALLASSSYDDTVRIWKDYDDDWECVAVLNGHEGTVWS
T 2hes X
                                                                                  202 (330)
 T ss_dssp
                  TTSCEEEEECCTTCCCCE--EEEEECCCSSCEEEEECSS--SSEEEEEETTSCEEEEEEETTEEEEEEECCCSSCEEE
 T ss_pred
                  CCCeEEEEECCCCCcee--eeeccccCCceEEEECCC--CCEEEEEeCCCCCEEEEeccCCCCceeeEEecccCCCEEE
```

```
Q ss pred
                          EEECCCcccccccCCcce--EEEEEeCCceEEEEEcc----CCceeEEEEEec-cCCCCEEEE
 Q Fri Mar 04 23: 151 ASWAPATIEEDGEHNGTKESR--KFVTGGADNLVKIWKYNS----DAQTYVLESTLE-GHSDWVRDVAWSPTVLLRSYLA
                                                                                                                        223 (297)
                      O Consensus
                                                                                                                        223 (297)
                                               203 ~~
                                                                                                                        265 (330)
                      203 SDFDKTE-----GVFRLCSGSDDSTVRVWKYMGDDEDDQQEWVCEAILPDVHKRQVYNVAWGFN----GLIA
 T 2hes X
                                                                                                                        265 (330)
 T ss_dssp
                          EEECCSS-----SCEEEEEETTSCEEEEEECTTSCEEEEEECCSCCSCEEEEEECTT----SCEE
 T ss_pred
                          eEEcCCC-----CGEEEEEcCCCCEEEEEEcCCCcccccccceeeeecCcCCCccEEEEEECCC----CeEE
                          EEeCCCeEEEEEccCCCCceeEEEeccccC-ceEEEEEECC--CCCEEEEEECC
 Q ss_pred
 Q Fri_Mar_04_23: 224 SVSQDRTCIIWTQDNEQGPWKKTLLKEEKFP-DVLWRASWSL--SGNVLALSGGDNKVTLWKEN 284 (297)
 O Consensus
                     224 s-s-Dg-i-iw----d--i-iw---
                                                                                                     284 (297)
                          +++.||.|++|++...... +. ..|.+++|+| ++++|++++.||.|++|+...
                      266 ----v-dg-i-v-d------v----v
 T Consensus
                                                                              ----l----dg-i-iw---
                                                                                                     327 (330)
                      266 SVGADGVLAVYEEVDGEWKVFAKRALC--HGVYEINVVKWLELNGKTILATGGDDGIVNFWSLE 327 (330)
 T 2hes X
                          EEETTSCEEEEEETTEEEEEEESCT--TTTSCEEEEEEC-----CCEEEEETTSEEEEEEC-
 T ss dssp
 T ss pred
                          EECCCCEEEEECCCCceeeeeecccc--cCcceeeEEecccCCcEEEEEccCCCEEEEEecc
                                       POTEN DATA BANK
PROTEIN DATA BANK
PROTEIN DATA BANK
PUBLICATION
PU
 No 76
🗌 >5cvo_A WD repeat-containing protein 48; WDR48, WD repeat, beta propeller, USP46, covalent DUB, deubiquitinase,
 hydrolase-protein binding complex; 3.89A {Homo sapiens}
 Probab=100.00 E-value=7.3e-35 Score=266.34 Aligned_cols=248 Identities=18% Similarity=0.240 Sum probs=0.0
 Q ss_pred
                          EecCCcCeeeEEEEcCCCCEEEEEEcCCCc-cceeEEeccCCcCEEEEEccCCcCCEEEEE
 Q Fri Mar 04 23:
                       4 IANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGET-HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIW
                                                                                                                         82 (297)
 O Consensus
                        4 ----h---v------q--l-t-s-d--v-lwd------h---v-----h---v-----l-s-s-D--i-iw
                                                                                                                         82 (297)
                          T Consensus
                       25 VEKYNRNGVNALQLDPALNRLFTAGRDSIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCN--GKTLISASSDTTVKVW
 T 5cvo A
                                                                                                                        102 (677)
 T ss dssp
                          {\tt CCCSBSSCEEEEEETTTEEEEEETTSCEEEEECSSCCSCCEEEEECCSSCEEEEEECST--TCCEEEEETTSCEEEE}
 T ss pred
                          cccccCeEEEEEcCCCEEEEEcCCCeEEEEEcCCCCcceEEEEecCCCCCeEEEEEcCC--CCEEEEEECCCeEEEE
 Q ss pred
                          EccCCeEEEEEeccCcccEEEEEECCCccCcEEEEEECCCcc-----hhhhhhhccceeEEEECC
 Q Fri_Mar_04_23:
                       83 KEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTT-----SPIIIDAHAIGVNSASWAP
                                                                                                                        155 (297)
 Q Consensus
                       83 d~~~~
                                     155 (297)
                      T Consensus
                                                                                                                        178 (677)
                      103 NAHKGF--CMSTLRTHKDYVKALAYAKD--KELVASAGLDROIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNO
 T 5cvo A
                                                                                                                        178 (677)
                          ETTTTE--EEEEECCCSSCCCEEEEETT--TTEEEEECTTSCEEEEEHHHHHCSCCSSCCCCCEEECCCCSCEEEEECT
 T ss_dssp
                           ECCCCe--EeEEECCCCCcEEEEEEeCC--CCEEEEEECCCCEEEEEECCCCcccccCCCccceeeeeCCCCCEEEEEECC
 T ss_pred
 Q ss pred
                          Q Fri Mar 04 23: 156 ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWT
                                                                                                                        235 (297)
                               O Consensus
                      156
                                                                                                                        235 (297)
                                          .++++|+.|+.|++||++.. ....++|+...|..++|+|++ .+|++++.||.|++||
                      179 dg------Lasgs-dg-I-iwD--t------l--h---V--l--spdg----L-sgs-Dg-I-iwd
179 LG------TIIVSGSTEKVLRVWDPRTC---AKLMKLKGHTDNVKALLLNRDG---TOCLSGSSDGTIRLWS
 T Consensus
                                                                                                                        238 (677)
 T 5cvo A
                                                                                                                        238 (677)
                          TS------SEEEEETTSSEEEETTTT----EEEEEECCCSSCEEEEECTTS---SEEEEEETTSEEEEE
 T ss dssp
                          T ss pred
 Q ss_pred
                          ccCCCceeEEEecccCCceEEEEECCCCCEEEEE
 Q Fri_Mar_04_23: 236 QDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                                                               ~1~~~~d~~i~iw~
                                                                                  282 (297)
 Q Consensus
                      236
                          ~~~~i~~~
                          +.... +...|++++|+|++++|+|++++|
                      239 -----i----h---V--l--spdg--l-sgs-dg-V-vwd 280 (677)
                      239 LGQQR---CIATYRV--HDEGVWALQVNDAFTHVYSGGRDRKIYCTD 280 (677)
 T 5cvo A
 T ss dssp
                          TTTTE---EEEEEC--CSSCEEEEECTTSCEEEEETTCEEEEE
                          CCCCc---EEEEEec--CCCCEEEEEECCCCCEEEEEE
 T ss pred
                                       PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
 No 77
                                                                  Pub Med
->5cxb_A Ribosome biogenesis protein YTM1; ribosome assembly, WD40, beta-propeller, ubiquitin-like DOMA protein
 binding; 2.10A {Chaetomium thermophilum} PDB: 5cyk A 5cxc A
 Probab=100.00 E-value=9.5e-35 Score=258.95 Aligned_cols=250 Identities=18% Similarity=0.217 Sum_probs=0.0
                          GERGCCCCCeeeEEEEc-----CCCCEEEEEeCCCCGEEEEEccCCGGGGeeEEec------CCCCCE
 Q ss pred
 Q Fri_Mar_04_23:
                        2 VVIANAHNELIHDAVLD-----GHEGPV
                                                                                                                         56 (297)
                        2 -----h---v------h---v------h---v
                                                                                                                         56 (297)
 O Consensus
                                                                   |+|++|++|+.|++|++||+
                      123 -----H----V---v---s-------s-d----l-s-s-dg-v-iwd---------
 T 5cxb A
                      123 YEASFEHDDWVSAVDVLSATSPAGRWSSAANSSAAVOPGOERVLSASYDGLLRIWNA---SGSVIATSPSGSHGGHTASI
 T ss_dssp
                          EEEEEECSSCEEEEEECTTSHHHHHHHTCSSSCCCCTTCCEEEEEETTSCEEEEET---TSCEEEECCCGGGTSCSSCE
 T ss_pred
                          ccccccCceeeeEeecccccccccccccCCCCEEEEEeCCCCCEEEEEEC---CCCEEEeecCCcCCCCCcce
 Q ss pred
                          EEEEecCCccCCEEEEEcCCCeEEEEEccc-----CeEEEEEEecccCccEEEEEEECCCCEEEEEEE
                       57 WRVDWAHPKFGTILASCSYDGKVLIWKEEN-----GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFK 131 (297)
 Q Fri_Mar_04_23:
                       O Consensus
                                                                                                                        131 (297)
                          .+++|++ +..|++++|++||++| ++.....+..|..|.+++|+| +..++++++.|+.|++|++.
                      274 (514)
 T Consensus
                      200 KAAKFLT---SDRLASAGMDRTVRVWKYTESDHFTGELKPTLELYGHTGSVDWLDVDGH--SKHILTASADGAIGFWSAS 274 (514)
 T 5cxb_A
 T ss dssp
                           EEEEEEE---TTEEEEEETTSEEEEEEEESSSSCEEEEEEEECCSSCEEEEEETT--TTEEEEEETTSCEEEEECS
 T ss_pred
                          EEEEEeC---CCeEEEEecCCceceeEEEecCCcccceeEEEEecCc--CCEEEEEcCCccEEEEECC
```

```
Q ss_pred
                           C-----CCcchbbbbbbcccceeEEEECCCcccccCCccceEEE_EEeCCceE
 Q Fri Mar 04 23: 132 E-----NGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFV-TGGADNLV
                                                                                                                           182 (297)
 O Consensus
                      132 ~----
                                                                            ~~v~
                                                                                                        ----l--ta--d--i
                                                                                                                          182 (297)
                                                  .....+..|...|.+++|+|++
                      275 ~~~
                               T Consensus
                                                                                                       --~~l~~s~s~d~~i
 T 5cxb A
                      275 KASAPEPDASLLPGAHVSKRRKATSSVSTAQRGPLGLWSIHTAPATAAIFDPRD------RTVAYSASQDHTV
                                                                                                                           341 (514)
                           TTTCCCCCGGGSTTCCCC-----CEEECCSEEECCCSSCEEEEECSSC-----TTEEEEEETTSEE
 T ss_dssp
                           T ss pred
 Q ss_pred EEEEEccCCceeEEEEEcccCCceeEEEEEccCCcceeEEEEcccCCcceEE
Q Fri_Mar_04_23: 183 KIWKYNSDAQTYVLESTLEGHSDWVRDVAWSP----TVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLW 258 (297)
                      183 --wd------h---v--l--s-----las-s-Dg-i-iw-------i-
                                                                                                                           258 (297)
 O Consensus
                          T Consensus
                      342 RTLDLTTGQ----VVSTLT-LTHPLLSLSALTRAGTTS---PLLAAGTSAHIITMVDPRASSATTSVMTLRG--HANKVV 411 (514)
 T 5cxb A
 T ss_dssp
                           EEEETTTCC---EEEEEE-CSSCEEEEEECCTTCSS---CEEEEEETTSCEEEECSSSCSSCC-CEEECC--CSSCEE
 T ss_pred
                           EEEECCCCc---EEEEEe-cCCceeEEEEccCCCCC---CEEEEECCCCCeEEEEEcC--CCCcEE
                           EEEECCCCE-EEEEcCCCCEEEEE
 Q ss_pred
 Q Fri_Mar_04_23: 259 RASWSLSGNV-LALSGGDNKVTLWK 282 (297)
                      259 ~~~~~l~~~~d~~i~iw~ 282 (297)
 Q Consensus
                          +++|+|++++ |++++.||.|++|+
                      412 ~l~~sp~~~~ll~s~s~Dg~v~iwd 436 (514)
 T Consensus
                      412 SLSPSPENEYSLVSGSHDGTCRVWD 436 (514)
 T 5cxb A
                           EEEECSSCSSEEEEEETTSCEEEEE
 T ss dssp
                           EEEEccccceeeee
 T ss pred
                                       PDB™
PROTEIN DATA BANK

