

```
■ 14 41g9_A F-box-like/WD repeat-co 100.0 1.7E-36 4.6E-41 275.0 38.0
                                                                           296
                                                                                  4-343
                                                                                            50-367 (400)
  15 \ 4wju\_A Ribosome assembly prote 100.0 1.5E-37 4.2E-42
                                                              290.8
                                                                     31.3
                                                                           288
                                                                                  2-332
                                                                                           136-514 (515)
  16 2pbi B Guanine nucleotide-bind 100.0 1.3E-36 3.6E-41
                                                              271.2
                                                                     35.7
                                                                           293
                                                                                   2-332
                                                                                            57-354
                                                                                                   (354)
     3fm0 A Protein CIAO1: WDR39,SG 100.0 2.6E-36 7.3E-41
                                                              268.1
                                                                     36.5
                                                                           308
                                                                                   1-345
                                                                                             7-345
                                                                                                   (345)
  18 leri A Transcriptional repress 100.0 1.3E-36 3.7E-41
                                                              274.9
                                                                     33.8
                                                                                   7-334
                                                                                            62-388
                                                                                                   (393)
                                                              274.5
                                                                           287
                                                                                            43-340
  19 3jb9_L PRE-mRNA-splicing facto 100.0 2.3E-37 6.4E-42
                                                                     28.0
                                                                                   2-334
                                                                                                   (340)
  20 3frx A Guanine nucleotide-bind 100.0 5.1E-36 1.4E-40
                                                              263.4
                                                                     35.6
                                                                           295
                                                                                   2-337
                                                                                            10-319 (319)
  21 3jam_g RACK1; eukaryotic trans 100.0 5.9E-36 1.6E-40
                                                              263.7
                                                                     35.5
                                                                           298
                                                                                   1-337
                                                                                            10-326 (326)
  22 41g8 A PRE-mRNA-processing fac 100.0 3.2E-36 8.9E-41
                                                              268.7
                                                                     33.6
                                                                           280
                                                                                   8-333
                                                                                            67-354 (354)
  23 4j0w_A U3 small nucleolar RNA- 100.0 6.4E-36 1.8E-40
265.6
                                                                           303
                                                                                   2-349
                                                                                             7-336
                                                                                                   (343)
                                                                     34.0
  24 4j87 A Coatomer subunit alpha; 100.0 1.6E-35 4.4E-40
                                                              261.1
                                                                                   3-334
                                                                                            47-327
                                                                                                   (327)
  25 4wjs_A RSA4; ribosome assembly 100.0 7.2E-36
                                                              277.5
                                                                     34.8
                                                                           287
                                                                                   3-332
                                                                                           108-484
                                                                                                   (485)
  26 4bh6 A APC/C activator protein 100.0 2.2E-35
                                                      6E - 40
                                                              258.3
                                                                     35.4
                                                                           243
                                                                                   8-337
                                                                                            61-308
                                                                                                   (308)
  27 4d6v A GIB2, G protein beta su 100.0 5.3E-35 1.5E-39
                                                              256.2
                                                                     37.4
                                                                           289
                                                                                   5-333
                                                                                            11-312
                                                                                                   (314)
  28 4a11 B DNA excision repair pro 100.0 2.4E-35 6.6E-40
                                                                           296
                                                                                   2-336
                                                                                            36-366 (408)
                                                              268.1
                                                                     35.6
  29 5cxb_B Ribosome biogenesis pro 100.0 1.2E-35 3.3E-40
                                                              266.5
                                                                                   3-332
                                                                                            15-369
                                                                                                   (369)
  30 4jsn_D Target of rapamycin com 100.0 2.2E-34 6.1E-39
                                                              253.8
                                                                     34.2
                                                                           291
                                                                                  12-349
                                                                                             3-312 (326)
                                                                                           173-465 (465)
  31 5gan H U4/U6 small nuclear rib 100.0 2.4E-35 6.7E-40
                                                              272.5
                                                                     28.7
                                                                           285
                                                                                   7-332
  32 4j73 A Coatomer subunit beta'; 100.0
                                              4E-34 1.1E-38
                                                              249.4
                                                                     34.1
                                                                           247
                                                                                   3-330
                                                                                            49-298 (301)
  33 3ei3 B DNA damage-binding prot 100.0 1.9E-34 5.3E-39
                                                              259.8
                                                                           290
                                                                                   3-335
                                                                                            67-382 (383)
                                                                     32.8
  34 3w15 A Peroxisomal targeting s 100.0 5.3E-34 1.5E-38
                                                              255.6
                                                                     35.0
                                                                           271
                                                                                   1-349
                                                                                             3-335
                                                                                                   (368)
  35 4ery_A WD repeat-containing pr 100.0 1.7E-33 4.6E-38
                                                              246.1
                                                                     37.2
                                                                           295
                                                                                   1-335
                                                                                            15-312 (312)
  36 4yvd_A Pleiotropic regulator 1 100.0 1.8E-33
                                                                           294
                                                              252.1
                                                                     37.4
                                                                                   3-344
                                                                                            58-362
                                                                                                   (374)
  37 5ams_A SQT1, ribosome assembly 100.0 3.5E-34 9.6E-39
                                                              262.1
                                                                     33.3
                                                                           285
                                                                                   5-335
                                                                                           105-431 (431)
  38 4ggc_A P55CDC, cell division c 100.0 1.9E-33 5.2E-38
                                                              247.0
                                                                     36.5
                                                                           246
                                                                                   5-337
                                                                                            63-317 (318)
  39 41q9 A F-box-like/WD repeat-co 100.0 1.3E-33 3.5E-38
                                                                                   7-334
                                                                                           109-399 (400)
                                                              256.0
                                                                     35.8
                                                                           279
     4j0x A Ribosomal RNA-processin 100.0 2.4E-34 6.7E-39
                                                              264.2
                                                                           304
                                                                                   2-349
                                                                                            25-450
                                                                                                   (451)
                                                                     31.2
  41 1k8k_C P40, ARP2/3 complex 41 100.0 5.6E-34 1.5E-38
                                                              254.8
                                                                           296
                                                                                   3-334
                                                                                             2-360
                                                                                                   (372)
  42 4zoy_A SQT1; chaperone, riboso 100.0 1.5E-33 4.2E-38
                                                              261.0
                                                                     35.2
                                                                           311
                                                                                   1-338
                                                                                             7-488 (491)
  43 5ams A SQT1, ribosome assembly 100.0 1.2E-33 3.4E-38
                                                              258.5
                                                                     33.8
                                                                           301
                                                                                   1-349
                                                                                            57-392 (431)
  44 5cvl A WD repeat-containing pr 100.0 4.9E-34 1.4E-38
                                                              271.5
                                                                     32.0
                                                                           300
                                                                                   2-335
                                                                                            38-343 (598)
                                                                                   7-336
  45 4psw B Histone acetyltransfera 100.0 9.6E-34 2.6E-38
                                                              257.0
                                                                     32.4
                                                                           245
                                                                                           116-385 (401)
     4gga_A P55CDC, cell division c 100.0 4.4E-33 1.2E-37
                                                                                   5-338
                                                                                           143-398
                                                                                                   (420)
  47 3sfz_A APAF-1, apoptotic pepti 100.0 1.4E-33 3.9E-38
                                                              289.6
                                                                     35.9
                                                                           294
                                                                                   2-336
                                                                                           608-1035(1249
     5cvo_A WD repeat-containing pr 100.0 8.1E-34 2.2E-38
                                                              272.3
                                                                     31.9
                                                                           300
                                                                                   2-335
                                                                                            23-328 (677)
  49 3dwl_C Actin-related protein 2 100.0 8.4E-35 2.3E-39
                                                              261.0
                                                                     23.2
                                                                           293
                                                                                   1-333
                                                                                             3-377 (377)
  50 3jb9 K PRE-mRNA-splicing facto 100.0 1.9E-34 5.2E-39
                                                                           286
                                                                                   3-336
                                                                                           157-453 (473)
                                                              267.1
                                                                     26.1
  51 3dm0 A Maltose-binding peripla 100.0 6.3E-33 1.7E-37
                                                              268.7
                                                                     37.7
                                                                           295
                                                                                   2-334
                                                                                           375-692
                                                                                                   (694)
  52 2hes_X YDR267CP; beta-propelle 100.0 1.5E-32 4.2E-37
                                                              241.0
                                                                                   3-337
                                                                                             8-330
                                                                                                   (330)
  53 3gre_A Serine/threonine-protei 100.0 5.9E-34 1.6E-38
                                                                           288
                                                              260.9
                                                                     27.7
                                                                                   3-332
                                                                                            56-437
                                                                                                   (437)
  54 4nsx A U3 small nucleolar RNA- 100.0 1.1E-32 3.1E-37
                                                              266.4
                                                                     38.0
                                                                           315
                                                                                   5-343
                                                                                           244-624 (684)
  55 4e54 B DNA damage-binding prot 100.0 2.4E-34 6.7E-39
                                                              263.4
                                                                     23.6
                                                                           297
                                                                                   1 - 340
                                                                                           111-435 (435)
                                                                           298
                                                                                            10-357 (357)
  56 3i2n A WD repeat-containing pr 100.0 3.9E-33 1.1E-37
                                                              249.1
                                                                     30.7
                                                                                   1-339
  57 3sfz_A APAF-1, apoptotic pepti 100.0 3.1E-33 8.6E-38
                                                                           303
                                                                                           653-1160(1249
  58 5a31 R The anaphase-promoting 100.0 2.2E-32 6.1E-37
                                                              246.8
                                                                     35.5
                                                                           244
                                                                                   8-338
                                                                                           130-378 (386)
  59 3mmy_A MRNA export factor; mRN 100.0 3.6E-33
                                                              250.2
                                                                           273
                                                                                   1-340
                                                                                            31-354 (368)
                                                      1E-37
                                                                     30.0
  60 4zox A Ribosome assembly prote 100.0 1.8E-32
                                                      5E-37
                                                              245.7
                                                                     34.1
                                                                           305
                                                                                  1-335
                                                                                             7-381 (381)
  61 2j04_B YDR362CP, TAU91; beta p 100.0 8.9E-34 2.4E-38
                                                              266.0
                                                                     26.4
                                                                           281
                                                                                   5-336
                                                                                           203-518 (524)
                                                                                            92-420 (420)
  62 3vl1 A 26S proteasome regulato 100.0 1.5E-32 4.2E-37
                                                              250.2
                                                                     32.3
                                                                           294
                                                                                   5-336
     409d B RIK1-associated factor 100.0
                                                                           289
                                                                                   3-334
                                                                                            24-409 (428)
  64 lgxr_A ESG1, transducin-like e 100.0 4.7E-32 1.3E-36
                                                              239.1
                                                                                   7-335
                                                                                            49-337 (337)
                                                                     33.7
                                                                           285
     5dfz B Serine/threonine-protei 100.0 8.8E-35 2.4E-39
                                                              297.2
                                                                     17.8
                                                                           291
                                                                                   1-333
                                                                                          1062-1445(1460)
  66 4ci8 A Echinoderm microtubule- 100.0 5.2E-32 1.4E-36
                                                              260.6
                                                                     36.1
                                                                           320
                                                                                   2-349
                                                                                           104-512 (655)
                                                                           306
                                                                                   3-343
                                                                                            84-414 (598)
  67 5cvl_A WD repeat-containing pr 100.0
                                              4E-32 1.1E-36
                                                              258.4
                                                                     34.6
  68 4aez_A CDC20, WD repeat-contai 100.0 6.5E-32 1.8E-36
                                                              244.9
                                                                           254
                                                                                   2-340
                                                                                           127-385
                                                                                                   (401)
                                                                     34.4
  69 3mkq_A Coatomer beta'-subunit; 100.0 1.6E-32 4.3E-37
                                                              270.6
                                                                           257
                                                                                   1-342
                                                                           299
  70 3jro_A Fusion protein of prote 100.0 1.5E-32 4.1E-37
                                                              268.3
                                                                     32.2
                                                                                   1-333
                                                                                             1-327
                                                                                                   (753)
  71 4xyh_A Kinetochore protein MIS 100.0 1.2E-32 3.2E-37
                                                              252.1
                                                                     28.3
                                                                           251
                                                                                   7-334
                                                                                           129-413 (430)
  72 4ci8 A Echinoderm microtubule- 100.0 7.7E-32 2.1E-36
                                                                           295
                                                                                           255-624 (655)
                                                              259.4
                                                                     35.3
                                                                                   6-349
  73 1r5m A SIR4-interacting protei 100.0 2.1E-32 5.8E-37
                                                                           301
                                                                                            35-359 (425)
                                                              249.0
                                                                     29.7
                                                                                   1-333
  74 3k26_A Polycomb protein EED; W 100.0 4.9E-32 1.3E-36
                                                                                                   (366)
  75 5cvo_A WD repeat-containing pr 100.0 7.7E-32 2.1E-36
                                                              258.7
                                                                     34.0
                                                                           306
                                                                                   3-343
                                                                                            69-399
                                                                                                   (677)
  76 2ymu_A WD-40 repeat protein; u 100.0 9E-32 2.5E-36
                                                              254.8
                                                                     34.1
                                                                           280
                                                                                  2-332
                                                                                             9-290 (577)
  77 5cxb A Ribosome biogenesis pro 100.0 1.3E-31 3.6E-36
                                                              250.7
                                                                     34.6
                                                                           285
                                                                                   7-335
                                                                                           128-508 (514)
  78 4nsx A U3 small nucleolar RNA- 100.0
                                              3E-31 8.2E-36
                                                              256.4
                                                                     37.7
                                                                           299
                                                                                   5-349
                                                                                           202-585 (684)
  79 2pm9 A Protein WEB1, protein t 100.0
                                              1E-32 2.9E-37
                                                              251.1
                                                                     25.5
                                                                           268
                                                                                   7-338
                                                                                            65-340
                                                                                                   (416)
  80 4xfv_A Elongator complex prote 100.0 7.7E-32 2.1E-36
                                                              264.2
                                                                           321
                                                                                   2-349
                                                                                            12-443
                                                                                            10-295 (313)
  81 3odt_A Protein DOA1; ubiquitin 100.0 1.7E-31 4.6E-36
                                                              234.2
                                                                     32.1
                                                                           282
                                                                                   1-334
  82 2ymu_A WD-40 repeat protein; u 100.0 2.7E-31 7.4E-36
                                                              251.5
                                                                     35.4
                                                                           279
                                                                                   3-332
                                                                                           297-577
                                                                                                   (577)
  83 2xyi A Probable histone-bindin 100.0 3.3E-32 9.1E-37
                                                              249.1
                                                                     27.9
                                                                           272
                                                                                   7-334
                                                                                           126-409 (430)
                                                                                  50-349
                                                                                           103-380
  84 1vyh C Platelet-activating fac 100.0 5.5E-32 1.5E-36
                                                              246.1
                                                                     28.7
                                                                           255
                                                                                                   (410)
  85 4gqb_B Methylosome protein 50; 100.0
                                              3E-31 8.2E-36
                                                              235.1
                                                                     32.6
                                                                           250
                                                                                   7-336
                                                                                            80-332
                                                                                                   (344)
                                                                                           100-424
  86 1r5m_A SIR4-interacting protei 100.0 3.5E-31 9.7E-36
                                                              240.9
                                                                     33.2
                                                                           277
                                                                                   1-334
  87 4jsn_D Target of rapamycin com 100.0 3.4E-31 9.4E-36
                                                              233.5
                                                                     31.5
                                                                           272
                                                                                   3-315
                                                                                            36-323
                                                                                                   (326)
  88 5a9q 2 Nucleoporin NUP37; tran 100.0 7.1E-32
                                                      2E-36
                                                              237.1
                                                                     27.0
                                                                           285
                                                                                   7-335
                                                                                            14-326 (326)
  89 5alu D Coatomer subunit beta': 100.0 6.3E-31 1.7E-35
                                                              261.8
                                                                     35.8
                                                                           288
                                                                                   1-331
                                                                                             7-298
                                                                                                   (905)
  90 3vl1 A 26S proteasome regulato 100.0 1.4E-31 3.7E-36
                                                              243.9
                                                                     27.9
                                                                           286
                                                                                   5-333
                                                                                            24-362 (420)
  91 4g56_B MGC81050 protein; prote 100.0 6.2E-31 1.7E-35
                                                                           300
                                                                                            38-350 (357)
  92 2j04 B YDR362CP, TAU91; beta p 100.0 8.9E-33 2.5E-37
                                                              259.2
                                                                     20.3
                                                                           255
                                                                                   2-336
                                                                                           126-429
                                                                                                   (524)
                                                                                           184-611 (611)
  93 1nr0_A Actin interacting prote 100.0 3.5E-30 9.6E-35
                                                              244.5
                                                                     38.2
                                                                           309
                                                                                   3-335
  94 1sq9_A Antiviral protein SKI8; 100.0 2.1E-31 5.7E-36
                                                              240.5
                                                                     28.4
                                                                           295
                                                                                   2-336
                                                                                             9-396 (397)
  95 3v7d B Cell division control p 100.0 1.7E-30 4.6E-35
                                                              240.1
                                                                     34.8
                                                                           256
                                                                                   2-335
                                                                                           114-381 (464)
     4u7a_A Ribosome biogenesis pro 100.0 4.6E-31 1.3E-35
                                                                                           450-826 (826)
                                                              259.7
                                                                     31.1
                                                                           289
                                                                                   3-333
  97 4i79_A Nucleoporin NUP43; stru 100.0 1.3E-30 3.6E-35
                                                              235.9
                                                                           258
                                                                                   8-342
                                                                                            28-319
                                                                                                   (399)
  98 3jro_A Fusion protein of prote 100.0 9.9E-32 2.7E-36
                                                                           292
                                                                                   5-336
                                                              262.5
                                                                     24.0
                                                                                            49-377
                                                                                                   (753)
  99 2ovr_B FBW7, F-BOX/WD repeat p 100.0 1.4E-29 3.9E-34
                                                              232.7
                                                                     36.6
                                                                           290
                                                                                   2-349
                                                                                           111-405
                                                                                                   (445)
100 4ui9 R Fizzy-related protein h 100.0 9.3E-30 2.6E-34
                                                              236.7
                                                                     33.7
                                                                           248
                                                                                   5-338
                                                                                           225-477 (493)
                                     PDB<sup>IM</sup>
PROTEIN DATA BANK
  No 1
                                                 NCBI
                                                             Pub Med
```

🗌 >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=4.8e-52 Score=370.41 Aligned cols=349 Identities=100% Similarity=1.521 Sum probs=0.0
                                  \tt CCccCCCCCeEEEEEECCCCCEEEEEECCCCCCeeEeeeeccccceEEEEECCCCCCEEEEEeCCCc
0 ss pred
Q Fri_Mar_04_23:
                              1 MOPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                                                                                                   80 (349)
                              1 ~~~~~h~~~v~~~s~d~~lat~s~D~~v~iwd~~~~~~h~~~v~~v~~v~~~~~las~s~Dg~
Q Consensus
                                                                                                                                                                   80 (349)
                                 3 ----gh---V--v-s-dg--las-s-D--v-iWd------h---V--v-s---g--las-s-D--
T Consensus
                                                                                                                                                                   82 (351)
                              3 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
T 3f3f A
                                                                                                                                                                   82 (351)
                                  CCCEECCCSSCEEEEEECSSSSEEEEEETTSEEEEEEECSSSCCEEEEEEECCSSCEEEEEECCGGGCSEEEEEETTSC
T ss_dssp
T ss_pred
                                  EEEeeccCccccccccceeEEEEcCCCCcEEEEEEccCCCcEEEEEecCCCcceeeeccccEEEeecC
Q ss pred
                            81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
Q Fri Mar 04 23:
                                                                                                                                                                 160 (349)
                                                                                         ---p-----l-----d--i-iwd----
                                                                                                                                                                 160 (349)
O Consensus
                                  |+|||+..+...+..+..+..+..+|...|..||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...||...
T Consensus
                             83 v-iWd-----h---v--v--sp---g-1-s---d--v-lwd-------
                                                                                                                                                                 162 (351)
                             83 VKIWEEDPDOEECSGRRWNKI.CTI.NDSKGSI.YSVKFAPAHI.GI.KI.ACI.GNDGII.RI.YDAI.EPSDI.RSWTI.TSEMKVI.SIP
T 3f3f A
                                                                                                                                                                 162 (351)
                                  EEEEEECTTSCTTSSCSEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTCEEEEEECSSTTCTTCCEEEEEEESCSCC
T ss_dssp
T ss pred
                                  Q ss_pred
                                  Q Fri Mar 04_23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSALEQAIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
                                                                                                                                                                 240 (349)
                            Q Consensus
                                                                                                                                                                 240 (349)
                                  -----lasgs-D--v
T Consensus
                                                                                                                                                                 242 (351)
                            163 PANHLQSDFCLSWCPSRFSPEKLAVSALEQAIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
T 3f3f A
                                                                                                                                                                 242 (351)
T ss dssp
                                  CSSCSCCCERRECCCSSSCCERRERETTERERERECCTTSCERRECCCCCCCCERRERECCCCSSCSSERRERETTSCR
                                  CCcccCcEEEeECCCcCCceeEEecccceEEEEecCCCcEEEEEEeCCCCcceEEEECCCCcc
T ss_pred
Q ss_pred
                                  Q Fri_Mar_04_23: 241 RIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILS
                                                                                                                                                                 320 (349)
O Consensus
                            241 ~vwd~~~~i~v~spdg~~la
                                                                                                                                                                 320 (349)
                                 ~s~~~
                                                                                                                              ----h---V--v--spdg--la
T Consensus
                            243 ~iWd~~~~
                                                                                                                                                                 322 (351)
                            243 RIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILS
T 3f3f A
                                                                                                                                                                 322 (351)
                                  EEEEEEECC------CCSEEEEEEECTTSSCEEEEEECSSSCCEE
T ss_dssp
                                  T ss pred
Q ss_pred
                                  EecCCCeEEEEeccCCceEEEEeeccC
Q Fri_Mar_04_23: 321 SAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
O Consensus
                            321 s-s-D--v-iW------
                                                                                  349 (349)
                                 ||+.|++||||++...++|.|+.++++|
                            323 s~s~D~~v~lW~~~~~~~~~~
                                                                                  351 (351)
T Consensus
                            323 SAGDDGKVRLWKATYSNEFKCMSVITAQQ 351 (351)
T 3f3f A
T ss_dssp
                                  EEETTSCEEEEECTTSCEEEEEEC--
                                  EecCCCeEEEehhccCCcEEEEEeccCC
T ss pred
No 2
                                                                                                     Pub Med
             Eukaryotic translation initiation factor 3 subuni; EIF3 complex, beta-propeller; 2.00A {Saccharomyces
cerevisiae} PDB: 3zwl _B
Probab=100.00 E-value=1.1e-42 Score=309.62 Aligned_cols=307 Identities=18% Similarity=0.288 Sum_probs=0.0
                                  CCcc-cCCCcCeEEEEECCCCCEEEEEECCCCCCceeEeeecccccceEEEECCCCCCCEEEEEECCCCCCEEEEE
Q ss pred
                              1 \ \texttt{MQPF-DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDK}
Q Fri Mar 04 23:
                                                                                                                                                                   79 (349)
O Consensus
                              1 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v------las-s-Dq
                                                                                                                                                                   79 (349)
                                  T Consensus
                                                                                                                                                                   74 (347)
T 4ule_I
                              1 MKAIKLTGHERPLTQVKYNKEGDLLFSCSKDSSASVWYSLNG---ERLGTLDGHTGTIWSIDVDC--FTKYCVTGSADY
                                                                                                                                                                   74 (347)
                                  CEEEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEETTTC----CEEEEECCCCSCEEEEEECT-TSSEEEEEETTT
T ss dssp
                                  \texttt{CCceEecCCcceEeeeecCCceEeeeecCCceEeeeecCCc----ceeeeeccCccceeeeeecccc}
T ss pred
                                  eEEEeeccCcccccccceeEEEEccCCCcEEEEEEccC-----CeEEEEECCCCCceeeecccE
Q ss pred
Q Fri Mar 04 23:
                             \textbf{80} \ \ \textbf{TVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGND-----GILRLYDALEPSDLRSWTLTSEM}
                                                                                                                                                                 154 (349)
                             80 ~v~lwd~~~~iwd~~~iwd~~~
Q Consensus
                                                                                                                                                                 154 (349)
                                                               +.+..+. +..+|.+++|+|+ +..++++.+
                                                                                                                          +.+++||+....
                             T Consensus
                                                                                                                                                                 142 (347)
                                                                                                                                                                 142 (347)
T 4ule I
                                  EEEEEETTTC-----CEEEEEE-CSSCEEEEEECTT-SSEEEEEECCCTTCCCEEEEEEECTTTCCEEEECSS
T ss dssp
T ss_pred
                                  Q ss_pred
                                  EERRCCCCcccceREEECccCCCCccREEACCCCCCAREEEECCCCCCCAREEEECCCCCCCAREEEE
Q Fri Mar 04 23: 155 KVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIAT
                                                                                                                                                                 233 (349)
Q Consensus
                            155 -----
                                                                -----h---v--sp-----las
                                                                                                                                                                 233 (349)
                                  143 \hspace{0.1cm} \overset{\cdot}{\sim} \hspace{0.1cm} \overset{\cdot}{\sim} \hspace{0.1cm} \overset{\cdot}{\sim} \hspace{0.1cm} --dg \sim 1 - sg \sim dg \sim i - wd \sim --- -h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim dg \sim i - wd \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim dg \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim dg \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim dg \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim --- \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim --- \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim --- \sim --- \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim --- \sim --- \sim --- \sim h \sim v \sim 1 - fspdg --- \sim 1 - sg \sim --- \sim --- \sim --- \sim h \sim v \sim --- \sim ---
T Consensus
                                                                                                                                                                 213 (347)
T 4ule I
                            143 PIHKIITHEGLDAATVAGWST---KGKYIIAGHKDGKISKYDVSNNY--EYVDSIDLHEKSISDMOFSPDL----TYFIT
                                                                                                                                                                 213 (347)
                                  CSEEEECCTTSCCEEEEEECG---GGCEEEEEETTSCEEEEEGGGTT--EEEEEECCCSSCEEEEEECTTS----SEEEE
T ss_dssp
                                  cceeEecCCCceEEEECC---CCEEEEECCCc-chhhhhhhccCCCceEEEECCCC---CEEE
T ss pred
                                  Q ss pred
Q Fri Mar 04 23: 234 GCKDGRIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEE------KAELQSNLQVELLSEHDDHN 304 (349)
```

```
234 ~s~d~~v~vwd~~~~
 Q Consensus
                                                                                               ~~~~~h~ 304 (349)
                     T Consensus
                                                                                                                     293 (347)
                     214 SSRDTNSFLVDVSTLQVLKKYETDCPLNTAVITPLKEFIILGGGQEAKDVTTTSANEGKFEARFYHKIFEEEIGRVQGHF
 T 4ule I
                                                                                                                     293 (347)
                          EETTSEEEEETTTCCEEEEEECSSCEEEEECSSSSEEEEECC------CCEEEEEEETTTCCEEEEEEE
 T ss dssp
                          T ss pred
                         ceEEEEECCCCCEEEEecc
 Q ss pred
 Q Fri_Mar_04_23: 305 GEVWSVSWNLTGTILSSAGDDGKVRLWKAT 334 (349)
 Q Consensus
                     305 ~~i~~v~~spdg~~las~s~D~~v~iW~~~
                                                             334 (349)
                     +.|++|+||||++||||.|++|||+++
294 ~~V~~vafspdg~~laS~s~D~~vrlW~~~
 T Consensus
                                                             323 (347)
                     294 GPLNTVAISPOGTSYASGGEDGFIRLHHFE 323 (347)
 T 4ule I
 T ss_dssp
                         SCEEEEECTTSSEEEEEETTSCEEEEECC
 T ss_pred
                          eeEEEEECCCCCeEEeccCCccEEEecC
                                        PDB"
 No 3
                                                    NCBI
                                                                         Pub Med
           Nucleoporin SEH1; transport protein; 23.00A {Homo sapiens}
 Probab=100.00 E-value=2.5e-40 Score=295.91 Aligned cols=307 Identities=38% Similarity=0.751 Sum probs=0.0
                         Q ss pred
 Q Fri Mar 04 23:
                       1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                                                      80 (349)
                       1 ------h---v---s-d---l-t-s-D--v-iwd-------h---v--v-v-v------las-s-Dg-
 Q Consensus
                                                                                                                      80 (349)
                         ++..+.+|.+.|++++|+|||++|+||+.|++|+|||+...