NCBI
 No 78
                                                                             Pub Med
>1r5m_A SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A
 {Saccharomyces cerevisiae}
 Probab=100.00 E-value=2.4e-34 Score=249.39 Aligned cols=254 Identities=17% Similarity=0.225 Sum probs=0.0
 Q ss pred
                           CceEecCCcCeeeEEEccCCcEEEEEccCCcceeEEeccCCccceeEEeccCCccCEEEEEccCCccEEEEEccCCccEE
 Q Fri Mar 04 23:
                        1 \ \texttt{MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL}
                                                                                                                            80 (297)
 O Consensus
                        1 \  \  \, \hbox{$-\sim----}h - - \cdot v - v - - \cdot - \cdot g - \cdot 1 - t - s - d - \cdot v - 1 w d - - \cdot - \cdot - h - - \cdot v - v - - \cdot - - \cdot 1 - s - s - D - \cdot i - 1 - s - s - d - v - 1 - s - s - d - v - 1 - s - s - d - v - 1 - s - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 - s - d - v - 1 
                                                                                                                            80 (297)
                      T Consensus
                                                                                                                           174 (425)
                      100 LSASSGKTTNQVTCLAWSHDGNSIVTGVENGELRLWNK---TGALLNVLNFHRAPIVSVKWNKD--GTHIISMDVENVTI
 T 1r5m A
                                                                                                                          174 (425)
                           CC-----CBCEEEEECTTSSEEEEEETTSCEEEEET---TSCEEEEECCCCSCEEEEEECTT--SSEEEEEETTCCEE
 T ss_dssp
 T ss pred
                           hhhhhhccCCCeEEEEcCCCCEEEEEcCCCCEEEEEcC---CCCeEEEecCCCCCEEEEEccC--CCEEEEEcCCCeEE
 Q ss pred
                           EEEccCCeEEEEE.----eccCCcEEEEE
 Q Fri_Mar_04_23:
                       81 IWKEENGRWSOIAV-----HAVHSASVNSVO
                                                                                                                           106 (297)
                           +||++++.....
                      175 iwd-----g-i---d------
                                                                                                                           254 (425)
 T Consensus
                      175 LWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFVYQITEKTPTGKLIGHHGPISVLE
 T 1r5m A
                                                                                                                           254 (425)
                           EEETTTTEEEEEECCC-----CCCBSCCEEEETTEEEEECGGCEEEETTCSSCSEEECCCSSCEEEE
 T ss dssp
                           EEECCCCceeeeecccCccceeecccCCccEEEEEcCCCcEEEEEcCCCcEEeeeccCCCceeEEE
 T ss pred
                           eCCccCCcEEEEEECCCEEEEEEecCCCcchhhhhhhhccceeEEEECCCccccccccCCccceEEEEEECCceEEEEE
 Q ss_pred
 Q Fri Mar 04 23: 107 WAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWK
                                                                                                                          186 (297)
                      +.++++++|+.|+.|++||+....
 T Consensus
                      255 ~~
                              -----l----dg-i-i-d------v----v----
                                                                                                -----1~~~~d~~i~i~d 316 (425)
 T 1r5m A
                      255 FNDT--NKIJIJSASDDGTLRTWHGGNGN--SONCFYGHSOSTVSASWVGDD------KVTSCSMDGSVRLWS
                                                                                                                          316 (425)
                           EETT--TTEEEEEETTSCEEEECSSSBS--CSEEECCCSSCEEEEEETTT------EEEEEETTSEEEEE
 T ss dssp
                           ECCC--CCEEEEEeCCCEEEEEECCCc--ccchhcccceEEEEEEcCCC------eEEEEeCCCcEEEEE
 T ss_pred
 Q ss_pred
                           ECCCCceeEEEEEeccCCCCEEEEEECCCCCCCEEEEEEcCCCCCCC
 Q Fri_Mar_04_23: 187 YNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG------PWKKTLLK
                                                                                                                           249 (297)
                      Q Consensus
                                                                                                                           249 (297)
                                .++..+..|...|.+++|+|++ .+|++++.||.|++|+++....
                                  T Consensus
                      317 ~~~~
                      {\tt 317~LKQN----TLLALSIVDGVPIFAGRISQDG---QKYAVAFMDGQVNVYDLKKLNSKSRSLYGNRDGILNPLPIPLYASYQ}
 T 1r5m A
                                                                                                                          389 (425)
 T ss dssp
                           TTTT----EEEEEECTTCCEEEEEECTTS---SEEEEEETTSCEEEEECHHHHC------CEECCEEEEEC
                           T ss_pred
                           CCCCCEEEEECCCCCEEEEECC
 Q ss pred
 Q Fri_Mar_04_23: 250 EEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
 O Consensus
                      284 (297)
                           ...+...|.+++|+|+|++++.||.|++|+.+
-----v---s-dg-l----dg-v-i----
 T Consensus
                      390 SSQDNDYIFDLSWNCAGNKISVAYSLQEGSVVAIP 424 (425)
 T 1r5m A
                           CTTCCCCEEEEECTTSSEEEEEESSSCCEEEECC
 T ss_dssp
 T ss_pred
                           ccccCCceeEEEEccCCceEEEEeccC
                                          PDB
                                                      NCBI
 No 79
                                                                            Pub Med
->4zoy_A SQT1; chaperone, ribosome biogenesis, WD40-repeat; 1.50A {Chaetomium thermophilum} PDB: 4zn4 _A 4zoz_A
 Probab=100.00 E-value=7.7e-34 Score=250.40 Aligned_cols=253 Identities=18% Similarity=0.278 Sum_probs=0.0
```

```
Q ss_pred
                Q Fri_Mar_04_23: 1 MVVIANAHNELIHDAVLDYY-GKRLATCSSDK-----TIKIFEVEGETH------KLIDT
                                                                         48 (297)
              1 ~~~~~h~~~v~~~~~q~~l~t~s~d~~~~~v~lwd~~
O Consensus
                                                                         48 (297)
               .+..+.+|.+.|++++|+|+ +++|+.|+ .|++|+|+
              84 (491)
              7 SIAYFDGHKDSVFAIAQHPLYPNIVATGGSEGDADDAPGKGYVLDI--SAAAGRPVLPPSYNSDPSSAPQQNTSLNPIFE
                                                                         84 (491)
T 4zoy A
                T ss_dssp
                T ss pred
                eccCCCCEEEEEec-CCccCCEEEEEccCCeeEEEEEccCCe-----
Q ss_pred
Q Fri Mar 04 23:
             49 LTGHEGPVWRVDWA-HPKFGTILASCSYDGKVLIWKEENGR------
                                                                         88 (297)
             49 ~~~h~~~v~~~~~~l~s~s~D~i~iwd~~~~~
O Consensus
                                                                         88 (297)
              T Consensus
                                                                        162 (491)
              85 IDGHTDSINALTFTLPR--GDFLVSGGMDGRMRVYAVSVPQNGALAQFKFLAESQETEEINWFAPCPSPDHPNTIALGAS
T 4zoy A
T ss dssp
                ECCCSSCEEEEECTTT--CCEEEEEETTCCEEEEEECCTTTTCCEEEEEEECSSSCEEEEECCCTTSTTEEEEEET
                ECCCCCEEEEEecCC--CCEEEEEcCCCCeEEEEEccCCCCcceeeEeeccCCCccceeeccCCCCCCCEEEEEeC
T ss_pred
                   -----EEEEEEecccCccEEEEEeCCccCcEEEEEEECCCEEEEEE
Q ss_pred
Q Fri Mar 04 23:
             89 -----KENGTTSPII
                                                                        140 (297)
             89 -----land
Q Consensus
                                                                        140 (297)
                       .....+..|...|.+++|+|+ +.+|++++.|+.|++|++
                                        ----l-s---dg-i-iwd-----
             163 dg~v~i~d~~
T Consensus
                                                                        240 (491)
                                  ~~~v~~~~
             163 DGSVWVFTLDASDPSNPVQIVQSYFLHTGPCTAGAWSPD--GLLLATVSEDESLHVYDVFGVAASKSLVTDNGQTVVSLT
T 4zoy A
                                                                        240 (491)
                TSCEEEEECC----CCEEEEEEECCCSSCEEEEECTT-SSEEEEEETTSCEEEEETTSHHHHTTCCCTTSSEEEEEC
T ss dssp
                CCeEEEEEccCCCcceeEeeeccCCcceeEEEecCC--CCEEEEEecCCccceeeccCCCcceEEEee
T ss pred
               hhh----ccceeEEEECCCccccccCCcceEEEEEEeCcceEEEEE
Q ss pred
Q Fri Mar_04_23: 141 IDA----HAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKY--------
             T Consensus
                                                                        307 (491)
             241 NVDQRFAVEGGLFSVAVSPTG-----AVVAVGGAGGQIKIVGLPRLSQPQQPQSQSQSRTGKAPAGRAGRPS 307 (491)
T 4zoy A
                TTCTTTCCTTCEEEEEECTTS-----SEEEEEEGGGCEEEEECCCC-----
T ss dssp
                T ss pred
                -----cCCCceeEEEEEeccCCCcEeEEEECCCCCCCEEEEEeCCCeEEEEEccCCCCceeEEEeccCCCceeEEE
Q ss_pred
Q Fri_Mar_04_23: 188 -----NSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPD-VLW 258 (297)
                   O Consensus
                         T Consensus
             308 -----
             308 OOOOTTSHOAGT----ILASLOIOSDNIESLAFSPSA---PILAAGSTDGSIAVFDTSRSF---ALRRHLRGAHAEDPVV 377 (491)
T 4zoy A
               -----CTTC---EEEEECCSSSCEEEEECSSS--SEEEEEETTSCEEEEETTTTT--EEEEEETTTTTTSCEE
T ss dssp
T ss pred
                ccccccccce----EeeeccCCCcceEEEECCCC---CeEEEEcCCcEEEEEeCCCc---eeeeEecCCccCceeE
Q ss_pred
               EEEECC-----CCCEEEEEcCCCCEEEEE
Q Fri_Mar_04_23: 259 RASWSL-----SGNVLALSGGDNKVTLWK 282 (297)
             259 ~~~~d~i~iw~
Q Consensus
                                      282 (297)
                T Consensus
             378 KVEFVKSPPNAAMAGWLLTSCGMDGVVRRWD
T 4zoy A
                                      408 (491)
T ss dssp
                EEEECSSCSSGGGTTTEEEEEETTSCEEEE
                EEEecccccCCCCCEEEEE
T ss_pred
                       PDB"
PROTEIN DATA BANK

NCBI
                                       Pub Med
>3k26_A Polycomb protein EED; WD40, structural genomics, NPPSFA, national project on prote structural and
functional analysis, structural genomics CON SGC; HET: M3L; 1.58A {Homo sapiens} PDB: 3jzn_A* 3k27_A* 3jpx_A* 3jzg
3jzh_A* 3iiw_A* 4x3e_A* 3ijc_A* 3ijv_A* 3ij0_A* 3ij1_A* 2qxv_A
Probab=100.00 E-value=2.1e-34 Score=244.71 Aligned_cols=248 Identities=18% Similarity=0.232 Sum_probs=0.0
Q ss_pred
                CCcCeeeEEEEcCCC----CEEEEEeCCCcEEEEEccCCcceeEEEeccCCCCEEEEEecC-CccCCEEEEEccCCCeEEE
Q Fri_Mar_04_23:
                                                                         81 (297)
              7 AHNELIHDAVLDYYG----KRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAH-PKFGTILASCSYDGKVLI
              81 (297)
Q Consensus
               T Consensus
             67 DADENFYTCAWTYDSNTSHDLLAVAGSRGIIRIIND--ITMOCIKHYVGHGNAINELKEHPRD--PNLLISVSKDHALRI.
T 3k26 A
                                                                        142 (366)
               CTTCCEEEEEEECTTTCCEEEEEEETTCEEEEECT--TTCCEEEEEECSCC--TTEEEEEEETTSCEEE
T ss dssp
                ccCcceeeeecCcccceeeeecCccceeeecccceeeecccceeeecccceeeecccceee
T ss pred
Q ss_pred
                EECCCCEEEEEEe---cccCccEEEEEeCCccCcEEEEEECCCcchhhhhhhh------
Q Fri_Mar_04_23:
             82 WKEENGRWSQIAVH---AVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA----- 143 (297)
O Consensus
             143 wd-----
T Consensus
                                                                        216 (366)
             143 WNIQTDT--LVAIFGGVEGHRDEVLSADYDLL--GEKIMSCGMDHSLKLWRINSK--RMMNAIKESYDYNPNKTNRPFIS 216 (366)
T 3k26 A
T ss_dssp
                EETTTTE--EEEECSTTSCSSCEEEEECTT--SSEEEEEETTSCEEEEESCSH--HHHHHHHHHTCCGGGCSSCCCC
                T ss_pred
                -----ccceeEEEECCCccccccccCCcceEEEEEeCCceEEEEEE
Q ss pred
Q Fri_Mar_04_23: 144 ------HAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQ------TYVLESTL 200 (297)
                                                                        200 (297)
             144 -----v~~~v~~~~~v~~~~~~1~tg~~d~~i~~wd~~~~~~~~~~
```

```
.++++++.|+.|++||++....
T Consensus
               217 ~~~~~~~
                               ~~~v~~~
                                     281 (366)
               217 OKIHFPDFSTRDIHRNYVDCVRWLG------DLILSKSCENAIVCWKPGKMEDDIDKIKPSESNVTILGRF
T 3k26 A
                                                                                     281 (366)
                  EEECCCSEEECSSCSSCCCEEEET-----TEEEEECSSSEEEEEEESSTTCCGGGCCTTCCCEEEEEE
T ss dssp
 T ss_pred
                  eeeccCcccccccceEEEEecC------CEEEEEcCCCCEEEEEcccccccccCCccceeeecc
                  GCCCCGEEFFFFCCC--CCCCCFFFFFECCCCEEFFFCCCCC-CceeFFFECCCCCGEFFFFFECCCCCCFFFFFCCCCCC
Q ss pred
Q Fri_Mar_04_23: 201 EGHSDWVRDVAWSPT--VLLRSYLASVSQDRTCIIWTQDNEQ-GPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNK
                                                                                     277 (297)
               277 (297)
Q Consensus
                   ..|...|.+++|+|+ + .+|++++.||.|++|+++...
T Consensus
               282 ~~
                     ---v----s-----i----dg-i-vwd------dg
                                                                                     358 (366)
               282 DYSOCDIWYMRESMDEWO---KMIALGNOVGKLYVWDLEVEDPHKAKCTTLTHHKCGAALROTSESRDSSILIAVCDDAS
T 3k26 A
                                                                                     358 (366)
                  ECSSCCSSCCCEECTTS---SEEEEECTTSCEEEEECCSSSGGGCEEEEECCTTCCSCEEEEEECTTSSEEEEEETTSE
T ss dssp
T ss pred
                  CCCcCceEEEEEccCCCC---CEEEEEcCCCCeEEEEecCCCccceeEEeecccCCcEEEEEECCCC
                  EEEEE
Q ss pred
Q Fri_Mar_04_23: 278 VTLWK 282 (297)
               278 i~iw~ 282 (297)
Q Consensus
                   |++|+
               359 i~iw~
T Consensus
T 3k26_A
               359 IWRWD
                        363 (366)
T ss_dssp
                  EFFE
T ss_pred
                  EEEec
                             PDB
                                     NCBI
                                                     Pub Med
S3sfz_A APAF-1, apoptotic peptidase activating factor 1; apoptosis, caspase activation, cytochrome C,
procaspase-9, A nucleotide, cytosol; HET: ADP; 3.00A {Mus musculus} PDB: 3shf _A* 3j2t _A*
Probab=100.00 E-value=2.8e-34 Score=280.09 Aligned_cols=249 Identities=20% Similarity=0.376 Sum_probs=0.0
                  CceEccCccceeEEEccCccEEEEEccCccceEEEEccCccceeEEcccCccceEEEccCcccCEEEEEccCcccEE
Q Fri Mar 04 23:
                 1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                      80 (297)
                 1 -----h---v----q--1-t-s-d--v-1wd------h---v-
Q Consensus
                                                                     ~~~~~l~s~s~D~~i~
                                                                                      80 (297)
                  -----h---V----fs-dg--las-s-d--i-lwd------l--h---V--v-fspd--g--las-s-d--v-
T Consensus
                                                                                     682 (1249)
T 3sfz A
               607 SRLVVRPHTDAVYHACFSQDGQRIASCGADKTLQVFKA--ETGEKLLDIKAHEDEVLCCAFSSD--DSYIATCSADKKVK
                                                                                     682 (1249)
T ss_dssp
                  CSEEECCCSSCEEEEECTTSSEEEEETTSCEEEEET--TTCCEEEEECCCSSCEEEEECTT--SSEEEEEETTSEEE
T ss_pred
                  EEEccCCeEEEEEeccCccceEEEEEeCCccCcEEEEEECCCcchhhhhhhhccceeeEEEECCCccc
Q ss_pred
Q Fri_Mar_04_23:
                81 IWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEE
                                                                                     160 (297)
O Consensus
                160 (297)
               T Consensus
                                                                                     755 (1249)
               683 IWDSATGK--LVHTYDEHSEQVNCCHFTNKSNHLLLATGSNDFFLKLWDLNQKE--CRNTMFGHTNSVNHCRFSPDD---
T 3sfz A
                                                                                     755 (1249)
                  EEETTTCC--EEEEEECCSSCEEEEEECSSSSCCEEEEEETTSCEEEEETTSSS--EEEEECCCSSCEEEEEECSST---
T ss_dssp
T ss_pred
                  EEECCCCe--EEEEECCCCcEEEEEEECCCCeEEEEEccCCc--eEEEeecCCCcEEEEEECCCC---
                  ccccCCccceEEEEEeCCceeEEEEEec-----
Q ss pred
Q Fri_Mar_04_23:
               161 DGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTL-----
                  -----l-tg--d--i--wd-----
 Q Consensus
               161
                                                                                     200 (297)
                         .++++|+.|++||++.+ ....+
                                                                 ---v----s-dq--l---
T Consensus
               756 -----l~s~s~dq~v~vwd~~~~~
                                                                                     821 (1249)
               756 -----ELLASCSADGTLRLWDVRSA----NERKSINVKRFFLSSEDPPEDVEVIVKCCSWSADGDKIIVAAKNKV
T 3sfz A
                                                                                     821 (1249)
 T ss dssp
                  -----TEEEEEESSSEEEEEGGGT---EEEEEEECCCC-----CCCCCBCCCCBCTTSSEEEEEETTEE
T ss_pred
                   Q ss pred
O Fri Mar 04 23:
               201 -----EGHSDWVRDVAWSPTVLLRSYLASVSODRTCIIWTODNEOGPWKKTLLKEEKFPDVLWRASWSLS
                                                                                     265 (297)
               201 -----h---v--l--s-----las-s-Dg-i-iw--------
O Consensus
                                                                                     265 (297)
                              .+|...|.+++|+|++ .+++++.|+.|++|+.....
               T Consensus
                                                                                     893 (1249)
               822 LLFDIHTSGLLAEIHTGHHSTIOYCDFSPYD---HLAVIALSOYCVELWNIDSRL---KVADCRG--HLSWVHGVMFSPD
T 3sfz A
                                                                                     893 (1249)
                  EEEETTTCCEEEEECSSSCCCEEECSST---TEEEEECSSSCEEEEETTTTE---EEEEECC--CSSCEEEEECTT
T ss dssp
                  EEEEeCCCCeecccCCCCCEEEEEECCCC---CEEEEEECCCCe---eeeEecC--cccEEEEEECCC
T ss pred
Q ss_pred
                  CCEEEECCCCCEEEEE
Q Fri_Mar_04_23: 266 GNVLALSGGDNKVTLWK 282 (297)
               266 ~~~l~~~~d~~i~iw~ 282 (297)
Q Consensus
                  |++|++++.|++|++|+
                  g~~l~s~s~D~~i~vWd 910 (1249)
T Consensus
               894 GSSFLTASDDQTIRVWE 910 (1249)
T 3sfz A
T ss dssp
                  SSEEREETTSCEERE
T ss pred
                  CCEEEEeCCCCEEEE
                                               Pub Med
33gre A Serine/threonine-protein kinase VPS15; seven-bladed propeller, WD repeat, scaffold protein, ATP- binding,
 endosome, golgi apparatus; 1.80A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=2.5e-35 Score=257.24 Aligned_cols=254 Identities=13% Similarity=0.112 Sum_probs=0.0
Q ss_pred
                  CERECCC-cCeeeEEEEcCCCC-EEEEEecCC----CccceeEEeccCC-CCEEEEEcCCCccCCEEEEE
Q Fri_Mar_04_23: 2 VVIANAH-NELIHDAVLDYYGK-RLATCSSDKTIKIFEVEG---ETHKLIDTLTGHEGFVWRVDWAHPKFGTILASCSYD
                                                                                     76 (297)
```

```
Q Consensus
                                                                                                              76 (297)
                    T Consensus
                                                                                                             132 (437)
                    55 IATLMENEPNSITSSAVSPGETPYLITGSDQGVIKIWNLKEIIVGEVYSSSLTYDCSSTVTQITMIPN--FDAFAVSSKD
T 3gre A
                                                                                                             132 (437)
                       EEEECTTTTSCEEEEEEECSSSCEEEEEETTSEEEEEEHHHHHTTCCCSCSEEEECSSCEEEEECTT--SSEEEEEETT
T ss dssp
                       EEEEccccCCEEEEEECCCCcEEEEEECCCceEEEEECCccccccchhhhccCCCCEEEEEEECC--CCEEEEEECC
T ss pred
                       CeEEEEcc-----CCeEEEEEeccCc-cEEEEEeCCccCcEEEEEEcCCCcchhhhhhhh
Q ss pred
Q Fri_Mar_04_23:
                   77 GKVLIWKEE----NGRWSQIAVHAVHSA-SVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA
                                                                                                             143 (297)
Q Consensus
                                                                            ~~1~~~~d~~i~i~~
                                                                                                             143 (297)
                   T Consensus
                                                                                                             212 (437)
                   133 GQIIVLKVNHYQQESEVKFLNCECIRKINLKNFGKNEYAVRMRAFVNEEKSLLVALTNLSRVIIFDIRTLERLQIIENSP
T 3gre A
                                                                                                             212 (437)
T ss_dssp
                       SEEEEEEEEETTEEEEEEEEEGGGGSSCCCEEEEEEECSSCEEEEEETTSEEEEETTTCCEEEEEECCG
T ss_pred
                       Q ss_pred
                       Q Fri_Mar_04_23: 144 HAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE-GHSDWVRDVAWSP----TVLL
                                                                                                             218 (297)
                                    Q Consensus
                   144
                                                                                                             218 (297)
                                              -----i-s---dg-i-iwd------
T Consensus
                   213
                                                                                                             273 (437)
                   213 RHGAVSSICIDEEC-----CVLILGTTRGIIDIWDIRFN---VLIRSWSFGDHAPITHVEVCOFYGKNS-
                                                                                                             273 (437)
T 3gre A
                       GGCCEEEEECTTS-----CEEEEEETTSCEEEETTTT---EEEEEEBCTTCEEEEEEECTTTCTTE-
T ss_dssp
                       CCCceEEEECCCC----CceEEEECCCCceEEEEECCCC----CceEEEEECCCCCceEEEEEeccCCCc--
T ss pred
Q ss_pred
                       Q Fri Mar 04 23: 219 RSYLASVSQDRTCIIWTQDNEQGPWKKTLLK------EEKFPDVLWRASWSL-----SGNVLALSG 273 (297)
                                                                                                             273 (297)
O Consensus
                  .+|++++.|+.|++||+.... ...+. . +...|.+++|+|
                   -i-----i-s--
                                                                                                             347 (437)
T Consensus
                   274 -VIVVGGSSKTFLTIWNFVKGH---CQYAFINSDEQPSMEHFLP--IEKGLEELNFCGIRSLNALSTISVSNDKILLTDE
T 3gre A
T ss_dssp
                       -EEEEEESTTEEEEEETTTTE---EEEEEESSSSCCCGGGGSC-BCSSGGCCCCCCCSGGGGCCEEETTEEEEEG
T ss_pred
                       -eEEEEccCCCeEEEEecCCCce---eeeEeecccCCcceeecc--ccchheeEecccCCCceEEEEccC
                       CCCCEEEE
Q ss_pred
Q Fri_Mar_04_23: 274 GDNKVTLWK 282 (297)
                  274 ~d~~i~iw~ 282 (297)
Q Consensus
                  .||.|++|+
348 ~dg~i~iwd 356 (437)
T Consensus
T 3gre_A
                  348 ATSSIVMFS 356 (437)
T ss dssp
                       GGTEEEEE
                       CCCEEEEE
T ss pred
No 83
                                   PDB NCBI Pub Med
         WD repeat-containing protein 92; WD40 repeats, structural genomics, structural genomic consortium, SGC,
apoptosis, transcription; 1.95A (Homo sapiens)
Probab=100.00 E-value=9e-35 Score=247.57 Aligned cols=251 Identities=14% Similarity=0.184 Sum probs=0.0
                       CcCeeeEEEccCC---CEEEEEecCCccEEEEEccCCcc-eeEEeccCCcCEEEEE------ecCCccCCEEEEEccCC
Q ss pred
Q Fri Mar 04 23:
                     8 HNELIHDAVLDYYG---KRLATCSSDKTIKIFEVEGETHK-LIDTLTGHEGPVWRVD-----WAHPKFGTILASCSYDG
                                                                                                              77 (297)
                    Q Consensus
                                                                                                              77 (297)
                    | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... 
T Consensus
                                                                                                             139 (357)
                    64 KAKPIKCGTFGATSLQQRYLATGDFGGNLHIWNL--EAPEMPVYSVKGHKEIINAIDGIGGLGIGEG--APEIVTGSRDG 139 (357)
T 3i2n A
                       ESSCEEEECTTCCTTTCCEEEEETTSCEEECT--TSCSSCSEEECCCSSCEEEEEEESGGGCC-C--CCEEEEEETTS
T ss_dssp
T ss pred
                       eEEEEEccCC-eEEEEEecccC----ccEEEEEeC----CccCCcEEEEEEEcCCCcchhhhhhhhccce
0 ss pred
Q Fri_Mar_04_23:
                    78 KVLIWKEENG-RWSQIAVHAVHS----ASVNSVQWA----PHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGV
                                                                                                             148 (297)
                    +|++||++++ . ....+. ..+.++|+ |+ +.+++++.|+.|+.|++||++.. .....+
                   140 ~v~lWd~~~~~~v~lwd~~~~~v~lasg~~d~~i~lwd~~~~~v~212 (357)
T Consensus
                   140 TVKVWDPRQKDD--PVANMEPVQGENKRDCWTVAFGNAYNQE--ERVVCAGYDNGDIKLFDLRNM---ALRWETNIKNGV
T 3i2n A
                                                                                                             212 (357)
                       CEEECTTSCSS--CSEECCCTTSCCCCEEEEEEECCC-C--CCEEEEEETTSEEEEEETTTT---EEEEEEECSSCE
T ss dssp
                       CEEEEECCCCCC--ceeEeecccCCcceeEEEEeeeeeCCC--CCEEEEEECCCC---cEEEeecCCCce
T ss pred
                       Q ss pred
Q FTI Mar 04 23: 149 NSASWAP---ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVL-ESTLEGHSDWVRDVAWSPTVLLRSYLAS 224 (297)
                   149 ------l-tg--d--i--wd-------h---v--l-rs-----las 224 (297)
O Consensus
                  T Consensus
                  213 CSLEFDRKDISM-----NKLVATSLEGKFHVFDMRTOHPTKGFASVSEKAHKSTVWQVRHLPQN--RELFLT 277 (357)
T 3i2n A
                       EEEEESCSSSSC-----CEEEEEESTTEEEEEEEEEETTTEEEEEEECCSSCEEEEEETTE-EEEEE
T ss dssp
T ss_pred
                       EEEEecCCCCcc-----ceEEEEeCCCceEEEEECCCccceeeeccCccceEEEEECCCC--CCEEEE
Q ss_pred
                       EeCCCeEEEEccCCCCce-----eEEEeccccCceEEEEECCCCCEEE-EEcCCCCEEEEEE
Q Fri_Mar_04_23: 225 VSQDRTCIIWTQDNEQGPW------KKTLLKEEKFPDVLWRASWSLSGNVLA-LSGGDNKVTLWKEN
                                                                                                        284 (297)
Q Consensus
                  225 ~s~Dq~i~iw~~~~d~i~iw~~~
                                                                                                        284 (297)
                  352 (357)
T Consensus
                  278 AGGAGGLHLWKYEYPIQRSKKDSEGIEMGVAGSVSLLONVTLSTOPISSLDWSPDKRGLCVCSSFDOTVRVLTVT
T 3i2n A
                                                                                                        352 (357)
T ss_dssp
                       RETTSEERREERCCSCC--CCTTSCCCCCCCRERERERECCSSCEERRECCSSSTTERREFETTSEERREEC
```