                         ~~~l~gH~~~V~~v~fspdg~~las-s~D~ti~lWd~~~~~~l~gH~~~V~~v~~s~~~~g~~laS-s~D~t
 T Consensus
                                                                                                                      82 (360)
 T 5a9q_7
                       4 ARSTAADHKDI.THDVSFDFHGRRMATCSSDOSVKVWDKSES-GDWHCTASWKTHSGSVWRVTWAHPEFGOVI.ASCSFDRT
                                                                                                                      82 (360)
                         CCCEECCCSSCEEEEECSSSSEEEEEETTSEEEEEEECSS-BCEEEEEECCSSCEEEEEECCTTTCSEEEEEETTSC
 T ss dssp
 T ss pred
                         Q ss_pred
                         EEEeeccCccccccc---cceeEEEEcCCCCcEEEEECcCCCcEEEEEEecCCccceeeecccEEEe
 Q Fri_Mar_04_23:
                      81 VKLWEEDPDOEECSGR---RWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVL
                                                                                                                     157 (349)
                                                           ----v----p-----l-----d--i-iwd------
 Q Consensus
                      81 v~lwd~~~
                                                                                                                     157 (349)
                      |++||+.++...|
|++||+.++..|+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||+++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||++.||+
 T Consensus
 T 5a9q 7
                      83 AAVWEEIVGESNDKLRGQSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYEAPDVMNLSQWSLQHEI---
                                                                                                                     159 (360)
 T ss_dssp
                          EEEEEECSSSCCCSSTTCCSEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTCEEEEEECSCSSCSSCCEEEEE---
 T ss_pred
                          EEEEEccCcccccccccccccccccccceeeeeeeee---
                         ecccccceeEEEEccccc--CcceEEecccc------eEEEEecc-CccEEEEEEccccccccc
 Q ss_pred
 Q Fri_Mar_04_23: 158 SIPPANHLQSDFCLSWCPSRF--SPEKLAVSALEQ------AIIYQRGK-DGKLHVAAKLPGHKSLIRSISWAPSIGRW
                                                                                                                     227 (349)
 O Consensus
                     227 (349)
                     T Consensus
                                                                                                                     234 (360)
 T 5a9q_7
                     160 ----SCKLSCSCISWNPSSSRAHSPMIAVGSDDSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNLGRS
                                                                                                                     234 (360)
                         ----ECCSSCCEEEECCCCTTTSCCEEEEECCCCSSSCCCEEEEECSSSCSEEEEECCCCCSCCCEEEECCCSSCS
 T ss_dssp
 T ss_pred
                          ----eecCCccEEEECCcccCCCcEEEEEcCCCCcccceEEEEEecCcCccceEEEEEeccCCCcc
                         Q ss pred
 Q Fri_Mar_04_23: 228 YQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEV
                                                                                                                     307 (349)
                     228 ~~~las~s~d~~v~vwd~~~~~~
 Q Consensus
                                                                                                                     307 (349)
                     ..+++++.| +++|++.....
235 ~~~las~~d-v~iw~~~~~~~~~~~
                                                                                              .....
 T Consensus
                                                                                             V---Hp-----
                                                                                                                     281 (360)
                     235 FHILAIATKD-VRIFTLKPVRKELTSSGG------PTKFEIHIVAQFDNHNSQV
 T 5a9q 7
                                                                                                                     281 (360)
 T ss dssp
                          T ss_pred
                          Q ss pred
                         EEEEECCCCCEEEEecCCCceEEEEeccCC
 O Fri Mar 04 23: 308 WSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAOO 349 (349)
                     308 ~~v~~spdg~~las~s~D~~v~iW~~~~~~~~~
 O Consensus
                                                                           349 (349)
                         282 ~~V~fspdg~-las~s-D~v~iW~~~~1~gh~ 323 (360)
282 WRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGLLKGNG 323 (360)
 T Consensus
 T 5a9q 7
                         CEEEECSSSCCEEEECTTSCEEEEEECSSSCEEEEEEECC-
 T ss dssp
                          EEEEEcCCCCEEEEeccCcc
 T ss pred
                                      SCOPe PROTEIN DATA PANE
                                                                                      Pub Med
>\text{!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=6.9e-41 Score=304.71 Aligned_cols=286 Identities=19% Similarity=0.339 Sum_probs=0.0
 Q ss_pred
                         O Fri Mar 04 23:
                       2 OPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                                                      81 (349)
 Q Consensus
                       2 -----h---v---s-d---las-s-Dg-v
                                                                                                                      81 (349)
                     T Consensus
                                                                                                                     174 (410)
                     101 KYALSGHRSPVTRVIFHPVFSVMVSASEDATIKVWDYETG----DFERTLKGHTDSVQDISFDH--SGKLLASCSADMTI
 T 1vyh_C
                                                                                                                     174 (410)
                         SCEEECCSSCEEEEECSSSSEEEEEESSSCEEEEETTTC----CCCEEECCCSSCEEEEECT--TSSEEEEEETTSCC
 T ss dssp
                         ceEecCCCCEEEEEECCCCCEEEEECCCC----cEEEEEeccCccEEEEEcC--CCCEEEEEcCCCcE
 T ss_pred
 Q ss pred
                         Q Fri Mar 04 23: 82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP 161 (349)
```

```
Q Consensus
               82 ~1wd~~~~~~
                  T Consensus
               175 KLWDFQG-----FECIRTMHGHDHNVSSVSIMPN-GDHIVSASRDKTIKMWEVQTGYCVKTFT----- 231 (410)
T 1vvh C
                  CEEETTS-----SCEEECCCCSSCEEEEEECSS-SSEEEEEETTSEEEEEETTTCCEEEEEE
T ss dssp
                  EEEECCC-----CCEEEEEECCCCCEEEEEEeCC--CCEEEEEECCCCCEEEEEC
T ss pred
                  CcccceeEEEEccCCCCceEEecCCc-eEEEEecCCccEEEEEEccCCCcceeEEEECCC------
Q ss pred
Q Fri_Mar_04_23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPS------ 223 (349)
Q Consensus
                                                     ~~~~h~~~v~~sp~-----
                                                                                  223 (349)
               T Consensus
                                                                                  304 (410)
               232 -GHREWVRMVRPNQ---DGTLIASCSNDQTVRVWVVATKE---CKAELREHRHVVECISWAPESSYSSISEATGSETKKS 304 (410)
T 1vyh C
T ss_dssp
                  -CCSSCEEEEECT---TSSEEEEEETTSCEEEEETTTCC---EEEEECCCSSCEEEEEECCSCGGGGGGGCCSCC----
T ss_pred
                  -CCCCcEEEEECC---CCCEEEEEeCCCcEEEEECCCC---eEEEecCCCcEEEEEEcCccchhhhhhacccccc
Q ss_pred
                  Q Fri_Mar_04_23: 224 ---IGRWYQLIATGCKDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLS
                                                                                  298 (349)
Q Consensus
               224 ---~~las~s~d~~v~vwd~~~~-
                                                                                  298 (349)
               374 (410)
               305 GKPG---PFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHSGGKFILSCADDKT-----LRVWDYKNKRCMK
T lvyh_C
                                                                                  374 (410)
                  ---C---CEEEEEETTSEEEEEETTTTEEEEEEECCSSCEEEEECSSSSCEEEETTTE-----EEEECCTTSCCCE
T ss_dssp
                  CCCC----CEEEEECCCCeEEEEECCCCCEEEEEECCCCCEEEEEECCCCCEEEE
T ss pred
Q ss_pred
                  eccCCceeeeeeccccceeeeec
Q Fri Mar 04 23: 299 EHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKA 333 (349)
              299 ----h---i--v--spdg--las-s-D--v-iW-- 333 (349)
O Consensus
               .+.+|...|++|+|++++|||+.|++|+||+.
375 ~1~~h~~~V~~1~~~~~~1~sgs~Dg~i~vWd~
T Consensus
               375 TLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWEC 409 (410)
T lvyh_C
T ss_dssp
                  EEECCSSCEEEEECSSSSCEEEEETTSEEEEEC-
T ss_pred
                  EECCCCCCEEEEEecCCCCEEEEecCCCCeEEEeeC
No 5
                           SCOPe POB<sup>W</sup> PROTEIN DATA BANK
                                             NCBI
                                                             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=2.7e-40 Score=293.38 Aligned_cols=288 Identities=15% Similarity=0.227 Sum_probs=0.0
Q ss_pred
                  Q Fri Mar 04 23:
                2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                   81 (349)
                2 -----h---v---s-d---l-t-s-D--v-iwd-------h---v-v-v-v-----las-s-Dg-v
O Consensus
                                                                                   81 (349)
                  ++.+.||.+.|++++|+||+++|+||+...
                48 ~~~l~gH~~~V~~~~s~d~~~l~s~s~Dg~v~iWd~~~~~
                                                            ~~~v~~~~s~--~g~~l~sg~~d~~i
T 1got_B
                48 RRTLRGHLAKTYAMHWGTDSRLLLSASODGKT.TTWDSYTT----NKVHATPLRSSWVMTCAYAP--SGNYVACGGLDNTC
                                                                                  121 (340)
                  EERECCCSSCEEEEECTTSSEEEEETTTEEEEEETTTC----CEEEEEECSSSCEEEEEECT--TSSEEEEEETTCEE
T ss_dssp
                  ceeecCcCceeEEEEcCcCcEEEEEecCcceEEEEcccc----ccceEEeccccceEEEEccc--cccEEEEEecccceE
T ss pred
                  EEeeccCcccccccceeEEEEcCCCCcEEEEEECcCCCceEEEEEcCCCCcceeeeccccEEEeecCC
Q ss pred
 Q Fri_Mar_04_23:
               82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP
                                                                                  161 (349)
Q Consensus
               161 (349)
                  ++|++.+...