```
T ss_pred
                  ECCCCcEEEEeCCCccccccCCccceeeccccceeheeeccCCCeeEEEEECCCCEEEEEEEEE
                           PDB<sup>™</sup>
PROTEIN DATA BANK
                                   NCBI Pub Med
->4yvd_A Pleiotropic regulator 1; WD40 repeat, mRNA processing, mRNA splicing, structural GENO structural genomics
 consortium, SGC, RNA binding protein; 1.70A {Homo sapiens}
Probab=100.00 E-value=1.8e-33 Score=240.26 Aligned_cols=246 Identities=19% Similarity=0.376 Sum probs=0.0
                  \tt ceEecCCcCeeeEEEecCCCcEeEEEeccCCcceeEEeccCCccceeEEeccCCccCEEEEEeccCcccEEEEEccCCceEEE
Q ss pred
 Q Fri Mar 04 23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                    81 (297)
                2 ~~~~~h~~~v~~~~~g~~l~t~s~d~~v~lwd~~~~~~~h~~~v~~~~~~~l~s~s~D~~i~i
Q Consensus
                                                                                    81 (297)
                  T Consensus
                                                            ---v-----i----d--v--
                                                                                    174 (374)
T 4yvd_A
                99 KLSLTGHISTVRGVIVSTRSPYLFSCGEDKOVKCWDL--EYNKVIRHYHGHLSAVYGLDLHPT--IDVLVTCSRDSTARI
                                                                                    174 (374)
                  EEEECCCSSCEEEEECSSSSEEEEETTSCEEEET--TTTEEEEECCCCSSCEEEEECSS--SSEEEEETTSEEEE
T ss dssp
T ss pred
                  EEEEecCcCceeEEEECCCCEEEEEECCCeEEEEEC--CCCceEEEEEccccccEEEEEECCC--CCEEEEEeCCCcEEE
                  {\tt EEccCCeEEEEEeccCcccEEEEEEcCCcccEEEEEEcCCccceEEEEEEccCccchhhhhhhhccceeeEEEECCCccccc}
0 ss pred
Q Fri_Mar_04_23:
                \textbf{82} \ \ \textbf{WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED} \\
                                                                                    161 (297)
                           Q Consensus
                82 wd~~~~~
                                                                                    161 (297)
                  -d------v-----v------i-----ig-i-i-d------i-----i
T Consensus
                                                                                    244 (374)
               175 WDVRTKA--SVHTLSGHTNAVATVRCQAA--EPQIITGSHDTTIRLWDLVAG--KTRVTLTNHKKSVRAVVLHPRH----
T 4yvd A
                                                                                    244 (374)
 T ss_dssp
                  EETTTCC--EEEEEECCSSCEEEEECSS--SSCEEEEETTSCEEEEETTTT--EEEEEECCCSSCCEEEECTTS----
                  EECCCCc--eeEeeCCCCcEEEEEECCC--CCEEEEEECCCC--eEEEEecCCCCcEEEEEECCCC---
T ss pred
                  Q ss pred
O Fri Mar 04 23:
               162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                                    241 (297)
O Consensus
               162
                        ----l-tg--d--i--wd------h---v--l--s-----las-s-Dg-i-iw-
                                                                                    241 (297)
                      T Consensus
                                                                                    305 (374)
               245 -----YTFASGSPDN-IKOWKFPDG---SFIONISGHNAIINTLTVNSD---GVLVSGADNGTMHIWDWRTGY-
T 4yvd_A
                                                                                    305 (374)
                  -----SEEEEECSSC-EEEEETTTT---EEEEEECCCCSCEEEEEECTT---CEEEEEETTSCEEEEETTTCC-
T ss_dssp
T ss pred
                   -----CEEEEecCCc-EEEEECCCC----cEEeecccCcceeEEEEECCC----CEEEEccCCCeEEEEECCCCe-
Q ss_pred
                  ceeEEEecccc-----CceEEEEECCCCCEEEEEC
Q Fri_Mar_04_23: 242 PWKKTLLKEEKF-----PDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
Q Consensus
               242 ~~~~~d~i~iw~~~
                                                            284 (297)
                    ...+.. . ...|.+++|+|++++|++++|.|.|+|+|...
                                                             352 (374)
               306 --NFQRVHA--AVQPGSLDSESGIFACAFDQSESRLLTAEADKTIKVYRED 352 (374)
T 4yvd A
T ss dssp
                  --EEEEECC-----CCCEEEEEECTTSCEEEEEECT
T ss pred
                  --eeeeecc--ccCcccccCCceEEEECCCCCEEEEecCCCeEEEEECC
                            PDB<sup>™</sup>
PROTEIN DATA BANK
No 85
                                     NCBI
                                              Pub Med
>4g56_B MGC81050 protein; protein arginine methyltransferase, protein complexes, histo methylation, transferase;
HET: SAH; 2.95A {Xenopus laevis}
Probab=100.00 E-value=2.3e-34 Score=244.52 Aligned_cols=260 Identities=19% Similarity=0.219 Sum_probs=0.0
                  CCCCeeeEEEEcCCCCEEEEEcCCCc--cceeEEeccCCCCEEEEEccCCcCEEEEEccCCCCEEEEE
Q Fri_Mar_04_23:
                7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGET--HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKE
                                                                                    84 (297)
                7 -h---v-----q--l-t-s-d--v-lwd------h---v----h---v-----l-s-s-D--i-iwd-
Q Consensus
                                                                                    84 (297)
                  .|..|+++|++++. ++++.|+.|++||+... .....+.+|...|.++|+++ ++|++++.|+.|+.|+||+||+...
T 4q56 B
                92 OTEAGVTDVAWVSEKG-ILVASDSGAVELWEILEKESLLVNKFAKYEHDDIVKTLSVFSD--GTOAVSGGKDFSVKVWDL
                                                                                    168 (357)
T ss dssp
                  ECSSCEEEEETTTE-EEEEETTSCEEEC-----CCCCEEECCCSSCEEEEEECSS-SSEEEEEETTSCEEEEET
                  T ss_pred
Q ss_pred
                  cCCeEEEEEEeccCCccEEEEEECC-ccCCcEEEEEEECCCccchhhhhhhhcccceeEEEECCCccccc
                85 \ \ ENGRWSQIAVHAVHSASVNSVQWAP-HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGE
 Q Fri Mar 04 23:
                                                                                    163 (297)
O Consensus
                163 (297)
                  169 ~~~~
                                      ----l----d--i-iwd-----
                                                                                    239 (357)
T Consensus
T 4g56_B
               169 SQKA--VLKSYNAHSSEVNCVAACPGK--DTIFLSCGEDGRILLWDTRKPKPATRIDFCASDTIPTSVTWHPEKD----
                                                                                    239 (357)
                  T ss_dssp
                  CCCc--eEEEEecCcCceeEEEEcCCC--CCEEEEEECCCCeEEEEECCCCccceeeeecCCCCeEEEEECCCCC----
T ss_pred
Q ss_pred
                  ccCccceEEEEecCcceEEEEEccCCceeEEEEEccCCcce
Q Fri_Mar_04_23:
               164 HNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPW 243 (297)
O Consensus
               164 ------l-tg-d-i-wd------h---v-l--s----las-s-Dg-i-iw------
               T Consensus
                                                                                    303 (357)
T 4a56 B
               240 -----DTFACGDETGNVSLVNIKNPD----SAQTSAVHSQNITGLAYSYHS--SPFLASISEDCTVAVLDADFSE---
                                                                                   303 (357)
 T ss_dssp
                  -----TEEEEEESSCEEEEESSCGG----GCEEECCCSSCEEEEEECSSS--SCCEEEEETTSCEEECTTSCE---
T ss_pred
                  -----ceeeeccccceeeecccc---ceeeeccccc---ceeeecccc---ceeeecccc---
Q ss pred
                  eEEEeccccCceEEEEECCC-CCEEEEEccCCCcEEEeeeccC
               244 KKTLLKEEKFPDVLWRASWSLS-GNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (297)
O Fri Mar 04 23:
                   -----d--i-w-----
                                                                297 (297)
 Q Consensus
                    T Consensus
               355 (357)
               304 ---VFRDLSHRDFVTGVAWSPLDHSKFTTVGWDHKVLHHHLPSEGRTENLIATKA 355 (357)
 T 4q56 B
```

```
T ss_dssp
                  ---EEEECCCSSCEEEEECSSSTTEEEEEETTSCEEEEECC-----
 T ss pred
                  ---ereccCCCcrererecCCcccerereccCererecCcccccchhcccc
                           PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
 No 86
                                             Pub Med
>4ery A WD repeat-containing protein 5; WD40, WIN motif, beta propeller, 3-10 helix, lysine methyltransferase,
RBBP5, ASH2L, core complex; 1.30A {Homo sapiens} PDB: 2h6k _A* 2h68 _A* 2h6q _A* 3eg6 _A 4erq _A 2h6n _A 4erz _A 4e
4esg _A 4ewr _A 2gnq _A 2x12 _A 2x13 _A 3uvk _A* 3ps1 _A* 3uvl _A 3uvm _A 3uvn _A 3uvo _A 4cy2 _A ...
Probab=100.00 E-value=1.4e-33 Score=235.10 Aligned_cols=253 Identities=24% Similarity=0.383 Sum_probs=0.0
                  Q Fri_Mar_04_23:
                2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                   81 (297)
                2 -----h---v-----q--1-t-s-d--v-lwd------h---v---
                                                                 -----l-s-s-D--i-i
 Q Consensus
                                                                                   81 (297)
                  58 -----v----s----l----d--v-vwd-------
                                                                                   133 (312)
 T 4ery A
                58 EKTISGHKLGISDVAWSSDSNLLVSASDDKTLKIWDV--SSGKCLKTLKGHSNYVFCCNFNPO--SNLIVSGSFDESVRI
                                                                                   133 (312)
 T ss_dssp
                  ERRECCCSSCEREERCTTSSERERETTSERERET--TTCCREERECCSSCEREERCCSS--SSERERETTSCERE
 T ss_pred
                  eeeeccccceeEEECCCCCEEEEEcC-CCCeEEEEC--CCCeeEEEECCC--CCEEEEecCCCeEEE
                  EEccCCeEEEEEeccCcccEEEEEECCCccCcEEEEEECCCccchhhhhhhhcccceeEEEECCCcccc
 Q ss pred
 Q Fri_Mar_04_23:
                82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED 161 (297)
 Q Consensus
                161 (297)
                  T Consensus
               204 (312)
 T 4ery_A
               134 WDVKTGK--CLKTLPAHSDPVSAVHFNRD--GSLIVSSSYDGLCRIWDTASG-QCLKTLIDDDNPPVSFVKFSPNG----
                                                                                   204 (312)
                  EETTTCC--EEEEECCCSSCEEEEEECTT--SSEEEEEETTSCEEEEETTTC-CEEEEEECCSSCCEEEEEECTTS----
 T ss dssp
 T ss_pred
                  EECCCC---eeecccCCCCEEEEEcCC--CCEEEEcCCCCCEEEeeCCCC-cEEEEECCCCCceeEEEECCCC----
 Q ss pred
                  Q Fri Mar 04 23:
               162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                                  241 (297)
 O Consensus
               241 (297)
               270 (312)
 T Consensus
 T 4ery A
               205 -----KYILAATLDNTLKLWDYSKG---KCLKTYTGHKNEKYCIFANFSVTGGKWIVSGSEDNLVYIWNLQTKE-
                                                                                   270 (312)
                  -----SEEEEETTTEEEEEETTTT----EEEEEECSSCCSSSCCCEEEECSSSCEEEECCTTSCEEEEETTTCC-
 T ss_dssp
 T ss_pred
                  -----CEEEEEeCCCEEEEecCCCC----cEEEEEecCCCCcEEEEEEEcCCCeEEEEECCCce
 Q ss pred
                  ceeEEEecccCCceEEEEECC--CCCEEEEECC
 Q Fri_Mar_04_23: 242 PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGG--DNKVTLWKENL
                                                        285 (297)
               ....+.. +...|.+++|+|++++. |+.|++|+.+.
 T Consensus
               271 __~~~d~i~W~~~
                                                        312 (312)
               271 --IVOKLOG--HTDVVISTACHPTENIIASAALENDKTIKLWKSDC
 T 4erv A
                                                        312 (312)
 T ss_dssp
                 --EEEEECC--CSSCEEEEEECSSSSEEEEEECTTTCCEEEEECCC
 T ss_pred
                  --eeeeccC--CCcceEEEccCCCCcEEEeeccCCCceEEEeeccC
                          SCOPe PROTEIN DATA BANK
 No 87
                                             NCBI
                                                            Pub Med
->4gga_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; 2.04A
 {Homo sapiens} SCOP: b.69.4.0 PDB: 4ggd _A
 Probab=100.00 E-value=7.9e-34 Score=246.93 Aligned_cols=244 Identities=21% Similarity=0.361 Sum_probs=0.0
                  Q ss pred
 Q Fri_Mar_04_23:
                 7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEEN
                                                                                   86 (297)
                 86 (297)
               T Consensus
                                                                                   178 (420)
               103 RNDYYLNLVDWSSGN--VLAVALDNSVYLWSASSGDILOLLOMEOPGEYISSVAWIKE--GNYLAVGTSSAEVOLWDVOO
 T 4gga_A
                                                                                   178 (420)
                  T ss dssp
                  CCCceeEEEECCCC--EEEEECCCEEEEEECCCceEEEEeccCCCCeEEEEEECCC--CCEEEEEECCC
 T ss pred
 Q ss pred
                  Q Fri_Mar_04_23:
               87 GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNG
                                                                                   166 (297)
                                    -----l----d--i-i-----
                                                                                   166 (297)
 Q Consensus
                    .+..+..|...|.+++|++. .+++++.|+.|++||++.. .....+.+|...|.+++|+|++
               179 -----h---v--l--sgs-dg-i-iwd-----h---v--l--s-d----
                                                                                   242 (420)
               179 QK--RLRNMTSHSARVGSLSWNSY----ILSSGSRSGHIHHHDVRVA-EHHVATLSGHSQEVCGLRWAPDG-----
 T 4gga A
                                                                                   242 (420)
 T ss_dssp
                  TE--EEEECCCSSCEEEEEETT----EEEEEETTSEEEEEETTSS-SCEEEEEECCSSCEEEEECTTS-----
                  CE--EeEEcCCCCeEEEEEcCCC----EEEEECCCCcEEEEECCCCCCEEEEECCCCC-----
 T ss pred
 Q ss pred
                  CccceEEEEeCCceEEEEEcCCCceeEEEEEccCCCceeEEEEEccCCCccee
 Q Fri_Mar_04_23: 167 TKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS--QDRTCIIWTQDNEQGPWK 244 (297)
               167 -----l-tq--d--i--wd-------h---v--l--s----las-s---Dq-i-iw-----
                                                                                   244 (297)
 O Consensus
                  T Consensus
 T 4gga A
               243 ----RHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQ--SNVLATGGGTSDRHIRIWNVCSGA---- 312 (420)
 T ss_dssp
                  ----SEEEEEETTSCEEEEESSCCSSCSCCSEEECCCSSCEEEEECTTC--TTEEEEEECTTTCEEEEEETTTTE----
 T ss_pred
                  ----CEEEEEECCCeEEEEECCCCCcceEEEecCCCcceEEEEECCCC--CCEEEEECCCCCCEEEEEECCCCC----
 Q ss pred
                  EEEecccCCceEEEEECCCCCEEEEE
 Q Fri_Mar_04_23: 245 KTLLKEEKFPDVLWRASWSLSGNVLALSG--GDNKVTLWK
                                                  282 (297)
               245 -----i----i------l-----l--i-iw- 282 (297)
 O Consensus
                    .+......
```

```
T Consensus
                    313 --~~v~~l~~s~~~~l~~~g~~d~~i~iwd 350 (420)
                    313 -- CLSAVDAHSOVCSILWSPHYKELISGHGFAONOLVIWK 350 (420)
 T 4gga_A
 T ss dssp
                        --EEEEEECSSCEEEEEETTTTEEEEEECTTTCCEEEEE
                         --EeEEecCCCceEEEEECCCCCEEEEE
 T ss pred
                                     PDB PROTEIN DATA BANK PUBLICATION OF PUBLICATION OF
 No 88
>3gre_A Serine/threonine-protein kinase VPS15; seven-bladed propeller, WD repeat, scaffold protein, ATP- binding,
 endosome, golgi apparatus; 1.80A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=7.6e-35 Score=254.14 Aligned_cols=247 Identities=10% Similarity=0.104 Sum_probs=0.0
                         CCcCeeeEEEcCCCCEEEEEcC------CCccceeEeecCCC--CEEEEEecCCccCEEEEE
 0 ss pred
 Q Fri Mar 04 23:
                     7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVE-----GETHKLIDTLTGHEG--PVWRVDWAHPKFGTILASC
                                                                                                                   73 (297)
 O Consensus
                      73 (297)
                    T Consensus
                                                                                                                 188 (437)
                    109 DCSSTVTQITMIPNFDAFAVSSKDGQIIVLKVNHYQQESEVKFLNCECIRKINLKNFGKNEYAVRMRAFVNEEKSLLVAL 188 (437)
 T 3gre_A
                         T ss dssp
                         T ss pred
 Q ss_pred
                         Q Fri_Mar_04_23:
                     74 SYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIID-AHAIGVNSAS
                                                                                                                  152 (297)
 Q Consensus
                     74 s-D--i-iwd------v----v-----v------d--i-i------v----
                                                                                                                  152 (297)
                     +.|+.|++||++++......|...|...|.+++|+|+ +.+|++++.|+.|++||++......+..|...+..++++
189 ~-dg-i-iwd-------v----v----s----l-s---dg-i-iwd---------i-----
 T Consensus
                                                                                                                  264 (437)
                     189 TNLSRVIIFDIRTLERLQIIENSPRHGAVSSICIDEE--CCVLILGTTRGIIDIWDIRFN--VLIRSWSFGDHAPITHVE
 T 3gre A
 T ss dssp
                         ETTSEEEEETTTCCEEEEEECCGGCCEEEEEECTT--SCEEEEEETTSCEEEEETTTT--EEEEEEBCTTCEEEEEEE
                         eCCCeEEEECCCCcEEEEeccCCCCceEEEEECCC--CCEEEEECCCC--CceEEEEcCCCCCeeEEE
 T ss pred
 Q ss_pred
                         ECC----CcccccccCCccceEEEEEeCCceEEEEEEcCCcceeEEEEEcc------cCCCcEeEEEECC-
 Q Fri_Mar_04_23: 153 WAP----ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE------GHSDWVRDVAWSP-
                                                                                                                 214 (297)
                    153 ~~~----h-~v-l~tg~d~i~wd~~~~~~~h-tg~d~i~wd~~~~~214 (297)
 O Consensus
                                       T Consensus
                                                                                                                  327 (437)
                          ~p~
 T 3gre_A
                     265 VCQFYGKNS-----VIVVGGSSKTFLTIWNFVKG---HCQYAFINSDEQPSMEHFLPIEKGLEELNFCGIR 327 (437)
 T ss_dssp
                         T ss pred
                         EeeccCCc----eeeEEEccCCceEEEEeCCCc---eeeeEeecccCccceeeccccchheeEecccc
                         -----CCCCCCEEEEEeCCCeEEEEEccCCCCceeEEEec-----
 Q ss pred
 Q Fri_Mar_04_23: 215 -----TVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLK------
 Q Consensus
                    215 ------ 249 (297)
                                ++ .+|++++.||.|++|++.... ...+.
 T Consensus
                     401 (437)
 T 3gre_A
                    328 SLNALSTISVSND---KILLTDEATSSIVMFSLNELS---SSKAVISPSRFSDVFIPTQVTANLTMLLRKMKRTSTHSVD 401 (437)
                         SGGGGCCEEETT---EEEEEEGGGTEEEEETTCGG---GCEEEECC--CCCEEEEEEETTEEEEEECC-----
 T ss dssp
 T ss_pred
                         CCCceEEEEcCCC---CEEEEcCCCCEEEEEECCCCc---cceEeccCCccceeecccCCCceEEEEecCchhhcccc
                        ---cccCcceEEEEECC--CCCEEEEE
 Q ss pred
 Q Fri_Mar_04_23: 250 ---EEKFPDVLWRASWSL--SGNVLALSGGDNKVTLWK 282 (297)
 Q Consensus
                     . |...|++++|+| ++++|++++.||.|++|+
402 -----h---v--l-s----l-s---dg-v-iW-
 T Consensus
                                                                    437 (437)
                     402 DSLY--HHDIINSISTCEVDETPLLVACDNSGLIGIFO
 T 3gre A
                                                                    437 (437)
                         -----CCCEEEEEEESSSSEEEEEETTSCEEEEC
 T ss dssp
 T ss_pred
                         chhc--CcCeEEEEEEecCCCcEEEEEcCCCeEEEeC
                                    PDE NCBI Pub Med
 No 89
>4ci8_A Echinoderm microtubule-associated protein-like 1; structural protein, EML1, EML4-ALK, HSP90 inhibitors,
 tubulin-binding, beta propeller; 2.60A {Homo sapiens}
 Probab=100.00 E-value=8.9e-34 Score=259.66 Aligned_cols=265 Identities=14% Similarity=0.221 Sum_probs=0.0
                         ceEecC-CcCeeeEEEEcCCCcEEEEEccCCccee-----
 Q ss pred
 Q Fri Mar 04 23:
                      2 VVIANA-HNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLI------
                                                                                                                   46 (297)
                      +..+.+ |...|++++|+|+|+++++.|+.|++||+......
                    T Consensus
 T 4ci8 A
                         EEEETTSSSSCEEEEECTTSCEEEEETTTCEEEEECTTCCEEEEEECCTTTCSEEEEEECSTTCEEEEETTSCEEEECT
 T ss dssp
 T ss pred
                         Q ss_pred
                         Q Fri Mar 04 23:
                     47 ----DTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASS
                                                                                                                 121 (297)
                     O Consensus
                                                                                                                  121 (297)
                     T Consensus
                                                                                                                  444 (655)
                     372 SGDFTPITQGHTDELWGLAIHAS--KSQFLTCGHDKHATLWDAVGH---RPVWDKIIEDPAQSSGFHPS--GSVVAVGTL
 T 4ci8 A
                                                                                                                  444 (655)
 T ss_dssp
                         TCCCEEECCCSSCEEEEECSS--SSEEEEETTSEEEEEETTTT---EEEEEEECSSCEEEEEECTT--SSEEEEEES
 T ss pred
                         CCCeEEEEecCCCceEEEEECCC--CCEEEEECCCCeEEEEECCC--eEEEEEecCCccEEEEECCC--CCEEEEEEC
 Q ss pred
                         \tt CCEEEEEEecCCCcchhhhhhhhcccceeEEEEECCCccccccCCCcceEEEEEecCCcceeEEEEEecCCcceeEEEEEecCCcceeEEEEEecCCcceeEEEEEE
 Q Fri Mar 04 23: 122 DGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE 201 (297)
 O Consensus
                    201 (297)
```

```
++.+++|+.... ....+..|...+.+++|+|++
                                                                                                                            .+|++|+.|+.|++||+..+...+..+.
                                 445 dg~i~v~d~~~~~~v~~~~spdg------la~~~d~i~iw~~~~~~
  T Consensus
                                                                                                                                                                                     509 (655)
                                 445 TGRWFVFDTETKD--LVTVHTDGNEQLSVMRYSPDG-----NFLAIGSHDNCIYIYGVSDNGRKYTRVGKCS
  T 4ci8 A
                                                                                                                                                                                     509 (655)
                                       SSEEEEETTTCC--EEEEEECSSSCEEEEECTTS-----SEEEEEETTSCEEEEEEETTTTEEEEEEEEC
  T ss dssp
  T ss_pred
                                        CCEEEEECCCCc--EEEEEccCCCceeEEEECCCC------CEEEEEeCCCCEEEEEECCCCcceEEeEEC
                                       Q ss pred
  Q Fri Mar 04 23: 202 GHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEK-----FPD
                                                                                                                                                                                     255 (297)
                                 202 -h---v--las-s-Dg-i-iw------
                                                                                                                                                                                     255 (297)
  Q Consensus
                                 +|...|.+++|+|++ ..+.|+.|++|++... .+
510 ~h~~~v~-l~~s~d~----l~s~s~d~i~iwd~~~~----
  T Consensus
                                 510 GHSSFITHLDWSVNS---OFLVSNSGDYEILYWVPSACK-----OVVSVETTRDIEWATYTCTLGFHVFGVWPEGSDGT
  T 4ci8 A
                                                                                                                                                                                     580 (655)
                                       CCSSCEEEEEBTTS---SCEEEEETTCCCEEEEGGGTE-----ECCCHHHHTTCCBSCCCCSSSTTTTTSSCTTCCTT
  T ss dssp
  T ss pred
                                       CCCCCcEEEEECCCC---CEEEEECCCCeEEEEECCCCe-----ecCChhhcccceEEccccCCCcceeECcCCCCCC
  Q ss pred
                                       eEEEEECCCCCEEEEEcCCCCEEEEeccCC
  Q Fri Mar 04 23: 256 VLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ
                                                                                                                  297 (297)
                                 256 -i----l----d--i-iw------
  Q Consensus
                                                                                                                   297 (297)
                                        581 ~v~~~~s~~~~la~~~~dg~v~lw~~~~~~~~~~~~
  T Consensus
                                                                                                                    622 (655)
                                 581 DINAVCRAHEKKLLSTGDDFGKVHLFSYPCSQFRAPSHIYGG
  T 4ci8 A
                                                                                                                   622 (655)
  T ss_dssp
                                       SEEEEECSSSSEEEEETTSCEEEEESCCCSSSCCCEEECC
  T ss_pred
                                       SCOPe PDB<sup>™</sup> PROTEIN DATA BANK
                                                                                                    NCBI
                                                                                                                                     Pub Med
>lgxr_A ESG1, transducin-like enhancer protein 1; transcriptional CO-repressor, WD40, transcription repressor, WD
  repeat: 1.65A (Homo sapiens) SCOP: b.69.4.1 PDB: 2ce8 A 2ce9 A
  Probab=100.00 E-value=3e-33 Score=235.23 Aligned_cols=247 Identities=15% Similarity=0.252 Sum_probs=0.0
                                       ceEecCCcCeeeEEEEcCCCCEEEEEecCCccEEEEEccCC-ccceeEEec--cCCCCEEEEEEcCCCcCCEEEEEcCCCe
  Q Fri Mar 04 23:
                                    2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGE-THKLIDTLT--GHEGPVWRVDWAHPKFGTILASCSYDGK
                                                                                                                                                                                      78 (297)
                                    2 -----h---v-------l-s-s-b--
  Q Consensus
                                                                                                                                                                                       78 (297)
                                       T Consensus
                                                                                                                                                                                     120 (337)
  T 1gxr A
                                   44 QINTLNHGEVVCAVTISNPTRHVYTGG-KGCVKVWDISHPGNKSPVSQLDCLNRDNYIRSCKLLPD--GCTLIVGGEAST
                                                                                                                                                                                     120 (337)
  T ss_dssp
                                       EEEEECCSSCCCEEECSSSSEEEEC-BSEEEEETTSTTCCSCSEEEECSCTTSBEEEEEECTT--SSEEEEEESSSE
  T ss_pred
                                        EEEEEccCCeEEEEEecccCccEEEEEeCCCccCcEEEEEECCCcchhhhhhhhcccceeEEEECCCcc
  Q ss_pred
  Q Fri_Mar_04_23:
                                  79 VLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATI
                                                                                                                                                                                     158 (297)
  O Consensus
                                  158 (297)
                                 T Consensus
                                                                                                                                                                                     195 (337)
                                 121 LSIWDLAAPTPRIKAELTSSAPACYALAISPD--SKVCFSCCSDGNIAVWDLHNO--TLVROFOGHTDGASCIDISNDG-
                                                                                                                                                                                     195 (337)
  T 1gxr A
                                       EEEEECCCC--EEEEEECSSSCEEEEECTT--SSEEEEEETTSCEEEEETTTT--EEEEEECCCSSCEEEEECTTS-
  T ss_dssp
                                       EEEEeCCCCccceeeeccccccEEEEECCC--CCEEEEEcCCCeEEEEecCCC--ceeEEECCCCCeEEEEEcCCC-
  T ss pred
                                       Q ss pred
  Q Fri_Mar_04_23:
                                 \textbf{159} \hspace{0.2cm} \textbf{EEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDN} \\
                                                                                                                                                                                     238 (297)
                                                         -----l-tg--d--i--wd-----------h----v--l--s-----las-s-Dg-i-iw----
  Q Consensus
                                 159
                                                                                                                                                                                     238 (297)
                                                      .+++++.|+.|++||++.. ......|...+.++|+|++ ++++++.|+.|+|+|++++.
  T Consensus
                                                                                                                                                                                     255 (337)
                                 196 -----TKLWTGGLDNTVRSWDLREG----RQLQQHDFTSQIFSLGYCPTG--EWLAVGMESSNVEVLHVNK
  T 1gxr A
                                                                                                                                                                                     255 (337)
  T ss_dssp
                                       -----SEEEEEETTSEEEEEETTTT----EEEEEEECSSCEEEEECTTS---SEEEEEETTSCEEEEETTS
  T ss_pred
                                         -----CEEEEEeCCCCEEEEecCCC----ccccccCCCccEEEEECCCC---CEEEEEeCCCeEEEEeCCC
                                       CCCceeEEEecccCCceEEEEE
  Q ss pred
  O Fri Mar 04 23: 239 EOGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                                                -----d--i-iw-
  O Consensus
                                                                                                                      282 (297)
                                               ...+.. +...+.++|+|++++|++++.||.|++|+
  T Consensus
                                 256 -----dg-i-iw-
                                                                                                                      293 (337)
                                 256 PD----KYQLHL--HESCVLSLKFAYCGKWFVSTGKDNLLNAWR 293 (337)
  T 1gxr A
                                       SC---EEEECC--CSSCEEEEEECTTSSEEEEEETTSEEEEEE
  T ss dssp
                                       Cc---ceEEec--CCCCEEEEECCCCCEEEEE
  T ss pred
                                                              PDB'
  No 91
                                                                                                                  Pub Med
>3dwl_C Actin-related protein 2/3 complex subunit 1; propellor, actin-binding, ATP-binding, cytoskeleton, nucleot
  binding, WD repeat; HET: ATP; 3.78A {Schizosaccharomyces pombe}
  Probab=100.00 E-value=2.9e-35 Score=251.65 Aligned_cols=259 Identities=17% Similarity=0.154 Sum_probs=0.0
  Q ss_pred
                                       ceEecCCcCeeeEEEccCCCEEEEEecCCCc-cceeEEeccCCCCEEEEEccCCcCEEEEE
  O Fri Mar 04 23:
                                   2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGET-HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                                                                                       80 (297)
                                   2 -----h---v-------g--l-t-s-d--v-lwd-------h---v-------l-s-s-D--i-
+..+.+|...|++++|+|++++|++++|+.|+.|++||+...
  Q Consensus
                                                                                                                                                                                       80 (297)
                                   48 \hspace{0.1cm} \cdots \hspace{0.1cm} \overset{\cdot}{v} \cdots \overset{\cdot}{v} \overset{\cdot}{s} \cdots \overset{\cdot}{v} \overset{\cdot}{s} \cdots \overset{\cdot}{d} \cdots \overset{\cdot}{v} \overset{\cdot}{v} \cdots \overset{\cdot}{v} \cdots \overset{\cdot}{v} \cdots \overset{\cdot}{v} \cdots \overset{\cdot}{v} \cdots \overset{\cdot}{v} \cdots \overset{\cdot}{d} \cdots \overset{\cdot}{d} \cdots \overset{\cdot}{i} \cdots \overset{\cdot}{v} \overset{\cdot}{v} \overset{\cdot}{v}
  T Consensus
                                                                                                                                                                                     125 (377)
                                  48 ARTFSDHDKIVTCVDWAPKSNRIVTCSQDRNAYVYEKRPDGTWKQTLVLLRLNRAATFVRWSPN--EDKFAVGSGARVIS CCCBCCCSSCEEEEECTTTCCEEEEETTSSEEEC-----CCCCEEECCCCSSCEEEEECCTT--SSCCEEEESSSCEE
  T 3dwl C
                                                                                                                                                                                     125 (377)
  T ss dssp
                                        EEEeccCCCceEEEEEcCCCCEEEEEecCCeEEEEEccCCcceeeEEeccCCcceEEEEECCC--CCEEEEEECCCeEE
  T ss pred
  Q ss pred
                                       EEECCCCe-EEEEEecc-cCccEEEEEECCccCCcEEEEEECCCCEEEEE
  Q Fri Mar 04 23: 81 IWKEENGR-WSQIAVHAV-HSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFK------ENGTTSPIIID 142 (297)
```