                                             ----l-s-s-d--i-lwd-----
T Consensus
               122 ~iw~~~~~~--
                             __~~v~~~
               122 SIYNLKTREGN----VRVSRELAGHTGYLSCCRFLD--DNQIVTSSGDTTCALWDIETGQQTTTF-----
T 1got B
                                                                                  180 (340)
T ss_dssp
                  EEEETTTCSBS-----CEEEEEEECCSSCEEEEEEE---TTEEEEEETTSCEEEEETTTTEEEEE
T ss_pred
                  EEEEccCCCCc----cceeeeccCCCcceeeeeccC---CceeeeeecCCcceeeee
                  \texttt{CcccceeEEEEcccCCCCceEEeccCc-eEEEEeccCCcceEEEEEcccCCCceeEEEEEcccCCCc}
Q ss_pred
 Q Fri_Mar_04_23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
                                                                                  240 (349)
O Consensus
               162 -----h--v--y-sp-----las-s-d--v
                                                                                  240 (349)
               250 (340)
T Consensus
               181 TGHTGDVMSLSLAP---DTRLFVSGACDASAKLWDVREGM---CRQTFTGHESDINAICFFPNG---NAFATGSDDATC
T 1got B
                                                                                  250 (340)
                  CCCSSCEEEEECT---TSSEEEEEETTSCEEEEETTTCS---EEEEECCCSSCEEEEEECTTS----SEEEEEETTSCE
 T ss_dssp
                  eCCCCcEEEEECC---CCCEEEEEeCCCCe---eeeEEeCCCCEEEEEEcCCC----CEEEEECCCCeE
T ss_pred
Q ss pred
                  Q Fri_Mar_04_23: 241 RIFKITEKLSPLASEESL----TNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG 316 (349)
               ----v--spdq
              ..+|+...+.+..+|...|++++|+|+|
T Consensus
                                                                                  324 (340)
              251 RLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFN-----CNVWDALKADRAGVLAGHDNRVSCLGVTDDG
T lgot B
                                                                                  324 (340)
 T ss dssp
                  EEEETTTTEEEEEECCTTCCSCEEEEEECTTSSEEEEEETTSE-----EEEEETTTCCEEEEEEECCSSCEEEEEECTTS
 T ss_pred
                  EEEEcCCCCEEEEEccCCccceEEEEECCCCC
Q ss pred
                  CEEEEecCCCeEEEEe
Q Fri_Mar_04_23: 317 TILSSAGDDGKVRLWK 332 (349)
              317 ~~las~s~D~~v~iW~ 332 (349)
 Q Consensus
                 ++|||||.|++|+||+
              325 ~~1~sgs~D~~i~iWd 340 (340)
T Consensus
T 1got_B
              325 MAVATGSWDSFLKIWN 340 (340)
```

```
T ss_dssp
                         SCEEEETTSCEEEEC
 T ss_pred
                         CEEEEecCCCcEEeCC
                                       PDB<sup>®</sup>
PROTEIN DATA BANK
 No 6
                                                   NCBI Pub Med
🗌 >2pm7_B Protein transport protein SEC13, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A
 {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=7.6e-40 Score=285.00 Aligned_cols=275 Identities=27% Similarity=0.552 Sum_probs=0.0
                         Q Fri_Mar_04_23:
                       1 \ \texttt{MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT}
                                                                                                                     80 (349)
                       1 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v--v-----las-s-Dg-
 O Consensus
                                                                                                                     80 (349)
                         T Consensus
                            78 (297)
                       1 MVVIANAHNEMIHDAVMDYYGKRMATCSSDKTIKIFEVEGETHK--LIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGK
 T 2pm7_B
                                                                                                                      78 (297)
 T ss dssp
                         -CEECCSCSSCEEEEECTTSSEEEEEETTSCEEEEEBCSSCBC--CCEECCCSSCEEEEEECCGGGCSEEEEEETTTE
 T ss_pred
                         CCEEeccccceeEEEccCCCEEEEEecCCchh--eeEEecCCCCEEEEEecCCccC
 Q ss_pred
                         {\tt EEE}{\tt eecc}{\tt CccccccceeEEEEcccccceeEEEEcccccceeEEEEeccccceeeeccceEEEeecc}
 Q Fri Mar 04 23:
                      81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                                                    160 (349)
                      Q Consensus
                      |++||+.++.||+.++||+.++.||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++||+.++|
 T Consensus
                                                                                                                    142 (297)
 T 2pm7 B
                      79 VMIWKEENGRWSQ-----IAVHAVHSASVNSVQWAPHEYGPMLLVASSDGKVSVVEFKENGTTSPIIID----- 142 (297)
 T ss_dssp
                         EEEEEBSSSCBCC-----CEEECCCSSCEEEEEECCGGGCSEEEEEETTSEEEEEEBCSSSCBCCEEEE-----
                         EEEEEccCCceEe-----EEEecccCCcEEEEEECccCCCcEEEEEeccCCCceeecc-----
 T ss_pred
 0 ss pred
                         CCcccceeEEEEcccCCCC------CceEEecCCc-eEEEEecCCCceeEEEECcCCCC
 Q Fri_Mar_04_23: 161 PANHLQSDFCLSWCPSRFSP-----EKLAVSALEQ-AIIYQRGKDGKL-HVAAKLPGHKSLIRSISWAPSIG
                                                                                                                    225 (349)
                                             ~~~_____h~~v~~v~~sp~~~
                     T Consensus
                                                                                                                    215 (297)
 T 2pm7 B
                                                                                                                    215 (297)
 T ss dssp
                         T ss pred
                           -ccCceeEEEEcC---CCCcccccCCCcceEEEEEeCCCeEEEEEECCCCceEEEEEEcCCCceEEEEEECCC-
 Q ss_pred
                         Q FTI MAT 04 23: 226 RWY---QLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD
                                                                                                                    302 (349)
                     226 ~~~-las~s~d~~v~vwd~~~
 Q Consensus
                                                                                                                    302 (349)
                     + .+||+++.|++|+|||+...
216 -----las-s-D--v-iWd-----
 T Consensus
                                                                                                                    250 (297)
 T 2pm7_B
                     216 --VILRSYMASYSODRTCITWTODNE------OGPWKKTILKE
                                                                                                                    250 (297)
 T ss dssp
                         --CSSSEEEEEETTSCEEEEEESST-----TSCCEEEESSS
 T ss_pred
                         --CCCCceEEEEcCCC------CCceeeEEecc
 Q ss_pred
                         --CCGEEEEEECCCCCEEEEecCCCGEEEEEe
 Q Fri_Mar_04_23: 303 --HNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVI 345 (349)
                     303 --h---i--v--spdg--las-s-D--v-iW------
 Q Consensus
                                                                             345 (349)
                           |...|++++|+|+|++|+++.|++|+||+....++|.|+..+
                             ----v----s--g--las---d--v--W-----g-w----- 295 (297)
 T Consensus
                     251 EKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEV 295 (297)
 T 2pm7 B
 T ss_dssp
                         SCCSSCEEEEECSSSCCEEEEETTSCEEEEECTTSCEEEC---
 T ss_pred
                         PDB* PICBI Pub Med
>3bg1_A Protein SEC13 homolog; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
 complex, nucleus, phosphoprotein; 3.004 (Homo sapiens) PDB: 3bg0 A 5a9g 6

Probab=100.00 E-value=7.5e-41 Score=293.97 Aligned_cols=285 Identities=31% Similarity=0.582 Sum_probs=0.0
                         Q Fri_Mar_04_23:
                      1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                                                     80 (349)
                       1 ------h---v-----las-s-Dg-
 Q Consensus
                                                                                                                     80 (349)
                         T Consensus
                         -----h---v---s-dg--las-s-D--v-iWd-------l--h---V--v--s----g--l-s-s-D--
                                                                                                                      82 (316)
                       5 INTVDTSHEDMIHDAQMDYYGTRLATCSSDRSVKIFDVR--NGGQILIADLRGHEGPVWQVAWAHPMYGNILASCSYDRK
 T 3bq1 A
                                                                                                                      82 (316)
 T ss_dssp
                         -----CCEEEEECGGGCEEEEETTTEEEEEEEE--TTEEEEEEEECCSSCEEEEECCGGGSSCEEEETTSC
                         hhhhhhcaceEEEEEECCCCEEEEEeCCCcEEEEECC--CCCGEEEEEecaCCCcEEEEEeCCCCCCEEEEEeCCCC
 T ss_pred
 Q ss pred
                         EEEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCcEEEEEeccCccceeeecccEEEeecC
 Q Fri_Mar_04_23:
                     81 VKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                                                    160 (349)
 O Consensus
                      160 (349)
                         T Consensus
                      83 v-iwd--------h---v--v-sp---q--lasgs-D--i--w-------
                                                                                                                    145 (316)
 T 3bg1_A
                      83 VIIWREENGTWEK-----SHEHAGHDSSVNSVCWAPHDYGLILACGSSDGAISLLTYTGEGQWE-----VKKI
                                                                                                                    145 (316)
 T ss dssp
                         EEEECCSSSCCCE-----EEEECCCSSCCCEEEECCTTTCSCEEEECSSSCEEEEECSSSCEE-----ECCB
 T ss_pred
                         EEEEECCCCceee------EEEecCCCccEEEEEECCCCccEEEEEECCCCcee------EEEe
                         CCcccceeEEEEccCCCC------CCceEEecCCc-eEEEEecCCCcceeEEEECC
 Q ss pred
 Q Fri_Mar_04_23: 161 PANHLQSDFCLSWCPSRFS------PEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAP 222 (349)
 Q Consensus
                     161 ~~~~~h~~v~~v~sp 222 (349)
                                                              ...+...+.++|+| +
146 -----v----s-----
 T Consensus
                                                          -----l-sgs-D--i-iwd------l--h---v--v--sp 222 (316)
```

```
T 3bg1_A
              146 NNAHTIGCNAVSWAP---AVVPGSLIDHPSGQKPNYIKRFASGGCDNLIKLWKEEEDGQWKEEQKLEAHSDWVRDVAWAP 222 (316)
T ss_dssp
                TTSSSSCBCCCEECC---CCCC-----CCSCCCCCCCBEECCBTTSBCCEEEECTTSCEEEEECCBCCSSCEEEEECCC
T ss_pred
                 Q ss_pred
 Q Fri_Mar_04_23: 223 SIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD
                                                                             302 (349)
Q Consensus
              223 ~~~~~las~s~d~~v~vwd~~~~
                                                                             302 (349)
                +....+.+|++++.|++|+|||+...
                ----las-s-Dg-v-iWd--
                                                                             260 (316)
T Consensus
              223 SIGLPTSTIASCSQDGRVFIWTCDDA-----SNTWSPKLLHK
 T 3bg1_A
                                                                             260 (316)
                 CSSCSCCEEEEETTCEEEEEECSST-----TCCCCBCCEEEE
T ss_dssp
                 T ss_pred
Q ss_pred
                CCceEEEEECCCCCEEEEecCCCceEEEEeccCC
Q Fri_Mar_04_23:
              303 HNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
O Consensus
              303 h---i--v--spdg--las-s-D--v-iW------
                                                    349 (349)
                T Consensus
              261 FNDVVWHVSWSITANILAVSGGDNKVTLWKESVDGQWVCISDVNKGQ 307 (316)
T 3bq1 A
                 CSSCEEEEECTTTCCEEEEESSSCEEEEEECTTSCEEEEEECC---
T ss_dssp
                 cCcceeeeeccccceeeeecccc
T ss pred
                          PDB"
No 8
                                               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
 4179 A
Probab=100.00 E-value=8.7e-39 Score=278.90 Aligned cols=263 Identities=14% Similarity=0.261 Sum probs=0.0
Q ss_pred
                Q Fri_Mar_04_23:
               1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                             80 (349)
               1 -----h---v--v---s-d---l-t-s-D--v-iwd------h---v--v--v-----las-s-Dg-
                                                                             80 (349)
O Consensus
                -----i~sgs~d~~
                                                                             78 (301)
T Consensus
               5 IKKTFSNRSDRVKGIDFHPTEPWVLTTLYSGRVEIWNYETQ----VEVRSIQVTETPVRAGKFIA--RKNWIIVGSDDFR
T 4j73_A
                                                                             78 (301)
T ss_dssp
                 CEEEEEECSCEEEEECSSSSEEEEEETTSEEEEEETTTT----EEEEEEECCSSCEEEEEEG--GGTEEEEEETTSE
T ss pred
                hhhhhcCCCCceEEEECCCCCEEEEECCCCc===ceeEecccccEEEEEeC--CCCEEEECCCCc
                EEEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCcEEEEEeccCc-CcceeeeccccEEEeec
Q ss pred
              81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP-SDLRSWTLTSEMKVLSI
 Q Fri Mar 04 23:
                                                                             159 (349)
 O Consensus
              159 (349)
                         +.+..+.+|...|.+++|+|+ +..|++++|++||+...
                |++||+.++
T Consensus
              136 (301)
              79 IRVFNYNTG-----EKVVDFEAHPDYIRSIAVHPT--KPYVLSGSDDLTVKLWNWENNWALEQTF-----
T 4i73 A
                                                                             136 (301)
                EEEEETTTC-----CEEEEEECCSSCEEEEECSS-SSEEEEETTSCEEEEETTTTEEEEEE
T ss dssp
                 EEEEECCCC------cEEEEEeCCCCcEEEEEECCC--CCEEEEECCCCcchhhh
T ss_pred
                Q ss pred
Q Fri Mar 04 23: 160 PPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDG
                                                                             238 (349)
                      -----h---v--sp-----las-s-d-
                                                                             238 (349)
 Q Consensus
                  .+|...+.++|+|. ++..+++++++++++++++++|+.....