```
81 iwd-----d--i-i-----d
Q Consensus
                                                                           142 (297)
              T Consensus
                                                                           202 (377)
              126 VCYFEQENDWWVSKHLKRPLRSTILSLDWHPN--NVLLAAGCADRKAYVLSAYVRDVDAKPEASVWGSRLPFNTVCAEY-
T 3dwl C
                                                                           202 (377)
                ECCC----CCCCEEECSSCCSCEEEEECTT--SSEEEEEESSSCEEEEEECCSCC-CCCSCSSCSCCCEEEEEECC-
T ss dssp
                T ss pred
                hccceeEEEECCCccccccCCCcceEEEEEECCCceEEEEEEcCCCceeEEEEEEccCCCcEeEEEEECCCCCCCEE
Q ss pred
Q Fri_Mar_04_23: 143 AHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYL 222 (297)
Q Consensus
                                   ~~~~l~tg~~d~~i~~wd~~~~
                  T Consensus
              203 ~
              203 PSGGWVHAVGFSPSG-----NALAYAGHDSSVTIAYPSAPEQPPRALITVKLSQLPLRSLLWANES---AIV
T 3dwl C
                                                                           266 (377)
T ss_dssp
                CCSSSEEEEECTTS-----SCEEEEETTTEEC-CEECSTTSCEEECCCEECSSSCEEEEEEETT--EEE
T ss_pred
                Q ss_pred
                EEROCCCOEREERCCCCCCCOOOREERCCCCC------CC
Q Fri_Mar_04_23: 223 ASVSQDRTCIIWTQDNEQGPWKKTLLKEEK------FP
                                                                           254 (297)
Q Consensus
              254 (297)
T Consensus
T 3dwl C
              267 AAG-YNYSPILLQGNESG-WAHTRDLDAGTSKTSFTHTGNTGEGREEEGPVSFTALRSTFRNMDLKGSSQSISSLPTVHQ 344 (377)
                T ss_dssp
                T ss pred
Q ss_pred
                ceeeeeeccccc----eeeeeccccceeeee
Q Fri Mar 04 23: 255 DVLWRASWSLSGN----VLALSGGDNKVTLWKE 283 (297)
             255 ~~i~~~~~~l~~~~d~~i~iw~~ 283 (297)
O Consensus
              ..|++++|+|+++ +|++++.||+|++|+.
345 ~~V~~v~~~~~~1~s~s~Dg~v~iw~~
T Consensus
              345 NMIATLRPYAGTPGNITAFTSSGTDGRVVLWTL 377 (377)
T 3dwl C
T ss_dssp
                SCEEEEEEEETTEEEEEEEETTSEEEEECC
T ss_pred
                cceeeEEEecCCCCCeEEEEEecCCceEEEEeC
No 92
                        PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
                                               Pub Med
🗌 >1r5m_A SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A
 {Saccharomyces cerevisiae}
 Probab=100.00 E-value=6.3e-34 Score=246.78 Aligned cols=249 Identities=15% Similarity=0.259 Sum probs=0.0
Q ss pred
                CCEECCCC--CeeeEEECC-CCCEEEEECCCCCCEEEEE
Q Fri Mar 04 23:
              1 MVVIANAHN--ELIHDAVLDY-YGKRLATCSSDKTIKIFEVEGET------HKLIDTLTGHEGPVWRV
                                                                            59 (297)
O Consensus
              1 -----h-_--v---h-----h---v---h---v---
                                                                            59 (297)
                114 (425)
T Consensus
              35 FVKILKEIVKLDNIVSSTWNPLDESILAYGEKNSVARLARIVETDQEGKKYWKLTIIAELRHPFALSASSGKTTNQVTCL
T 1r5m A
T ss_dssp
                CCEECEREECSCCSEEEECSSCTTEEEEEETBTEEEEEEEC-----CEEEEEEEEECCCCCC-----CBCEEEE
                T ss_pred
Q ss_pred
                EecCCccCCEEEEEcCCCeEEEEEccCCceEEEEEeccCcccEEEEEecCcccCceEEEEE
 Q Fri Mar 04 23:
              60 DWAHPKFGTILASCSYDGKVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPI
                                                                           139 (297)
              60 -----l-s-s-D-i-iwd-------v------l-----d-i-i-----
Q Consensus
                                                                           139 (297)
                187 (425)
T Consensus
              115 AWSHD--GNSIVTGVENGELRLWN-KTGA--LLNVLNFHRAPIVSVKWNKD--GTHIISMDVENVTILWNVISGTVMQHF 187 (425)
T 1r5m A
                EECTT--SSEEEEEETTSCEEEEE-TTSC--EEEEECCCCSCEEEEEECTT--SSEEEEEETTCCEEEEETTTTEEEEEE
T ss_dssp
T ss pred
                EECCC--CCEEEEEcCCCEEEEE-CCCC--eEEEecCCCCCEEEEEccC--CCEEEEEcCCCceeeee
                h------hhhccceeEEEECCCcccccc
0 ss pred
Q Fri_Mar_04_23:
              140 I-----IDAHAIGVNSASWAPATIEEDGEHN
                                                                           165 (297)
                                                                            165 (297)
              188 -----d-----i----i
T Consensus
                                                                            259 (425)
              188 ELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPRGAIFVYQITEKTPTGKLIGHHGPISVLEFNDTN------
T 1r5m A
                                                                           259 (425)
                CCC-----CCCBSCCEEEETTEEEEECGGGCEEEETTCSSCSEEECCCSSCEEEEEETTT-----
T ss dssp
                eecccCccceeecccCCccEEEEEcCCCEEEEEcCCCcEEEEEcCCCcEEeeeccCCCceeEEEECCCC-----
 T ss pred
                CCccceEEEEEcCCcceEEEEEccCCcceeEEEEEccCCCccEEEEEEccCcccccEEEEE
Q ss pred
Q Fri Mar 04 23: 166 GTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKK 245 (297)
                .+|++++.|+.|++|++.+. ....+.+|...|.+++|+|+
                                                      ..+++++.|+.|++|+++...
              260 -----dg-i-i-d----- 323 (425)
T Consensus
              260 -----KLLLSASDDGTLRIWHGGNGN----SQNCFYGHSQSIVSASWVGD----DKVISCSMDGSVRLWSLKQNT---LL 323 (425)
T 1r5m A
                ----TEEEEEETTSCEEECSSSBS----CSEECCCSSCEEEEEETT----TEEEEEETTSEEEEEETTTTE---EE
T ss dssp
                ----CEEEEECCCEEEEEECCCc---ccchhcccceEEEEECCC---CeEEEEECCCC---ee
T ss_pred
Q ss_pred
                EEecccCCceEEEEECCCCCEEEEE
Q Fri_Mar_04_23: 246 TLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
              246 ----d-i-iw-
Q Consensus
                                             282 (297)
                ..+.. +...+.++|+|++++|++++.||.|++|+
              324 -----s---i----s----l-----dg-v-iwd 358 (425)
T Consensus
 T 1r5m A
             324 ALSIV--DGVPIFAGRISODGOKYAVAFMDGOVNVYD
                                            358 (425)
 T ss dssp
                EEEEC--TTCCEEEEEECTTSSEEEEEETTSCEEEEE
```

```
T ss_pred
                            EEEec--CCCCeEEEEECCCCCEEEEE
                                            PDB"
                                                          NCBI Pub Med
3mmy_A MRNA export factor; mRNA export, nuclear protein; HET: MES; 1.65A {Homo sapiens} PDB: 4owr_A
 Probab=100.00 E-value=4.7e-34 Score=244.11 Aligned_cols=248 Identities=17% Similarity=0.256 Sum_probs=0.0
                            CceEecCCcCeeeEEEcCCC---CEEEEEeCCCcEEEEEccCCcceeEEeccCCCCCEEEEEecCCccCEEEEEcCCC
 Q ss pred
 Q Fri_Mar_04_23:
                         1 MVVIANAHNELIHDAVLDYYG---KRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDG
                                                                                                                                     77 (297)
                         1 ------h---v-l-t-s-d--v-lwd------h---vh---v-l-s-s-b-
                                                                                                                                     77 (297)
                         T Consensus
                                                                                                                                    108 (368)
 T 3mmy_A
                         31 DIEVTSSPDDSIGCLSFSPPTLPGNFLIAGSWANDVRCWEVQDSGQTIPKAQQMHTGPVLDVCWSDD--GSKVFTASCDK
                                                                                                                                    108 (368)
 T ss dssp
                            CEECSSCCSSCEEEEECCTTSSSEEEEEEETTSEEEEEEECTTSCEEEEEEECSSCEEEEEECTT--SSEEEEEETTS
 T ss_pred
                             eeecCCCCCCEEEEEeCCCCCCCEEEEEecCCCCEEEEEcCCCCcceeeccCCcceEEEEEEcCC--CCEEEEEcCCC
                            Q ss_pred
 O Fri Mar 04 23:
                         78 KVLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA-----
                                                                                                                                    143 (297)
                         78 ~i~iwd~~~~d~i~i~i~~~d~i~i~~~~~
 Q Consensus
                            T Consensus
                        109 -v-iWd-----h---v--v--v-----l-s-s-d--i-iWd------
                                                                                                                                    185 (368)
                        109 TAKMWDI.SSN---OATOTAOHDAPVKTTHWIKAPNYSCVMTGSWDKTI.KFWDTRSSNPMMVI.OI.PERCYCADVIYPMAVV
 T 3mmy A
                                                                                                                                    185 (368)
                            EEEEEETTT---EEEEEEECSSCEEEEEEECSSCEEEEEETTSEEEEECSSCSEEEECSSCEEEEEETTEEEE
 T ss dssp
 T ss_pred
                            CEEEEECCCC---cEEEeccCCcceEEEEEecCCCCEEEEEecCCCCeEEEeecCCCCeEEE
 Q ss_pred
                            Q Fri Mar 04 23: 144 -------HAIGVNSASWAPATIEEDGEHNGTKESR----KFVTGGADNLVKIWKYNSDAQTY
                                                                                                                                    194 (297)
                        144 -----l>tq~d~i~wd~~~~~
 O Consensus
                                                                                                                                    194 (297)
                                                           +...+.+++++ |+.
                                                                                                   .+++ |+.|+.+++|+++.....
                        186 ~~~d~~i~vwd~~~~~~
                                                                                              ----a-gs-dg-v-iw----
 T 3mmy A
                        186 ATAERGLIVYOLENOPSEFRRIESPLKHOHRCVAIFKDK-----ONKPTGFALGSIEGRVAIHYINPPNPA-
                                                                                                                                    251 (368)
 T ss dssp
                            EEGGGCEEEECSSSCEEEECCCSCSSCEEEEEEECT-----TSCEEEEEEETTSEEEEEESSCSCHH-
                             T ss pred
 Q ss pred
                            EEEEEeccCCC-----cEeEEEECCCCCCCEEEEEEccCCCCCceeEEEEeccCCCCceeEEEEE
 Q Fri_Mar_04_23: 195 VLESTLEGHSD-------WVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASW
                                                                                                                                    262 (297)
 Q Consensus
                        195 -----h-----v--l--s-----las-s-Dg-i-iw------i-----i-----i
                                                                                                                                    262 (297)
                                             .|.+++|+|++ .+||+++||+||+.... ....+.. +...|.+++|
                             ....+.+|..
                                  T Consensus
                                                                                                                                    323 (368)
                        252 KDNFTFKCHRSNGTNTSAPQDIYAVNGIAFHPVH---GTLATVGSDGRFSFWDKDART---KLKTSEQ--LDQPISACCF
 T 3mmy_A
                                                                                                                                    323 (368)
 T ss_dssp
                            HHSEEEECSEEC----CCCEEECCEEEEEECTTT---CCEEEEETTSCEEEEETTTTE---EEEECCC--CSSCEEEEE
 T ss_pred
                            CCCEEEeecccCCccCCCCcceeEEEEEEECCCC---CeEEEecCCCEEEEEECccc---EEEecCC--CCCCEEEEEE
 Q ss_pred
                            CCCCCEEEECCC
 Q Fri_Mar_04_23: 263 SLSGNVLALSGGD 275 (297)
 O Consensus
                       263 ~~~~l~~~~d 275 (297)
                       +|+|++||++..
324 spdg~~las~s~~
 T Consensus
                                               336 (368)
                        324 NHNGNIFAYASSY 336 (368)
 T 3mmy A
 T ss_dssp
                             CTTSSCEEEEECC
                            CCCCCEEEEECC
 T ss_pred
                                            PDB"
PROTEIN DATA BANK
 No 94
                                                          NCBI Pub Med
🗌 >5dfz_B Serine/threonine-protein kinase VPS15; autophagy, vacuolar protein SORT yeast, complex II, PI3P, kinase,
 lipid, WD40, BARA; 4.40A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.2e-36 Score=295.83 Aligned cols=250 Identities=13% Similarity=0.164 Sum probs=0.0
                            CceEe-cCCcCeeeEEEEcCCCC-EEEEEeCCCcEEEEEccCCccceeEEeccC-----CCCEEEEEeccCccCCEEEEE
 Q ss pred
 Q Fri_Mar_04_23:
                         1 MVVIA-NAHNELIHDAVLDYYGK-RLATCSSDKTIKIFEVEGETHKLIDTLTGH----EGPVWRVDWAHPKFGTILASC
                                                                                                                                     73 (297)
                          1 \  \  \, \sim \sim \sim \sim \sim h \sim \sim v \sim \sim \sim - g \sim \sim 1 - t \sim s \sim d \sim v \sim 1 \\ w d \sim \sim \sim \sim \sim \sim h \sim \sim \sim v \sim \sim \sim \sim \sim \sim 1 - s \sim 1 - 
 O Consensus
                                                                                                                                     73 (297)
                      .+.|.+++|+++ |+.|++|
 T Consensus
                                                                                                   ~~~H~~~V~svafspd--g~~laSg 1136 (1460)
                      1061 LIATLMENEPNSITSSAVSPGETPYLITGSDOGVIKIWNL--KEILVGEVYSSSLTYDCSSTVTQITMIPN--FDAFAVS 1136 (1460)
 T 5dfz B
 T ss_dssp
                             EEEEECSCSSSCCSCEEECSSSCEEEECTTSEEEEEH--HHHHTTCCCSCSEEEECSSCEEEEECTT--SSCEEE
                             T ss_pred
 0 ss pred
                            cccceeeeecccceeeeecccccceeeeeeccccccc
 Q Fri_Mar_04_23:
                        74 SYDGKVLIWKEENGRWSQ-----IAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTS 137 (297)
                         74 s-D--i-iwd-----d--i-i----d--i-i------
                                                                     +..+.+|...|.+++|+|++ +.++++|+.|++|++||++.....
                            +.|++|++||+++++ .
 T Consensus
                      1137 s-DgtI-iWd--tg-----ir-----l-gH---V--v-fsp-g----L-Sgs-D-tI-iWDl-tg--l- 1213 (1460)
                      1137 SKDGQIIVLKVNHYQ--QESEVKFLNCECIRKINLKNFGKNEYAVRMRAFVNEE-KSLLVALTNLSRVIIFDIRTLERLQ 1213 (1460)
 T 5dfz B
 T ss_dssp
                            ETTTEEEEEEEE--ETTEEEEEEEEEEGGGGSSCCCCCEEEEECSS-CEEEEECTTCEEEEEETTTTEEEE
 T ss pred
                             Q ss_pred
                            hhhhhhccceeEEEECCCccccccccCccceEEEEEECCceEEEEEEcCCCceeEEEEEec-cCCCcEeEEE----E
 Q Fri_Mar_04_23: 138 PIIIDAHAIGVNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLE-GHSDWVRDVA----W 212 (297)
                                                     Q Consensus
                       138 ~~~~~
                                                                     .++++|+-|++|++|+++
                                                                                                                                  1276 (1460)
 T Consensus
                      1214 tl-g~~H~~~V~svafspdg---------LaSgs~DgtIrlWDl~tg----~~tl~~gh~~~V~~v~~~~
                      1214 IIENSPRHGAVSSICIDEEC------CVLILGTTRGIIDIWDIRFN---VLIRSWSFGDHAPITHVEVCQFY 1276 (1460)
 T 5dfz B
 T ss dssp
                            EEECCGGGCSBCCCEECSSS-----SEEEEEBTTSCEEEEETTTT---EEEEEEBCTTCCCCCEEECCSTT
```

```
T ss_pred
                  eecCCcccCeEEEEecCCC-----CeEEEEccCCCeEEEEEcCCC----ceeEEEecCCCCceeEEEecccc
                  CCCCCCCEEEEEeCCCCCceeEEEeccCCCCceeEEEeccCCCceEEEEECCC------CC
0 ss pred
 Q Fri_Mar_04_23: 213 SPTVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLS------GN 267 (297)
              267 (297)
              ~~~~q~ 1348 (1460)
T Consensus
              1277 GKNS---VIVVGGSSKTFLTIWNFVKGH---CQYAFIN--SDEQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVSNDK 1348 (1460)
T 5dfz B
                  CTTE---EEEECSSSSEEEEEEETTTTE---EEEEEEE-BSSCCCHHHHSCBCSCCTTCCCCCCCSTTSCCCEEEETTE
T ss_dssp
T ss_pred
                  CCCC---EEEEEECCCCeEEEEECCCCc---EEEEEEC--CCCCccceeccchhhhhhhhccccccccceeEEEECCCC
                  EEEEEcCCCCEEEEE
Q ss pred
Q Fri_Mar_04_23: 268 VLALSGGDNKVTLWK 282 (297)
Q Consensus 268 ~1~~~~d~~i~iw~ 282 (297)
                 + | ++ | +. | ++ | ++ | +
T Consensus
             1349 ~1~Sgs~Dg~IrvWd 1363 (1460)
T 5dfz_B
             1349 ILLTDEATSSIVMFS 1363 (1460)
T ss_dssp
                  EEEEETTTTEEEEEE
T ss pred
                  EEEEeCCCCEEEEE
No 95
                          PDB™
PROTEIN DATA BANK
                                             Pub Med
□ >3v11_A 26S proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A {Saccharomyces
 cerevisiae} PDB: 3acp _A
 Probab=100.00 E-value=1.1e-33 Score=245.38 Aligned_cols=245 Identities=15% Similarity=0.173 Sum_probs=0.0
                  ecCCcCeeeEEEcCCCC-EEEEEcCCCcEEEEEccCCcceeEEeccCCCCEEEEEccCCcCEEEEEE
0 ss pred
Q Fri Mar 04 23:
                5 ANAHNELIHDAVLDYYGK-RLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWK
                                                                                    83 (297)
O Consensus
                83 (297)
               T Consensus
               92 KMLKRADYTAVDTAKLOMRRFILGTTEGDIKVLDS--NFNLOREIDQAHVSEITKLKFFPS--GEALISSSODMOLKIWS 167 (420)
T 3vl1 A
                  TTSCSCCEEEEEECSSSCEEEEETTSCEEEECT--TSCEEEEETTSSSSCEEEEEECTT--SSEEEEEETTSEEEEE
T ss dssp
T ss pred
                  cccCCCeEEEEEcCCCceEEEEcCCCcEEEEEC--CCCceeeeecccCceeEEEEeCC--CCEEEEE
Q ss_pred
                  Q Fri_Mar_04_23:
               84 EENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPII-IDAHAIGVNSASWAP-----
Q Consensus
               84 -----v----v----v-----v-----v-----v-----
                                                                          ~~~---- 155 (297)
               168 VKDGS--NPRTLIGHRATVTDIAIIDR--GRNVLSASLDGTIRLWECGTGTTIHTFNRKENPHDGVNSIALFVGTDRQLH 243 (420)
T 3vll A
T ss dssp
                  TTTCC--CCEEEECCSSCEEEEEETT--TTEEEEEETTSCEEEEETTTTEEEEEECCBTTBTTCCEEEEEEECCCSSCG
T ss pred
                  CCCCC--chhhhhcCcccEEEEEcCC--CCEEEEEcCCCcEEEEEeccCCCcceEEEEccCCcceEE
                  -----CcccccccCCccceEEEEEcCCcceEEEEEEcCCCcceEEEEEEccCCCc
Q ss_pred
 Q Fri_Mar_04_23: 156 -----ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDW-VRDVAWSP-TVLLR 219 (297)
               Q Consensus
                                                                                   219 (297)
T Consensus
                                                                                   303 (420)
               244 EISTSKKNNLEFGTYG-----KYVIAGHVSGVITVHNVFSKE---QTIQLPSKFTCSCNSLTVDGNNA-- 303 (420)
T 3vl1 A
                  GGCCCCCTTCSSCTT----EEEEEEETTSCEEEEETTTCC---EEEEECCTTSSCEEEEECSSCT--
T ss_dssp
                  ecccCceeEEEEcCCC-----CEEEEEcCCCEEEEEECCCCC----cceecCCCCceeeEeEeecCCCC---
T ss pred
                  CEEEEEeCCCeEEEEEccCCCceeEE-EecccCCceEEEEECCCCCEEEEEE
Q ss pred
Q Fri_Mar_04_23: 220 SYLASVSQDRTCIIWTQDNEQGPWKKT-LLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKE 283 (297)
               O Consensus
               T Consensus
                                                                       362 (420)
               304 NYIYAGYENGMLAQWDLRSPECPVGEFLIN----EGTPINNVYFA-AGALFVSSGFDTSIK-LDI 362 (420)
T 3vl1 A
                  TEEEEEETTSEEEEEETTCTTSCSEEEEES----TTSCEEEEEEE-TTEEEEEEETTTEEEE-EEE
T ss dssp
                  CEEEEEcCCCceEEEecCCCCchheeccc----CCCceeEEEEC-CCCEEEEEeCCCCEE-EEE
T ss pred
             PDB™ SMDB
PROTEIN DATA BANK
No 96
                                             Pub Med
       Cell division control protein 4; WD 40 domain, phospho-peptide complex, E3 ubiquitin ligase, cell cycle,

── >3v7d B
 phospho binding protein, phosphorylation; HET: SEP; 2.31A {Saccharomyces cerevisiae} PDB: 1nex _B* 3mks _B*
Probab=100.00 E-value=2.6e-33 Score=246.70 Aligned_cols=242 Identities=22% Similarity=0.337 Sum_probs=0.0
Q ss pred
                  eEecCCcCe=eeEEEEcCCCCEEEEEecCCcceeEEeccCCccceeEEeccCCccCEEEEEecCCccCeEEE
Q Fri_Mar_04_23:
                3 VIANAHNEL-IHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                    81 (297)
                3 ----h----v-----g--1-t-s-d--v-lwd-----h---v----h---v------1-s-s-D--i-i
               .+.+|... +.++| +++|+|+|+|+|+|+| .+.++.+|... +|++++|+ +...|+|+|.+|++|
115 ~-l-gh---vv------l-sgs-D--i-vwd-------l-gh---V-l------l-sgs-D-tv-v
                                                                                  187 (464)
T Consensus
T 3v7d_B
               115 TTLRGHMTSVITCLQF--EDNYVITGADDKMIRVYDS--INKKFLLQLSGHDGGVWALKYAH---GGILVSGSTDRTVRV
                                                                                   187 (464)
T ss_dssp
                  EEEECCSSSCEEEEE--ETTEEEEEETTSCEEEEET--TTTEEEEEEECCSSCEEEEECS---TTEEEEEETTSCEEE
T ss_pred
                  EEECCCCCCEEEEEE--CCCEEEEEECCCCeEEEEEC--CCCeEEEEECC---CCeEEEECCC---CCeEEE
Q ss pred
                  EECCCCeEEEEEeccCccEEEEEeCCccCcEEEEEECCccCch-----hhh
Q Fri Mar 04 23:
               82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTS-----PII
                                                                                  140 (297)
               Q Consensus
                  188 Wd---g------h---V--1------l-sgs-D--i-vWd------------
T Consensus
                                                                                   265 (464)
 T 3v7d B
               188 WDIKKGC--CTHVFEGHNSTVRCLDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGV 265 (464)
```