T Consensus
              137 ----h---v--v---p-----l-sgs-D--v-iwd------
                                                       208 (301)
              137 --EGHEHFVMCVAFNPK--DPSTFASGCLDRTVKVWSLGQSTP--NFTLTTGOERGVNYVDYYPLPDK--PYMITASDDL
T 4j73 A
                                                                             208 (301)
                --CCCSSCEEEEECTT--CTTEEEEEETTSEEEEEETTCSSC--SEEEECCCTTCCCEEEECCSTTC--CEEEEECTTS
T ss dssp
T ss_pred
                 Q ss_pred
                Q Fri Mar 04 23: 239 RIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTI
                                                                            318 (349)
              239 ~v~vwd~~~~
                                                          -----h---i--v--spdg--
                                                                             318 (349)
O Consensus
                +|++||+..+
              209 ~i~iwd~~~~
T Consensus
                                                             ~~~~h~~~v~~
                                                                             242 (301)
т 4ј73_А
              209 TIKTWDYOTK-----SCVATLEGHMSNVSFAVFHPTLPT
                                                                             242 (301)
                EEEEEETTTC------CEEEEEECCSSCEEEEECSSSSE
T ss_dssp
                ceeeecccc-----chhhhhcccccceeeeeeccccc
T ss pred
                EEEecCCCeEEEEeccc
Q ss pred
Q Fri Mar 04 23: 319 LSSAGDDGKVRLWKATYSNEFKCMSVITAQ 348 (349)
O Consensus
             319 las~s~D~~v~iW~~~~~~~~~~~~
                                        348 (349)
                 |++|+.|++|+||++. ...++..+
              243 l~s~s~Dg~i~iWd~~---
T Consensus
T 4j73 A
              243 IISGSEDGTLKIWNSS---TYKVEKTLNVG 269 (301)
T ss_dssp
                EEEEETTSCEEEEETT---TCCEEEEECCS
                EEEEcCCCeEEEEeCC---CceeEEecccC
T ss_pred
                         PDB<sup>™</sup>
PROTEIN DATA BANK
                                NCBI Pub Med
>4j87_A Coatomer subunit alpha; beta propeller domain, vesicle trafficking, protein transpor; 1.67A
 {Schizosaccharomyces pombe} PDB: 4;8b A 4;8g A
 Probab=100.00 E-value=1.5e-38 Score=280.50 Aligned cols=265 Identities=15% Similarity=0.262 Sum probs=0.0
                 Q Fri Mar 04 23:
               1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                             80 (349)
O Consensus
               1 -----h---y----s-d---l-t-s-D--y-iwd------h---y--y--y------las-s-Dg-
                                                                             80 (349)
```

```
T Consensus
                                                                             76 (327)
              3 MLTKFESRSSRAKGVAFHPTQPWILTSLHNGRIQLWDYRMG---TLLDRFDGHDGPVRGIAFHP--TQPIFVSGGDDYK
T 4i87 A
                                                                             76 (327)
                EEEEEEECSCEEEEECSSSEEEEEETTSEEEEEETTTT----EEEEEEECCSSCEEEEEECS--SSSEEEEEETTSC
T ss dssp
T ss_pred
                hheeeccCccEEEEECCCCCeEEEEcCCCC----eEEEEEcCCCcEEEEECC--CCCEEEEECCCCe
                EEEeeccCccccccccceeerreccCCCcreeercccccceeeecccceeeeccccreeeeccccreeeecc
Q ss pred
Q Fri_Mar_04_23:
              81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                            160 (349)
              81 v-lwd----d--i-iwd-----
                                                                            160 (349)
Q Consensus
                             |++||+.++
                                            -----l-s-s-D--i-iwd------
T Consensus
                                                                            133 (327)
              77 VNVWNYKSR-----KILFSLCGHMDYVRVCTFHHE--YPWILSCSDDOTIRIWNWOSRNCIAII.-----
T 4j87 A
                                                                            133 (327)
                EEEEETTTT-----EEEEEECCCSSCEEEEEECSS-SSEEEEEETTSCEEEEETTTTEEEEE
T ss dssp
                EEEEECCCC-----eEEEEEcCCCCcEEEEEEcCC--CCEEEEEECCCCceeeEE-----
T ss pred
Q ss pred
                CCcccceeEEEEcccCCCCCceEEecCCc-eEEEEec------CCcEEEEEEcc
Q Fri Mar 04 23:
             161 PANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRG------KDGKLHVAAKLP
                                                                            209 (349)
                                   ~~~~i~~~~i
Q Consensus
             161 ~~~
                                                                            209 (349)
                134 ---h---v------p-----1-s-s-b--v-iwd-------
T Consensus
             134\ - \texttt{TGHSHYVMCAAFHP} - - - \texttt{SEDLIVSASLDQTVRVWDISGLRMKNAAPVSMSKEDQKAQAHNSISNDLFGSADAIVKFVLE}
T 4j87 A
                                                                            209 (327)
T ss_dssp
                -CCCSSCEEEEECS---SSSEEEEEETTSEEEEEECHHHHHHHHHSCCCCCGGGSCTTC-----CCSEEEEEEE
T ss_pred
                Q ss pred
Q Fri_Mar_04_23: 210 GHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQ
                                                                            289 (349)
O Consensus
             210 -h---v--v--sp------las-s-d--v-vwd------
                                                                            289 (349)
                +|...|.+++|+|++
                             .+|++++.|++|++||+...
             210 -h---v-----p-----1-s---D--i--w----
T Consensus
                                                                            244 (327)
т 4ј87_А
             210 GHDRGVNWCAFHPTL---PLILSAGDDRLVKLWRMTAS-----
                                                                            244 (327)
                CCSSCEEEEECSSS---SEEEEEETTSEEEEEECSS------
T ss dssp
T ss_pred
                cccceeeeeccc----ceeeeeccceeeeeecc------
Q ss pred
                Q Fri_Mar_04_23:
             290 SNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
             290 ~~~~h~~i~~v~~spdg~~las~s~D~~v~iW~~~~~~~~~~
Q Consensus
                                                             349 (349)
             T Consensus
T 4j87 A
T ss_dssp
                ---CEEEEEEECCSSCEEEEEECSSSSEEEEEETTSEEEEEETT---TCCEEEEEECSS
                ---ceEEEEEEeCccCcEEEEEECCCCCEEEEEeCCCeEEEEECC---CCChhhhhhhhcC
T ss_pred
No 10
                         PDB"
                                 NCBI
                                               Pub Med
      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=2.5e-37 Score=275.29 Aligned cols=278 Identities=29% Similarity=0.588 Sum probs=0.0
                Q ss pred
Q Fri_Mar_04_23:
              3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                             82 (349)
              Q Consensus
                                                                             82 (349)
                T Consensus
                                                                            140 (349)
              63 TIGNAHDDLIHDAVLDYYGRRLATCSSDKTIKIFEIDGENQ--RLVETLIGHEGPVWQVAWAHPKFGVILASCSYDGKVL
T 4190 A
                                                                            140 (349)
T ss dssp
                EEECSCSSCEEEEECTTSSEEEEEETTSEEEEEC----C-EEEEEEECCSSCEEEEEECCGGGCEEEEEETTSCEE
                T ss_pred
                EeeccCcccccccceeEEEccCCCcEEEEECcCCCcEEEEEecCCCcceeeeccccEEEeecCCC
Q ss pred
O Fri Mar 04 23:
              83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                            162 (349)
                                        ---p----l----d--i-iwd------
              83 lwd~~
O Consensus
                                                                            162 (349)
                        T Consensus
             141 iWd~~---
                       -----h---v--p---g--l-s-s-D--i-iwd-------
                                                                            202 (349)
             141 IWKED-----NGVWNKVAEHSVHOASVNSVSWAPHEYGPVLLCASSDGKISIVEFKDGGALEPIVIQ-----
T 4190 A
                                                                            202 (349)
                EEEEE-----TTEEEEEEEECCCSSCEEEEEECCGGGCSEEEEEETTSEEEEECBTTBCCSCEEEE
T ss dssp
                EEEcC-----CCCceeeeeeccCCCcEEEEEEeCCCCCEEEEEecCCCCcceeeEEe-----
T ss pred
Q ss_pred
                CCCCCeeEEEECCCC--CCCCceEEecCCc-eEEEEecCCCcE-EEEEEccCCCCceeEEEEECCCCCCc---eEEEEE
Q Fri Mar 04 23: 163 NHLQSDFCLSWCPSR--FSPEKLAVSALEQ-AIIYQRGKDGKL-HVAAKLPGHKSLIRSISWAPSIGRWY---QLIATGC
                                                                            235 (349)
                                      ---i----v--sp--
Q Consensus
             163
                                                                  ~~---~las~s
                                                                            235 (349)
                +|...+.++|+|.. .++..++++++++++|+...... .....+.+|...|++++|+|+
                         -----l-sgs-D--v-iwd------las-s
             203 GHAIGVNAASWAPISLPDNTRRFVSGGCDNLVKIWRYDDAAKTFIEEEAFQGHSDWVRDVAWSPS----RLSKSYIATAS
T 4190 A
                                                                            278 (349)
T ss dssp
                CSSSCEEEEECCCC---CCCEEEEEETTSCEEEEEETTTTEEEEEEECCCSSCEEEEEECCC----CSSSEEEEEE
T ss_pred
                ccCCceeEEEcccCCcccCEEEEeeCCCceeeEeeecCCCCceeEEEeCCC----cCCCCEEEEEe
                Q ss_pred
Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD--HNGEVWSVSWN
                                                                            313 (349)
Q Consensus
             236 ~d~~v~vwd~~~~~~~~~~~
                                                      -----i--v--s
                                                                            313 (349)
                .|++|+|||+...
                                                                   |...|++++|+
                ~D~~v~iWd~~~
                                                                            315 (349)
T Consensus
                                                                          ~s
                                                                            315 (349)
T 4190 A
T ss_dssp
                TTSCEEEEECTT-----CSCEEEEESCSSCCSSCEEEEEC
T ss pred
                CCCeEEEEeCCC------CCceeeeeeccccCCceEEEEEE
```

```
Q ss pred
                         CCCCEEEEecCCCceEEEEeec
 Q Fri Mar 04 23: 314 LTGTILSSAGDDGKVRLWKATYSNEFKCMSVITA 347 (349)
                     314 pdg~~las~s~D~~v~iW~~~~~~~
                          |+|++||+++.|++|+||+....++|.|+..+..
 T Consensus
                     316 pdg-~las-~~D-~v-lW-~-~-w-----
                                                                 349 (349)
                     316 LSGNVLAISGGDNKVTLWKENIQGKWESAGEVDQ 349 (349)
 T 4190 A
                         SSSCCEEEEETTSCEEEEEECTTSCEEEEECC-
 T ss dssp
                         CCCCEEEEcCCCCEEEEecCCC
 T ss pred
 No 11
                                                                         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=2.2e-37 Score=278.74 Aligned_cols=276 Identities=27% Similarity=0.566 Sum_probs=0.0
                         CCccCCCcceEEEEECCCCCEEEEEeCCCceEEEEECCCCCcceeEeeeccccceEEEEECCCCCCEEEEEeCCCc
 Q ss_pred
 O Fri Mar 04 23:
                     1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                                                      80 (349)
                       80 (349)
 Q Consensus
 T Consensus
                       3 ------l-gH---V--v--s-dg--lasgs-D--v-iWd------l-gH---V--v------g--lasgs-D--
                                                                                                                      80 (379)
                       3 MVVTANAHNELTHDAVLDYYGKRLATCSSDKTTKTFEVEGETH--KLIDTLTGHEGPVWRVDWAHPKFGTTLASCSYDGK
 T 3jrp A
                                                                                                                      80 (379)
                         --\mathtt{CCEEECCCCEEEEEECSSSSEEEEEETTSCEEEEEETTEE} -- \mathtt{EEEEEECCCSSCEEEEEECCGGGCSEEEEEETTSC}
 T ss dssp
                         T ss pred
 Q ss_pred
                         PROPRIES DO CONTROL DE LA PROPRIES DE LA CONTROL DE LA CON
 Q Fri Mar 04 23:
                     81 VKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                                                     160 (349)
                      81 v-lwd-----d--i-iwd------
                                                                                                                     160 (349)
 O Consensus
                                        |++||+.++..
                      144 (379)
 T 3jrp A
                      81 VLIWKEENGRW-----SOIAVHAVHSASVNSVOWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIID------
                                                                                                                     144 (379)
 T ss dssp
                         ERREREETTER-----ERRERECCCSSCREERECCGGGCSEREREETTSERERECCTTSCCCREERE-----
                         EEEEecCCCce-----EEEEEEeccCcceEEEEeccCCcceehhc-----
 T ss pred
 Q ss_pred
                         CCcccceeEEEEccCCCC------CceEEecCCc-eEEEEecCCCceeEEEECCCCC
 Q Fri_Mar_04_23: 161 PANHLQSDFCLSWCPSRFSP------EKLAVSALEQ-AIIYQRGKDGKL-HVAAKLPGHKSLIRSISWAPSIG 225 (349)
 Q Consensus
                     161 -----h---v--v--sp---
                                                                                                                     225 (349)
                     217 (379)
 T Consensus
                     145 -- AHAIGVNSASWAP---ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT--
 T 3jrp_A
                                                                                                                     217 (379)
 T ss_dssp
                         --CCTTCEEEEEECC---CC------CTTCEEEEEETTSCEEEEEETTTTEEEEEEEECCCSSCEEEEEECCC-
 T ss_pred
                          --cccceEEeeecc---cccccccCCCcccEEEEEcCCCCEEEEEecCCCCceEEEEEecCCCccceeEecCC--
                         Q ss pred
 Q Fri Mar 04 23: 226 RWY---QLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE---LLSE 299 (349)
 O Consensus
                     226 ----las-s-d--v-vwd------
                                                                                                                     299 (349)
                     + .+|++++.|++|++|+...
218 -----las-s-D--v-iWd-----
 T Consensus
                                                                                                                     249 (379)
                     218 --VLLRSYLASVSQDRTCIIWTQDNE-----QGPWKKTL
 T 3jrp A
                                                                                                                     249 (379)
 T ss_dssp
                        --CSSSEEEEEEETTSCEEEEEESST-----TSCCEEEE
                          T ss_pred
 Q ss pred
                         ccC--CCceEEEEECCCCCEEEEecCCCceEEEEecccC
 Q Fri_Mar_04_23: 300 HDD--HNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
                     300 ----h---i--v--spdg--las-s-D--v-iW-------
                                                                                      349 (349)
                         T Consensus
                     250 ~~~~
                     250 LKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLEGKWEPAGEVHQGG 301 (379)
 T 3jrp A
 T ss_dssp
                         SSSSCCSSCEEEEECSSSCCEEEEESSSSEEEEEEETTEEEEEEEC---
 T ss_pred
                         ccccCCCcEEEEECCCCCEEEEecCCCceEEeeecC
                                        PDB"
 No 12
                                                 Pub Med
🗌 >30w8_A WD repeat-containing protein 61; structural genomics consortium, SGC, transcriptio; 2.30A (Homo sapiens)
   Probab=100.00 E-value=7.7e-37 Score=268.96 Aligned cols=289 Identities=21% Similarity=0.353 Sum probs=0.0
                         CCGCCCCCCEEEEEECCC----CCEEEEEeCCCeEEEEECCCCCCceeEeeeccacceEEEEEECCCCCCEEEEEe
 Q ss_pred
 Q Fri Mar 04 23:
                       1 MQPFDSGHDDLVHDVVYDFY----GRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASAS
                                                                                                                      76 (349)
 O Consensus
                       1 ------h---v--s-d----s-d-----l-t-s-D--v-iwd--------h---v--v--v--v--v--las-s
                                                                                                                      76 (349)
                      T Consensus
                                                                                                                      99 (321)
 T 3ow8 A
                      24 LFKQEQAHDDAIWSVAWGTNKKENSETVVTGSLDDLVKVWKWR--DERLDLQWSLEGHQLGVVSVDISH--TLPIAASSS
                                                                                                                      99 (321)
                         EEEETTSSSSCEEEEEC-----CEEEEEETTSCEEEEEE--TTEEEEEEECCCSSCEEEEECS--SSSEEEEE
 T ss dssp
 T ss_pred
                         EEeehhcCCCcEEEEEecCCCCCCEEEEEeCC--CCceeeEEEeCC--CCCeEEEEE
 Q ss_pred
                         Q Fri_Mar_04_23:
                      77 YDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKV
                                                                                                                     156 (349)
 Q Consensus
                      77 -Dq-v-lwd------d--i-iwd------
                                                                                                                     156 (349)
                                               +.+..+..+..+..+.|+|+ +..|++++.++++||+......
                         . | + . | + + | | + . + +
                     100 ~d~~i~iwd~~~~~d~i~iwd~~~~~dg~i~i~d~~~~~~~
 T Consensus
                                                                                                                     161 (321)
 T 3ow8 A
                     100 LDAHIRLWDLENG-----KQIKSIDAGPVDAWTLAFSPD--SQYLATGTHVGKVNIFGVESGKKEYSLD-----
                         TTSEEEEEETTTT-----EEEEEEECCTTCCCCEEECTT-SSEEEEECTTSEEEEEETTTCSEEEEEE-----
 T ss dssp
 T ss_pred
                         CCCCEEEECCCC-----ceeeeeccccceeeeeccc--cceeeeeccccceeeeec-----
```

```
Q ss pred
                           eecCCCcccceeEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEccCCCCceeEEEECCCCCCceEEEEE
 Q Fri Mar 04 23: 157 LSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC
                                                                                                                          235 (349)
                                      235 (349)
                      T Consensus
                                                                                                                          225 (321)
 T 3ow8 A
                                                                                                                          225 (321)
                          -----CSSSCEEEEECT---TSSEEEEEETTSCEEEEETTTT---EEEEEECCCSSCCCEEEECTTS----CEEEEC
 T ss dssp
                           -----CCCCeEEEEEcC---CCCEEEEEcCCCcEEEEECCCC---cEEEEecCCCCCeEEEEEcCCC----CEEEEE
 T ss pred
 Q ss_pred
                           Q Fri Mar 04 23: 236 KDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWN
                                                                                                                          313 (349)
                      236 ~d~~v~vwd~~~~-
                                                                                                        ~~~h~~~i~~v~~s
 Q Consensus
                                                                                                                          313 (349)
                      T Consensus
 T 3ow8 A
                      226 DDGYIKIYDVOHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKS-----VKVWDVGTRTCVHTFFDHODOVWGVKYN
                                                                                                                          299 (321)
 T ss dssp
                           TTSCREEEETTTCCEREEECCCSSCREEEEECTTSSEEEEEETTSC-----EEEEETTTTTEEEEEECCCSSCEEEEEC
                           CCCeEEEECCCCceEEEecCCCCcEEEEECCCCCe====-==EEEECCCccceeeecCccceEEEEECC
 T ss pred
                           CCCCEEEEecCCCeEEEec
 Q ss pred
 Q Fri_Mar_04_23: 314 LTGTILSSAGDDGKVRLWKA 333 (349)
 Q Consensus
                      314 pdg~~las~s~D~~v~iW~~
                                                    333 (349)
                          |+|++|+++.|++|+||+.
-----l-s---d-i-iwd- 319 (321)
 T Consensus
                      300 GNGSKIVSVGDDQEIHIYDC 319 (321)
 T 3ow8 A
 T ss_dssp
                           TTSSEEEEETTCCEEEEC
 T ss_pred
                           CCCCEEEECCCCEEEEEC
                                         PDB™
PROTEIN DATA BANK
                                                      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=6e-37 Score=274.78 Aligned cols=249 Identities=17% Similarity=0.336 Sum probs=0.0
                           CCCEEEEEECC-CCCEEEEEeCCCeEEEEECCCCCceeEeeeeccccceEEEEEECCCCCCEEEEEecCC
 Q Fri_Mar_04_23:
                        {\bf 8} \ \ {\bf HDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEE}
                                                                                                                           86 (349)
 Q Consensus
                        8 h---v---s--d---l-t-s-D--v-iwd-------h---v--h---v---las-s-Dq-v-lwd-
                                                                                                                           86 (349)
                           |.+.|.+++|+| ++++|++++.|++|+|||+..+.. +...+.+|...|++++|+|. ++++|+||+.|++|+||+
                              --v--v--sp-----las-s-D--i-lWd------l-gh---V--v--sp-----l-s-s-D-ti-lWd-
 T Consensus
                                                                                                                          136 (368)
                        61 TQDCLFDLAWNESHENQVLVAQGDGTLRLFDTTFKEF---PIAIFKEHEREVFSCNWNLV-NRQNFLSSSWDGSIKIWSP
 T 3w15 A
                                                                                                                          136 (368)
 T ss_dssp
                           ESSCEEEEECTTCTTEEEEEETTSEEEEEETTSCSS---CSEEEECCSSCEEEEEECSS-SSSCEEEEETTSCEEEECT
                           CCCCCEEEECCCCCEEEEECCCCCEEEEECCCCCC---CccceehbcccceEEEECCCC-CCCEEEEecCCCCeEEEECC
 T ss_pred
                           Q ss pred
                       87 DPDQEECSGRRWNKLCTLNDS-----KGSLYSVKFAPAHLGLKLACLGNDGILRLYDA
 Q Fri Mar 04 23:
                                                                                                                          139 (349)
 O Consensus
                       87 ~~~~~~~\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagger_v=\dagge
                                                                                                                          139 (349)
                      ----v--v-fsp-----las-s-D--i-lWd-
 T Consensus
                                                                                                                          206 (368)
                      137 LRKQS-----LMTLTPRPLEITKMVDPLNAIILKKKSFTGISKNRNCVYQAQFSPHD-QNLVLSCSGNSYASLFDI
 T 3w15 A
                                                                                                                          206 (368)
                           TCSSC-----SEEECCCCHHHHHHHSCTTGGGSCC-----CCEEEEEECSSC-TTEEEEEETTSEEEEEET
 T ss_dssp
                           CCCcc-----eeecCCccceeccccccccccccCCCcEEEEECCCC-CCEEEEE
 T ss_pred
 Q ss pred
                           CCCCcc-eeeeccccEEEeecCCCcccceeEEEEcccCCCCceEEecCcc-eEEEEc--CCCcEE----EEEEc-
 Q Fri_Mar_04_23:
                      140 LEPSDL--RSWTLTSEMKVLSIPPANHLOSDFCLSWCPSRFSPEKLAVSALEO-AIIYORG--KDGKLH-----VAAKL- 208 (349)
                      140 -----
                     T Consensus
                                                                                                                          272 (368)
                      207 RLPSGKNONNFL------VHSGLEALTCDFNKY--RPYVVATGGVDNAIRIWDIRMLNKNPGQLHNSSCINEIP
 T 3w15 A
                                                                                                                          272 (368)
                           TSCTTSSEEEEE-----CSTTSCEEEEEECSS--CTTEEEEEETTSCEEEEETTC------CEEEEET
 T ss dssp
                           cCCCCccceeEEecCCC--CCCEEEEecCCCcceEEEECCccccCcCccccchhhhcc
 T ss pred
                           Q ss pred
 Q Fri_Mar_04_23: 209 PGHKSLIRSISWAPS-IGRWYQLIATGCKDGRIRIFKITE------KLSPLASEESLTNSNMFDNSADVDMDAQGR 277 (349)
                      209 ~~h~~~v~~sp~~~~~las~s~d~~v~vwd~~~~
 Q Consensus
                                                                                                                          277 (349)
                          .+|...|++++|+|+ + + +|++++|+|+|+++
                      273 ~~h~~~V~~v~fsp~~~----las~s~D~~vrlWd~~~~~~~~
 T Consensus
                                                                                                                          319 (368)
 T 3w15 A
                      273 NAHGLATRKUTWSPHHS---NILMSASYDMTCRIWRDLSNDGAKETYKTN-----
                                                                                                                          319 (368)
                           TSSSSCEEEEECSSCT---TEEEEEETTSCEEEEECTTC-----CCT-------
 T ss dssp
                           T ss pred
 Q ss_pred
                           cccccccccccccce----eeeeccCCcceEEEEECCC--CCEEEEecCCCeEEEEecc
 Q Fri_Mar_04_23: 278 SDSNTEEKAELQSNLQVE-----LLSEHDDHNGEVWSVSWNLT--GTILSSAGDDGKVRLWKAT 334 (349)
                      278 ~~~~~h~~i~~v~~spd--g~~las~s~D~~v~iW~~~ 334 (349)
 O Consensus
                      320 -----H----V--v-sp-g----las-s-D--v--W---
 T Consensus
                      320 -----STDATKGSIFNFTQHSEFVFGADWSLWGKPGYVASTAWDGNLFVWNGL 367 (368)
 T 3w15 A
 T ss_dssp
                          -----TTSTTTTEEEEECCCSSCEEEEECSSSSTTEEEEEETTSEEEEEECC
 T ss_pred
                           -----cccccccchhhcCcceeeeeecccCCCcEEEeecCCcEEEEecC
                                      PDB 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=1.7e-36 Score=274.98 Aligned cols=296 Identities=19% Similarity=0.346 Sum probs=0.0
                  cccccceeeeeecc-----ccceeeeeeccccccceee
Q ss pred
Q Fri_Mar_04_23:
                4 FDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRA-----HDSSIVAIDWASPEYGRIIA
                                                                                   73 (349)
                4 \  \  \, \sim \sim \sim h \sim \sim v \sim \sim \sim s \sim d \sim \sim 1 - t \sim s \sim D \sim v \sim iwd \sim \sim \sim \sim \sim \sim \sim \sim -1 - h \sim \sim v \sim v \sim \sim v \sim \sim \sim \sim \sim 1 a 
Q Consensus
                                                                                   73 (349)
                                                                 |...|++++|+| ++++|+
                  T Consensus
                                                                  ~~~~v~~l~~s~--~a~~l~
                                                                                  127 (400)
               50 VLRGHESEVFICAWNPVSDLLASGSGDSTARIWNLSENSTSGSTQLVLRHCIREGGQDVPSNKDVTSLDWNS--EGTLLA
T 41q9 A
                                                                                  127 (400)
                  EECCCSSCEEEEECSSSSEEEEETTSEEEEEECCC----CEEEEECC-----CCSSCCEEEEECT--TSSEEE
T ss dssp
                  EEEcccCCEEEEECCCCCEEEEECCCCcCCCCcceeeEeeccccccCCCCccEEEEEECC--CCCEE
T ss_pred
                  EEECCCeEEEeeccCcccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCcceeeecccc
Q ss pred
               74 SASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSE 153 (349)
Q Fri Mar 04 23:
               74 s-s-Dg~v-lwd~~~~~~~~v~~~~p~~~~l~~~d~i~iwd~~~~~~
                                                                                  153 (349)
O Consensus
                                     +....+..|...|.+++|+|+ +..|++++.|+.+++||+.+.....
                 +|+.|+.|++|+...