```
T ss_dssp
                            EETTTTE--EEEEECCCSSCEEEEEEESSSCEEEEEETTSCEEEEECCCCCC-----CCSSEEESCGGGCTTEEEE
 T ss_pred
                             Q ss_pred
 Q Fri_Mar_04_23: 141 IDAHAIGUNSASWAPATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRS
                                                                                                                                   220 (297)
                        141 -----v--1-tq--d--i--wd------h---v--1--s-----
 O Consensus
                                                                                                                                   220 (297)
                                                                  .++++|+.|++|++|
                                                                                             .++..+.+|...|.+++|+|++
                        266 l~gh~~~v~~s~~g-----h~~~l~sgs~D~~i~vWd~~~~----h~~v~~v~~~
 T Consensus
                                                                                                                                   323 (464)
                        266 LRGHMASVRTVSGHG-----NIVVSGSYDNTLIVWDVAQM----KCLYILSGHTDRIYSTIYDHER---K
 T 3v7d B
                                                                                                                                   323 (464)
 T ss_dssp
                             ECCCSSCEEEEET----TEEEEEETTSCEEEEETTT---EEEEEECCCSSCEEEEEETTT--T
 T ss pred
                             eecccceEEecCCC-----CEEEEecCCCeEEEEECCCC----cEEEEEECCccccEEEEEECCCC---C
                            EEEEEeCCCceeEEEeccCCCceeEEEeccccCceEEEE
 Q ss pred
 Q Fri_Mar_04_23: 221 YLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
                                                                      ---i----d--i-iw-
                            ++++|+.|++|++||++...
                                                         ....+.. |...+.++|+ +++|++++.||+|++|+
                        324 ~l~sgs~D~~i~iWd~~~g~--~~~l~~-h~~~v~~~~s--~~l~s~s~D~~i~vWd 378 (464)
 T Consensus
                        324 RCISASMDTTIRIWDLENGE---LMYTLQG--HTALVGLLRLS--DKFLVSAAADGSIRGWD
 T 3v7d B
                                                                                                            378 (464)
                             EEEEEETTSCEEEEETTTTE---EEEEECC--CSSCEEEEEC--SSEEEEEETTSEEEEEE
 T ss dssp
                             EEEEEeCCCcEEEEECCCc---EEEEEcC--cCCcEEEEEec--CCEEEEE
 T ss_pred
                                            PDB"
 No 97
                                                          NCBI
                                                                        Pub Med
>2pm9_A Protein WEB1, protein transport protein SEC31; beta propeller; 3.30A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=4.5e-35 Score=254.07 Aligned cols=253 Identities=15% Similarity=0.282 Sum probs=0.0
 0 ss pred
                            CCcCeeeEEEcCCCCEEEEEcCCC--ccceeEEeccCCCCEEEEEccCCcCCEEEEEc
 Q Fri Mar 04 23:
                          7 AHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGE--THKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKE
                                                                                                                                    84 (297)
 O Consensus
                          84 (297)
                            T Consensus
                                                                                                    -----l-s---d--i-iwd-
                                                                                                                                   143 (416)
 T 2pm9_A
                         65 OVDSKENDLDWSHNNKTTAGALDNGSLELYSTNEANNATNSMARFSNHSSSVKTVKENAKO-DNVLASGGNNGELETWDM
                                                                                                                                   143 (416)
                            CCSSCEEEECSSSSCEEEEESSSCEEECCSSTTSCCCEEEECCCSSSCCCEEECSSS-TTBEEEECSSSCEEBCBT
 T ss dssp
 T ss pred
                             Q ss_pred
                            ccce-----EEEEEEecccccccEEEEEEccccEEEEEEcccCcEEEEEE
 Q Fri_Mar_04_23:
                         153 (297)
 Q Consensus
                         85 ~~~~v~~~v~~~
                                                                     -----l----d--i-i------
                                                                                                                                   153 (297)
                                  ----l-s---dg-v-iwd-----
                                                                                                                                   222 (416)
 T 2pm9_A
                        144 NKCTESPSNYTPLTPGOSMSSVDEVISLAWNOSL-AHVFASAGSSNFASIWDLKAKKEVIHLSYTSPNSGIKOOLSVVEW
                                                                                                                                   222 (416)
 T ss dssp
                            TTTSSCTTTCCCBCCCCSCCSCCCCEEECSSC-TTEEEEESSSSCEEEEETTTTEEEEEECCCCCSSCCCCCEEEEEE
 T ss pred
                            CCCcccccCcCcCCCCCCCCEEEEECCCC-CCEEEEECCCCcEEEEECCCCcceEeecCCcccCCCCcceEEEEE
                            Q ss_pred
 Q Fri_Mar_04_23: 154 APATIEEDGEHNGTKESRKFVTGGADN---LVKIWKYNSDAQTYVLESTL-EGHSDWVRDVAWSP-TVLLRSYLASVSQD
                                                                                                                                   228 (297)
 Q Consensus
                        154
                            -----l-tq-d----i-wd------h---v-l--s----las-s-D
                                                                                                                                   228 (297)
                                                  .++++++.|+ .|++||++.... +...+.+|...|.+++|+|| ++
                                               ----l----d----i-iwd-------h---v----s--
                                                                                                                   --~-i~s~-
                                                                                                                                   284 (416)
 T Consensus
                                                                                                                              ~~d
                                       -----TRVATATGSDNDPSILIWDLRNANT---PLQTLNQGHQKGILSLDWCHQDE---HLLLSSGRD
 T 2pm9_A
                                                                                                                                   284 (416)
                             CSSCT-----TEEEEEECCSSSCCCCEEETTSTTS--CSBCCCSCCSSCEEEEECSSCS--SCEEEEESS
 T ss_dssp
                             CCCCC-----CEEEEECCCCCceEEEEeccCCC---cceeeccCcCCEEEEEecCCCC---CeEEEEeCC
 T ss pred
                            Q ss pred
                       229 RTCIIWTQDNEQGPWKKTLLKEEKFPDVLWRASWSLSG-NVLALSGGDNKVTLWKEN
 Q Fri Mar 04 23:
                       229 g-i-iw----d--i-iw---
 O Consensus
                                             ....+.. +...|.+++|+|++ ++|++++.||.|++|+..
                             |.|++||+....
                        T Consensus
                                                                                                      336 (416)
                        285 NTVLLWNPESAE---QLSQFPA--RGNWCFKTKFAPEAPDLFACASFDNKIEVQTLQ
 T 2pm9 A
                                                                                                      336 (416)
                             SEEEEECSSSCC---EEEEEEC--SSSCCCCEEECTTCTTEEEECCSSEEEEEESC
 T ss dssp
                             CCEEEECCCCc---eeeeccC--CCcceEEEEECCCCCEEEEEeCCC
 T ss pred
                                            PDB"
                     No 98
                                                          NCBI
                                                                        Pub Med
            Protein DOA1; ubiquitin, nuclear protein; HET: MSE MES; 1.35A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.8e-33 Score=235.26 Aligned_cols=253 Identities=20% Similarity=0.328 Sum_probs=0.0
                            ceEecCCcCeeeEEEccCCcEEEEEcCCCcEEEEEccCC-ccceeEEeccCCcCEEEEEccCCcCEEEEEccCCceEE
 0 ss pred
 Q Fri_Mar_04_23:
                          2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGE-THKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL
                                                                                                                                    80 (297)
                          2 \  \  \, \sim \sim \sim \sim h \sim \sim v \sim \sim \sim \sim g \sim 1 - t \sim s - d \sim v \sim 1 w d \sim \sim \sim \sim \sim \sim h \sim \sim v \sim \sim \sim \sim \sim \sim \sim 1 - s \sim s - D \sim i \sim s \sim 1 - s s 
                                                                                                                                    80 (297)
                             T Consensus
                                                                                                                                   127 (313)
                         52 GTVVYTGQGFLNSVCYDSEKELLLFGGKDTMINGVPLFATSGEDPLYTLIGHQGNVCSLSFQ----DGVVISGSWDKTAK
 T 3odt A
                                                                                                                                   127 (313)
 T ss dssp
                            EEEEEECSSCEEEEEETTTTEEEEEETTSCEEEEETTCCTTSCC-CEECCCSSCEEEEEE----TTEEEEEETTSEEE
 T ss_pred
                            eeEEecCCceEEEEECCCCCEEEEecCCCCceeEEccCCCCceeEEEecccCCCCEE
 Q ss_pred
                            EEEccCCeEEEEEecccCccEEEEEEcCC-ccCCcEEEEEECCCCEEEEEEecCCCcchhhhhhhh-cccceeEEEECCCcc
 Q Fri_Mar_04_23:
                        81 IWKEENGRWSQIAVHAVHSASVNSVQWAP-HEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDA-HAIGVNSASWAPATI
                                                                                                                                   158 (297)
                                                                -----l----d--i-i-----------
 Q Consensus
                         81 iwd~~~~
                                                                                                                                   158 (297)
                                         ....+..|...+.++.+.| + +..++++.|+.|++|+....
 T Consensus
                        128 iW~~~~h~~~v~~~~
                                                                  -----l-s-s-D--i--W------
                                                                                                                                   196 (313)
                        128 VWKEGS----LVYNLQAHNASVWDAKVVSFS--ENKFLTASADKTIKLWQNDKV----IKTFSGIHNDVVRHLAVVDDG-
 T 3odt A
                                                                                                                                   196 (313)
 T ss dssp
                            EEETTE----EEEEEECCSSCEEEEEEETT--TTEEEEEETTSCEEEEETTEE----EEEECSSCSSCEEEEEEETT-
```

```
T ss_pred
                  EEECCC----eEEEEeCCCCcEEEEEEECCC--CCeEEEEeCCCceEEEeeCCCc----cceeccCCCCeEEEEECCCC-
                  \verb|cccccCCcceeEEEEeCCceeEEEEeccCCceeEEEEeccCCceeEEEEEcccCcceeEEEEeccCceeEEEEeccc||
 0 ss pred
 Q Fri_Mar_04_23: 159 EEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDN
                                                                                    238 (297)
               238 (297)
               T Consensus
                                                                                    255 (313)
               197 -----HFISCSNDGLIKLVDMHTGD----VLRTYEGHESFVYCIKLLPN----GDIVSCGEDRTVRIWSKEN
 T 3odt A
                                                                                    255 (313)
                     -----EEEEEETTSEEEEETTTCC---EEEEEECCSSCEEEEECTT----SCEEEEETTSEEEEECTT
 T ss dssp
 T ss_pred
                      CCCceeEEEecccCCceEEEEECCCCCEEEEECCCCCEEEeeeccC
 Q ss pred
 Q Fri Mar 04 23: 239 EQGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQ 297 (297)
               O Consensus
                     ....+.. +...++++|+|+++ +++++.|++|+||+....++|....
                                                                   307 (313)
 T Consensus
               256 ----s-D--i-iw-----
               256 GS---LKQVITL--PAISIWSVDCMSNGD-IIVGSSDNLVRIFSQE-KSRWASEDEIKG 307 (313)
 T 3odt A
                  CC---EEEEEEC--SSSCEEEEEECTTSC-EEEEETTSCEEEEESC-GGGCCC-----
 T ss_dssp
 T ss pred
                  Ce---eEEEEEc--CCccEEEEEecCCCC-EEEEeCCCceEEEEECC-cccccHHHHHHh
                           PDB<sup>N</sup>
PROTEIN DATA BANK
                                              Pub Med
 No 99
>4ery A WD repeat-containing protein 5; WD40, WIN motif, beta propeller, 3-10 helix, lysine methyltransferase,
RBBP5, ASH2L, core complex; 1.30A {Homo sapiens} PDB: 2h6k A* 2h68 A* 2h6q A* 3eg6 A 4erq A 2h6n A 4erz A 4e
4esg A 4ewr A 2gnq A 2x12 A 2x13 A 3uvk A* 3ps1 A* 3uvl A 3uvm A 3uvn A 3uvo A 4cy2 A ...
Probab=100.00 E-value=1e-32 Score=229.93 Aligned_cols=250 Identities=23% Similarity=0.349 Sum_probs=0.0
                  ceEecCCcCeeeEEEccCCcEEEEEccCCcceeEEeccCCcceeEEeccCCccCEEEEE
 Q ss pred
 Q Fri_Mar_04_23:
                 2 VVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLI
                                                                                     81 (297)
                 2 -----h---v-----g--l-t-s-d--v-lwd------h---v----
                T Consensus
                                                                                     91 (312)
                16 KFTLAGHTKAVSSVKFSPNGEWLASSSADKLIKIWGA--YDGKFEKTISGHKLGISDVAWSSD--SNLLVSASDDKTLKI
 T 4ery A
                                                                                     91 (312)
 T ss_dssp
                  EEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEET--TTCCEEEEECCCSSCEEEEEECTT--SSEEEEEETTSEEEE
                  EEEcccCCCceeEEEECCCCCEEEEeeCCCcEEEEec--CCCceeeeeccccceeEEEECCC--CCEEEEEeCCCCEEE
 T ss pred
                  Q ss pred
 Q Fri Mar 04 23:
                82 WKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEED
                                                                                    161 (297)
                82 wd~~~~
                       Q Consensus
                                                                                    161 (297)
                   ||+++++ ....+..|...+.+++|+|+ +..+++++.|+.|++||+.... ....+..|...+..+++|+|++
 T Consensus
                161 (312)
                92 WDVSSGK--CLKTLKGHSNYVFCCNFNPO--SNLIVSGSFDESVRIWDVKTGK--CLKTLPAHSDPVSAVHFNRDG----
 T 4ery_A
                                                                                    161 (312)
                  EETTTCC--EEEEECCSSCEEEEECSS--SSEEEEEETTSCEEEEETTTCC--EEEEECCCSSCEEEEECTTS----
 T ss dssp
                  EECCCCe--eEEEEeCCCCceEEEEECCC--CCEEEEecCCCceEEEEECCCC--eeeecccCCCCEEEEEEcCCC---
 T ss pred
 Q ss_pred
                  Q Fri_Mar_04_23:
               162 GEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQG
                                                                                    241 (297)
               162 -----latg-d-i-wd-----h--v-l-ss-s-Dg-i-iw-----
 Q Consensus
                                                                                    241 (297)
                        T Consensus
               162 -----SLIVSSSYDGLCRIWDTASGQ---CLKTLIDDDNPPVSFVKFSPNG---KYILAATLDNTLKLWDYSKGK-
 T 4ery A
                                                                                    225 (312)
 T ss_dssp
                  -----SEEEEEETTSCEEEEETTTCC---EEEEECCSSCCCEEEEEECTTS---SEEEEEETTTEEEEEETTTTE-
                  -----CEEEEecCCCcEEEeeCCCCc--EEEEEECCCCC--CEEEEECCCCC--CEEEEE
 T ss_pred
                  ceeEEEecccCCceEEEEE
 Q ss pred
 Q Fri_Mar_04_23: 242 PWKKTLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
               242 ----d--i-iw-
                                                    282 (297)
 O Consensus
                   .....+++++|++++.||.|++|+
 T Consensus
               226 -----1-s---d--i-vwd 265 (312)
               226 -CLKTYTGHKNEKYCIFANFSVTGGKWIVSGSEDNLVYIWN 265 (312)
 T 4ery A
                  -EEEEECSSCCSSSCCCEEEECSSSCEEEECCTTSCEEEEE
 T ss_dssp
 T ss_pred
                  -EEEEEecCCCceeeeeee
 No 100
                            SCOPe PODE"
                                               NCBI
                                                              Pub Med
->4ggc_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; HET:
 MRD; 1.35A {Homo sapiens} SCOP: b.69.4.0 PDB: 4n14 A*
Probab=100.00 E-value=3.3e-33 Score=234.19 Aligned cols=243 Identities=21% Similarity=0.364 Sum probs=0.0
 Q ss_pred
                  CcCeeeEEEccCCcEEEEEccCCcceeEEccCCccceeEEccCCccceEEEEccCCccCeEEEEEccCCc
 Q Fri_Mar_04_23:
                8 HNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEENG
                                                                                     87 (297)
 O Consensus
                 8 h---v-----g--1-t-s-d--v-lwd-------h---v------l-s-s-D--i-iwd----
                                                                                     87 (297)
                T Consensus
                                                                                     99 (318)
 T 4ggc A
                99 (318)
 T ss dssp
                  {\tt CCTTCBCEEECTTS--EEEEEETTEEEEEETTTCCEEEEEEECCSTTCCEEEEEECTT--SSEEEEEETTSEEEEEETTTT}
 T ss_pred
                  cccccccCCC--eEEEEcCCEEEEEeCCCcceeeeeecCCCcEEEEEECCC--CCEEEEEECCCC
                  Q ss pred
 Q Fri_Mar_04_23:
                88 RWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIIDAHAIGVNSASWAPATIEEDGEHNGT
                                                                                    167 (297)
                  + .+..+..|...|.+++|++. ++++++.|+..+++||+... .....+.+||...|.+++|+|++
 Q Consensus
                88 ~~~
                                                                                    167 (297)
               T Consensus
```

```
100 K--RLRNMTSHSARVGSLSWNSY----ILSSGSRSGHIHHHDVRVA-EHHVATLSGHSQEVCGLRWAPDG------ 162 (318)
E--EEEEEECCSSCEEEEEETT----EEEEEETTSEEEEEETTSS-SCEEEEEECCSSCERRRFFCTTG.
T 4ggc_A
T ss_dssp
                   c--eeeccccCceeeeecCcc---EEEEEcCCCCEEEEecccc-ccceeeecCCCCCEeEEEECCCC-----
T ss_pred
Q ss_pred
                   CCCEEEEEECCCCCEEEEEECCCCCceeEEEEEECCCCCCCEEEEEE.
Q Fri_Mar_04_23: 168 KESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS--QDRTCIIWTQDNEQGPWKK 245 (297)
Q Consensus
               168 -----l-tq--d--i--wd-------h---v--l--s-----las-s---Dq-i-iw------
                                                                                             245 (297)
                     .+|++|+.|+.|++||+..+....+..+|...|.+++|+|++ ..++++++ .|++|++|++|
T Consensus
               163 ----las-s-D--v-vwd--------h---v-v--p-----l-s--s-b-i-iwd-----
                                                                                         --- 232 (318)
T 4ggc_A
             163 ---RHLASGGNDNLVNVWPSAPGEGGWVPLQTFTQHQGAVKAVAWCPWQ--SNVLATGGGTSDRHIRIWNVCSGA---- 232 (318)
T ss_dssp
                ---seeeeeettsceeeeesscbttbsccseeecccsceeeeeectts--tteeeeeectttceeeeeetttcc----
                   ---CEEEEEeCCCeEEEecCCCcCcccceeeecCCCceEEEEEccCC--CCEEEEeccCCCcEEEEECCCC----
T ss_pred
                   EEecccCCceEEEEECCCCCEEEEc--CCCCEEEEE
Q ss_pred
Q Fri_Mar_04_23: 246 TLLKEEKFPDVLWRASWSLSGNVLALSG--GDNKVTLWK 282 (297)
            246 ----i---i-----l-----l--i-iw- 282 (297)
O Consensus
               T Consensus
              233 -CLSAVDAHSQVCSILWSPHYKELISGHGFAQNQLVIWK 270 (318)
T 4ggc_A
T ss_dssp
                -EEEEEECSSCEEEEEETTTTEEEEEECTTTCCEEEEE
T ss_pred
                   -EeEEeccCCceeEEEECccCceEEEE
```

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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