T Consensus
               190 (400)
              128 TGSYDGFARIWTKDG-----NLASTLGQHKGPIFALKWNKK-GNFILSAGVDKTTIIWDAHTGEAKQQF---- 190 (400)
T 41q9 A
                  EEETTSEEEEEETTS-----CEBEEEEECSSCEEBEECSS-SSEEBEEETTSCEEEEETTTTEEEEE
T ss_dssp
T ss pred
                  EEECCCeEEEEcCCC-----cEEEEeccCCccEEEEEECCC--CCEEEEEecCCCccceec----
Q ss_pred
                 EEEeecCCCccccceEEEEcccCCCCceEEEEccCCCcEEEEEEccCCCCceEEE
Q Fri_Mar_04_23: 154 MKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIA 232 (349)
              154 -----h---y--y--sp-----la 232 (349)
Q Consensus
                     ..+...+..|.+ ...+++..+. +..+|+..... +..+..+|...|.+++|+|+|+
                                  ~~_____h~~v~~sp~g-___~l~
                                                                                  251 (400)
T Consensus
               191 -----PFHSAPALDVDWQS----NNTFASCSTDMCIHVCKLGQDRP---IKTFQGHTNEVNAIKWDPTG----NLLA 251 (400)
T 41g9_A
T ss_dssp
                 -----CCCSSCERERESS----SSERERETTSCERERETTCSSC---SREECCCSSCERERECTTS----SEER
                  T ss_pred
Q ss_pred
                  Q Fri_Mar_04_23: 233 TGCKDGRIRIFKITEK-LSPLASEESLTNSNMFDNSAD------VDMDAQGRSDSNTEEKAELQSNLQVELLSEHD 301 (349)
O Consensus
               233 s~s~d~~v~vwd~~~~
                                                                                  301 (349)
               T Consensus
                                                                                  325 (400)
               252 SCSDDMTLKIWSMKQDNCVHDLQAHNKEIYTIKWSPTGPGTNNPNANLMLASASFDST-----VRLWDVDRGICIHTMT
T 41g9_A
                                                                                  325 (400)
                  EEETTSEEEEEETTCSSCSEEEECCSSCEEEEECSCSTTSSSTTSCCCEEEEETTSC-----EEEEETTTTEEEEEEC
T ss_dssp
                  EEECCCcEEEEECCCCceeeehhhCCCcEEEEEEcCCCCCCCcceEEEEEcCCCc-----EEEEeCCCCcEeEEEc
T ss pred
Q ss_pred
                  CCCceEEEEECCCCCEEEEecCCCceEEEE
               302 DHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMS 343 (349)
Q Fri Mar 04 23:
               O Consensus
                                                    367 (400)
T Consensus
T 41g9_A
               326 KHQEPVYSVAFSPDGRYLASGSFDKCVHIWNTQTGALVHSYR 367 (400)
T ss_dssp
                  \tt CCCSCEEEEEECTTSSEEEEEETTSEEEEEETTTCCEEEEEE
                  cCCceEEEECCCCCEEEEEcCCCceEEEEc
T ss pred
No 15
                           PDB<sup>™</sup>
PROTEIN DATA BANK
                                                    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=1.5e-37 Score=290.79 Aligned_cols=288 Identities=18% Similarity=0.361 Sum_probs=0.0
                  CccCCCcCeEEEEECCCCCE-EEEEeCCCeEEEEECCCCCcceeEeeeccccceEEEEEECCCCCCEEEEEECCCc
Q ss pred
                2 QPFDSGHDDLVHDVVYDFYGRH-VATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
Q Fri Mar 04 23:
                                                                                   80 (349)
               2 ~~~~h~~v~~~s-d~~-l~t~s-D~v~iwd~~~~~h~~v~v~v~~~~las~s-Dg~
...+.||.+.|.+++|+|++...|+||+.|+|||+.+.
136 ~~l~gh~~v~~fsp~~~l~sgs-D~v~iwd~t~----l~gH~~v~v~sp-dg~lasgs-D~
O Consensus
                                                                                   80 (349)
T Consensus
                                                                                  209 (515)
               136 SSAIAGHGSTILCSAFAPHTSSRMVTGAGDNTARIWDCDTQ----TPMHTLKGHYNWVLCVSWSP--DGEVIATGSMDNT
T 4wju_A
                                                                                  209 (515)
                  T ss dssp
                  eeeecCCCccEEEEEccCCCceEEEEeCCCeEEEEECCCC----cEeEEECCCCcEEEEEECC--CCCEEEEEECCCe
T ss pred
                  EEEeeccCcccccccceeEEEEcCCCCcEEEEEECc------CCCCcEEEEEECCCCcceeeecccc
Q ss pred
Q Fri Mar 04 23:
               81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP-----AHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSE
                                                                                  153 (349)
                                                                                  153 (349)
               81 v-lwd-----d--i-iwd------
Q Consensus
                                 ...+.+|...|.+++|+| + +..|++++.|++|++||+.+.....
               T Consensus
                                                                                  274 (515)
              210 IRLWDPKSGQCL-----GDALRGHSKWITSLSWEPIHLVKPGS-KPRLASSSKDGTIKIWDTVSRVCQYTM----
T 4wju A
                                                                                  274 (515)
                  EEEECTTTCCBC----SSCBCCCSSCEEEEECCGGGSCTTS--CCCEEEEETTSCEEEEETTTTEEEEEC----
T ss dssp
T ss_pred
                  EEEEECCCCcCc-----cceecCCCceEEEEEcccccCCC--CcEEEEEcCCCEEEEEe----
Q ss_pred
                  EEEeecCCCccceeEEEcccCCCCceEEecCc-eEEEEecC------
Q Fri Mar 04 23: 154 MKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGK------
                                                                                  198 (349)
                          Q Consensus
                                                                                  198 (349)
               T Consensus
T 4wju_A
               275 -----SGHTNSVSCVKWGG---QGLLYSGSHDRTVRVWDINSQGRCINILKSHAHWVNHLSLSTDYALRIGAFDHT
                                                                                  342 (515)
                 -----CCCSSCEEEEECT----TSEEEEEETTSCEEEEEGGGTTEEEEECCCSSCEEEEEESSHHHHHHTTCCTT
T ss_dssp
                  T ss pred
                  -----CCcEEEEEccCCCCceeEEE
Q ss pred
Q Fri Mar 04 23: 199 ------DGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIA 232 (349)
```

```
Q Consensus
               199 -----
                                                               ---h---v--v--sp-----la 232 (349)
                                                       .....+.+|...|++++|+|++
                                 -----l-s-s-d-i-lwd------h---y--y-fspdg-----la 418 (515)
T Consensus
               343 GKKPSTPEEAQKKALENYEKICKKNGNSEEMMVTASDDYTMFLWNPLKSTKPIARMTGHQKLVNHVAFSPDG----RYIV
T 4wiu A
                                                                                     418 (515)
                  CCCCSSHHHHHHHHHHHHBSSSSBCCCEEEEETTSCEEECTTTCSSCSEEECCCSSCEEEEECTTS----SEEE
T ss dssp
                  CccCChHHHHHHhhhhhhheeccCCCCceEEEEEcCCCceEEEEEcCCCCeEEEEECCCC----CEEE
T ss pred
Q ss pred
                  Q Fri_Mar_04_23: 233 TGCKDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSV
                                                                                     310 (349)
Q Consensus
                                                                                     310 (349)
               T Consensus
                                                                                     492 (515)
               419 SASFDNSIKLWDGRDGKFISTFRGHVASVYQVAWSSDCRLLVSCSKDTT-----LKVWDVRTRKLSVDLPGHKDEVYTV
T 4wju A
                                                                                     492 (515)
T ss_dssp
                  EEETTSCEEEEETTTCCEEEEECCCSSCEEEEECTTSSEEEEEETTSE-----EEEEETTTTEEEEEEECCSSCEEEE
T ss_pred
                  EEECCCeEEEEECCCCcEEEEECCCcceEEEEECCCCCEEEEECCCCe-----EEEEECCCCceeeECCCCCCEEEE
Q ss_pred
                  EECCCCCEEEEecCCCCeEEEEe
Q Fri_Mar_04_23: 311 SWNLTGTILSSAGDDGKVRLWK 332 (349)
Q Consensus
               311 ~~spdg~~las~s~D~~v~iW~
                                     332 (349)
                  +|+||++|++|++|+|+
                    ~spdg~~lasg~~D~~v~lW~
T Consensus
               493 DWSVDGKRVCSGGKDKMVRLWT 514 (515)
T 4wju_A
T ss_dssp
                  EECTTSCEEEEETTSCEEEEE
                  EECCCCCEEEECCCCCEEecC
T ss pred
No 16
                            SCOPe
                                                              Pub Med
>2pbi B 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=1.3e-36 Score=271.24 Aligned_cols=293 Identities=18% Similarity=0.215 Sum_probs=0.0
Q ss_pred
                  Q Fri_Mar_04_23:
                2 OPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                      81 (349)
Q Consensus
                2 -----h---v---s-d---l-t-s-D--v-iwd------h---v-v-v--v-----las-s-Dg-v
                                                                                      81 (349)
                  T Consensus
                57 ~~~l~gH~~~V~~~~s~d~~~l~sgs~Dg~i~iWd~~~~---
                                                              ---v---sp---g--l----d---
                                                                                     130 (354)
                57 RRTLKGHGNKVLCMDWCKDKRRIVSSSQDGKVIVWDSFTT----NKEHAVTMPCTWVMACAYAP--SGCAIACGGLDNKC
T 2pbi_B
                                                                                     130 (354)
                  EEEEECCSSCEEEEECTTSSEEEEEETTSEEEEEETTTC----CEEEEEECSSSCCCEEEECT--TSSEEEEESTTSEE
T ss_dssp
T ss pred
                  eeEecCCCccEEEEECCCCCEEEEEcCCCC=---ccceeEeccCceEEEEECC--CCCeEEecccCCeE
Q ss_pred
                  EEeeccCccccccccceeEEEccCCCcEEEEEEccCCCccEEEEEecCCCcceeeecccEEEeecCC
Q Fri Mar 04 23:
                82 KLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP 161 (349)
O Consensus
                161 (349)
                  193 (354)
T Consensus
               131 SVYPLTFDKN---ENMAAKKKSVAMHTNYLSACSFTNS--DMQILTASGDGTCALWDVESGQLLQSFH-----
T 2pbi_B
T ss_dssp
                  EEEECCCCTT---CCSGGGCEEEEECSSCEEEEECSS--SSEEEEEETTSEEEEEETTTCCEEEEEE------
                  EEEECcccc---cccccceEeeccCceEEEEEccC--CCEEEEEccCCcEEEEEc
T ss_pred
Q ss_pred
                  CcccceeEEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEECCCCCCeEEEEEccCCCCE
 Q Fri Mar_04 23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
                                                                                     240 (349)
               162 ------las-s-d--v
Q Consensus
                                                                                     240 (349)
               ++...+.+.+.|... +...++++++++++|+.... +...+.+|...|.+++|+|+++++|++|
194 --h--v-------1-sg-d-v-iwd----------h--v-v-v-v--p------1-s-s-d--i
T Consensus
                                                                                     264 (354)
               194 -GHGADVLCLDLAPSET-GNTFVSGGCDKKAMVWDMRSGQ---CVQAFETHESDVNSVRYYPSG----DAFASGSDDATC
T 2pbi_B
                                                                                     264 (354)
                  T ss_dssp
T ss pred
                  -CCCCcEEEEeccCCC-CCEEEEECCCCcEEEEECCCCC---EeEEEccCCCCeEEEEEcCCC----CEEEEEcCCCCeE
                  0 ss pred
Q Fri_Mar_04_23: 241 RIFKITEK----LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG
                                                                                     316 (349)
               241 ~vwd~~~~---
                                                                 -----h---i--v--spdg
               T Consensus
                                                                                     338 (354)
               265 RLYDLRADREVAIYSKESIIFGASSVDFSLSGRLLFAGYNDYT-----INVWDVLKGSRVSILFGHENRVSTLRVSPDG
T 2pbi B
                                                                                     338 (354)
                  EEEETTTEEEEEECCTTCCSCEEEEEECTTSSEEEEEETTSC-----EEEEETTTCSEEEEEECCCSSCEEEEEECTTS
T ss dssp
                  EEEECCCCceeeEecCCcccceEEEEECCCCC=----EEEEECCCCeEEEEECCCC
T ss pred
                  CEEEEecCCCeEEEe
Q ss pred
Q Fri Mar 04 23: 317 TILSSAGDDGKVRLWK 332 (349)
               317 ~~las~s~D~~v~iW~
                                 332 (349)
                  ++|++|+.|++|+|
T Consensus
               339 ~~1~sgs~D~~i~iW~ 354 (354)
T 2pbi_B
               339 TAFCSGSWDHTLRVWA 354 (354)
T ss dssp
                  SCEEEETTSEEEEC
T ss pred
                  CEEEEEcccceeec
No 17
                                                    Pub Med
3fm0 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=2.6e-36 Score=268.13 Aligned cols=308 Identities=22% Similarity=0.382 Sum probs=0.0
Q ss_pred
                  CCccCCCcc-eEEEEECCCCCEEEEEeCCCcceeEeeec-cccceEEEEEcCCCCCCEEEEEeCC
```

```
Q Fri_Mar_04_23:
             1 MOPFDSGHDD-LVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWR-AHDSSIVAIDWASPEYGRIIASASYD
                                                                        78 (349)
O Consensus
              1 -----h---v---s-d---l-t-s-D--v-iwd-------h---v--v--v--v----las-s-D
                                                                        78 (349)
               T Consensus
                                                                        82 (345)
              7 LLGRVPAHPDSRCWFLAWNPAGTLLASCGGDRRIRIWGTE--GDSWICKSVLSEGHQRTVRKVAWSP--CGNYLASASFD
T 3fm0 A
                                                                        82 (345)
               EEEEECCSTTSCEEEEECTTSSCEEEEETTSCEEEEEE--TTEEEEEEECSSCSSCEEEEEECT--TSSEEEEEETT
T ss_dssp
               heeecccccCceEEEEECCCCCEEEEEeCCCeEEEEECC--CCceEEEEEEcCCCCCGEEEEEECC--CCCEEEEEECC
T ss pred
               Q ss pred
Q Fri_Mar_04_23:
             79 KTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLS
                                                                       158 (349)
             147 (345)
T Consensus
T 3fm0 A
             83 ATTCIWKKN-----QDDFECVTTLEGHENEVKSVAWAPS--GNLLATCSRDKSVWVWEVDEEDEYECVSVLN----- 147 (345)
T ss_dssp
               SCEEEEEC-----CC-EEEEEEECCCSSCEEEEEECTT-SSEEEEEETTSCEEEEEECTTSCEEEEEEC----
T ss_pred
               CeEEEEECC-----CCCceEEEEEECCcCcEEEEEEeCc--CCEEEEEECCCCCceeEEEec-----
               Q ss pred
Q Fri Mar_04 23: 159 IPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKD
                                                                       237 (349)
                                                                       237 (349)
                                      ---i-----las-s-d
Q Consensus
             T Consensus
             148 ----SHTQDVKHVVWHP---SQELLASASYDDTVKLYRE-EEDDWVCCATLEGHESTVWSLAFDPSG----QRLASCSDD
T 3fm0 A
                                                                       215 (345)
               ----CCCSCEEEEECS---SSSCEEEEETTSCEEEEE-ETTEEEEEEECCCSSCEEEEECTTS----SEEEEEETT
T ss_dssp
               ----cCCCceEEEEECC---CCCEEEEEeCCCEEEEEEC-CCCcEEEEEeecCccceEEEEEECCCC----CEEEEEECC
T ss_pred
Q ss_pred
               Q Fri Mar 04 23: 238 GRIRIFKIT-----EKLSPLAS-EESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQV----
                                                                       294 (349)
             238 ~~v~vwd~~-----
Q Consensus
                                                                       294 (349)
               ++|++|+..
                                ....+.. +......++++....+.+..
             216 ~~v~iw~~~~~~d~~~-i~vw~~~
T Consensus
             216 RTVRIWRQYLPGNEQGVACSGSDPSWKCICTLSGFHSRTIYDIAWCQLTGALATACGDDA-----IRVFQEDPNSDPQQ 289 (345)
T 3fm0 A
               SCEEEEEECTTCTTCCCCC---CEEEEEEECSSCSSCEEEEECTTTCCEEEEETTSC-----EEEEEECTTSCTTS
T ss_dssp
               CEEEEEeCcCccceeeecCCCcceEeeEecccCCceEEEEEcCCCcceEEEEEcCCCccc
T ss pred
                  -eeeeeccCCceEEEEECC-CCCEEEEecCCCceEEEEee
Q ss pred
Q Fri_Mar_04_23: 295 ---ELLSEHDDHNGEVWSVSWNL-TGTILSSAGDDGKVRLWKATYSNEFKCMSVI 345 (349)
             Q Consensus
                                                       345 (349)
T Consensus
             290 PTFSLTAHLHQAHSQDVNCVAWNPKEPGLLASCSDDGEVAFWKYQRPEGLHHHHHH 345 (345)
T 3fm0 A
T ss_dssp
               CCEEEEEETTSSSSCEEEEEECSSSTTEEEEEETTSCEEEEEECC-----
T ss_pred
               SCOPe PODE PROTEIN DATA BANK
                                       NCBI
                                              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=1.3e-36 Score=274.94 Aligned cols=281 Identities=16% Similarity=0.281 Sum probs=0.0
               CCcCeEEEEECCCCCEEEEEECCCCceeEeeeeccccce-----
Q Fri_Mar_04_23:
              7 GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSS-----IVAIDWASPEY
                                                                        68 (349)
Q Consensus
              68 (349)
             |++++|+| +
T Consensus
                                                               v~~v~~sp--d 134 (393)
              62 DHTSVVCCVKFSNDGEYLATGC-NKTTQVYRVSDG----SLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFSP--D
T lerj A
                                                                       134 (393)
T ss_dssp
               ECSSCCCEEECTTSSEEEEC-BSCEEEETTTC----CEEEEECC-----------CCCCBEEEEEECT--T
T ss_pred
               Q ss_pred
Q Fri_Mar_04_23:
             69 \ \ GRIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSW
                                                                       148 (349)
             O Consensus
                                                                       148 (349)
T Consensus
                                                                       203 (393)
             135 GKFLATGAEDRLIRIWDIENR------KIVMILQGHEQDIYSLDYFPS--GDKLVSGSGDRTVRIWDLRTGQCSLTL
                                                                       203 (393)
T lerj A
               SSEEEEETTSCEEEEETTTT-----EEEEEECCCSSCEEEEEECTT-SSEEEEEETTSEEEEEETTTTEEEEEE
T ss_dssp
               T ss_pred
               ecccEEEeecCCCccceeEEEcccCCCCceEEecCCc-eEEEEecCCccEEEEE
Q ss pred
Q Fri_Mar_04_23: 149 TLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLP-----GHKSLIRSISW
                                                                       220 (349)
             149 ~~~~~~
                                                                       220 (349)
                         .+...+.++++|. ++.++++...++ +++|+..... .+..+.
T Consensus
             264 (393)
                                                              ~~~h~~~v~~~
T lerj_A
             204 -----SIEDGVTTVAVSPG-DGKYIAAGSLDRAVRVWDSETGF--LVERLDSENESGTGHKDSVYSVVF
                                                                       264 (393)
T ss dssp
               -----ECSSCEEEEECST--TCCEEEEEETTSCEEEEETTTCC--EEEEEC-----CCCSSCEEEEE
T ss_pred
                  Q ss_pred
               Q Fri_Mar_04_23: 221 APSIGRWYQLIATGCKDGRIRIFKIT-----EKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKA 286 (349)
             221 sp-----las-s-d--v-vwd------
Q Consensus
                                                         ----- 286 (349)
            T Consensus
             265 TRDG---QSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQNDEYILSGSKDRG-----V 334 (393)
T lerj_A
```

```
T ss_dssp
                 CTTS----SEEEEEETTSEEEEEC----------CEEEEEECCSSCEEEEEECGGGCEEEEETTSE-----E
T ss_pred
                 ccccccceeeeccCCcceEEEEEC-----CCCCEEEEecCCCeEEEEecc
Q ss_pred
 Q Fri_Mar_04_23: 287 ELQSNLQVELLSEHDDHNGEVWSVSWN-----LTGTILSSAGDDGKVRLWKAT
                                                            334 (349)
              Q Consensus
                                                            334 (349)
              T Consensus
                                                            388 (393)
              335 LFWDKKSGNPLLMLQGHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYK
T lerj_A
                                                            388 (393)
                 T ss_dssp
                 EEEECCCCCEEEEEecCCCCCEEEEEccCCCCCCEEEEE
T ss pred
                          PDB NCBI Pub Med
No 19
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=2.3e-37 Score=274.49 Aligned cols=287 Identities=15% Similarity=0.206 Sum probs=0.0
                 Q ss pred
Q Fri Mar 04 23:
                2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                 81 (349)
               O Consensus
T Consensus
                                                                                117 (340)
T 3jb9 L
               43 NLQMFGHTAEVLVARFDPSGSYFASGMDRQILLWNVFGDVK---NYGVLNGCKGAITDLQWSR--DSRVVYCSSSDTHL
                                                                                117 (340)
 T ss_dssp
                 T ss_pred
                 eEEEecCCCCEEEEECCCCCEEEEecCCCcEEEeeCCCCc---eeEEEecCCCCEeEEEEcC--CCCEEEEEeCCCCE
0 ss pred
                 EEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCccEEEEEeccCccceeeeccccEEEeecCC
Q Fri_Mar_04_23:
               82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP
                                                                                161 (349)
               82 ~lwd~~~~d~i~iwd~~~~~~
                ++||+.++
                             +.+..+.|...|.+++|...|. ....+++++.|++|++||+++......
T Consensus
              118 ~~wd~~~~l~s~s~d~i~iwd~~~~~~~~~
                                                                                174 (340)
              118 MSWDAVSG-----QKIRKHKGHAGVVNALDVLKVG-SELLTSVSDDCTMKVWDSRSKDCIKTI----- 174 (340)
T 3jb9 L
T ss dssp
                 EEEETTTC-----CEEEECCCCSSCCCEEEECCC--CCEEEEECSSSEEEEEETTTSSEEEEE
                 EEEECCCC-----ceeeeccccceeeeeeccc-cceeeeeccccceeeee-----
 T ss pred
Q ss_pred
                 CCCCCeeEEEECCCCCCceEEECCCC-eEEEECCCCCEEEEEECCCCCCceeEEEECCCCCCceEEEEECCCCCC
Q Fri Mar 04 23: 162 ANHLOSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
                                                                                240 (349)
              162 ------las-s-d--v
Q Consensus
                                                                                240 (349)
T Consensus
              175 \ - - - - - - - - - 1 - - g - - dg - i - iwd - - - - - - - - - h - - v - 1 - sp - g - - - - - 1 - s - s - d - - v
                                                                               243 (340)
T 3jb9_L
              175 - EEKYPLTAVATAO---OGTOVFTGGTDGATKTWDLRNNH---CSHVLKGHKDTTTSLATSKDG----SSLLSNSMDNTV
                                                                                243 (340)
                 -ECSSCCCEEECS---SSCEEEECSSSCCEEETTTCS---CCEECCCCSCEEECCCSSS----SEEEEEETTSBC
T ss dssp
T ss pred
                 -ccccceeEEEcC---CCCEEEEEcCCccEEEEEcCCcc---cceeeEccCCCEEEEEECCCC----CEEEEEECCCCeE
Q ss pred
                 Q Fri_Mar_04_23: 241 RIFKITE-----KLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSV
                                                                                310 (349)
Q Consensus
              241 ~vwd~~~----
                                                               ----h---i--v
                                                                                310 (349)
                 ++||++.
                        T Consensus
              {\tt 244~RIFDVKPFASAQRQLQIFEGAIHGQEHNLLGVAWSRNSRFVGAGSSDKN------VYVWSA-TGDLRYVLPGHEGSVNHV}
T 3jb9 L
                                                                                316 (340)
T ss_dssp
                 CEEECC----CCCBCCCCBCCCCCTCCCCCCCCCCCTTSSCBEEECTTSC-----EEEECS-SSCEEEEECCCSSCEEEE
T ss_pred
                 EEEECchhcCCcceeEEeeecCccCEEEEEECCCCeEEEEccCCc-----EEEEEC-CCceeEEEecCCCCeeEE
Q ss_pred
                 EECCCCCEEEEecCCCeEEEEecc
Q Fri_Mar_04_23: 311 SWNLTGTILSSAGDDGKVRLWKAT 334 (349)
              311 ~~spdg~~las~s~D~~v~iW~~~
O Consensus
                                     334 (349)
                 +|+|++++|++|++|++|++|++|
T Consensus
              317 ~fsp~~~~l~s~s~Dg~i~lw~l~ 340 (340)
              317 DFHPHQDIILSCSSDRTIFLGELN 340 (340)
T 3jb9 L
T ss_dssp
                 CCCSSSCEEEEETTTEEEEECC
T ss_pred
                 EECCCCCEEEEECCCCeEEEE
                         SCOPe PDB<sup>W</sup> PROTEIN DATA BANK
                                            NCBI Publed
□ >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 3izl
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=5.1e-36 Score=263.39 Aligned_cols=295 Identities=18% Similarity=0.222 Sum_probs=0.0
                 Q ss_pred
Q Fri Mar 04 23:
                2 QPFDSGHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSN-WELSDSWRAHDSSIVAIDWASPEYGRIIASASYDK
                                                                                 79 (349)
                2 -----h---v---s--d---l-t-s-D--v-iwd-------h---v--v--v----las-s-Dq
O Consensus
                                                                                 79 (349)
               T Consensus
                                                                                 87 (319)
               10 RGTLEGHNGWVTSLATSAGQPNLLLSASRDKTLISWKLTGDDQKFGVPVRSFKGHSHIVQDCTLTA--DGAYALSASWDK
T 3frx A
                                                                                 87 (319)
T ss_dssp
                 T ss pred
                 EEEEcccceEEEEcCCCccEEEEEcCCCceEEEEccCCcccCCCccEEeEEEECC--CCCEEEEEECCC
 Q ss pred
                 eEEEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCccEEEEEeccCccceeeeccccEEEeec
 Q Fri Mar 04 23:
               80 TVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSI
                                                                                159 (349)
O Consensus
               159 (349)
```

```
.|++||+.++
               T Consensus
               88 TLRLWDVATG-----ETYQRFVGHKSDVMSVDIDKK-ASMIISGSRDKTIKVWTIKGQCLATL----- 144 (319)
T 3frx A
                 EEEEEETTTT----EEEEEEECCSSCEEEEEECTT-SCEEEEEETTSCEEEEE-----
T ss dssp
                 eEEEEECCCC-----ceeeEecCCCceEEEEEcCC--CCEEEEEECCCcEEEE
 T ss_pred
                 CCCcccceeEEEEccCCC---CCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEEEC
Q ss pred
Q Fri Mar 04 23: 160 PPANHLQSDFCLSWCPSRF---SPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC
                                                                               235 (349)
              235 (349)
Q Consensus
              T Consensus
T 3frx A
              145 --I.GHNDWVSOVRVVPNEKADDDSVTTTSAGNDKMVKAWNI.NOF---OTEADFTGHNSNTNTI.TASPDG----TI.TASAG
                                                                               215 (319)
                 --CCCSSCEEEEECCC-----CCEEEEEETTSCEEEEETTTT---EEEEEECCCCSCEEEEEECTTS----SEEEEE
T ss dssp
                 --EccCCceeeEEecCCCcCcCccEEEEEeCCCe==eeeEecCCccceEEEEECCCc----CEEEEE
T ss pred
Q ss pred
                 Q Fri Mar 04 23: 236 KDGRIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDH-----NGE
                                                                               306 (349)
                                                           ----h----
Q Consensus
              236 ~d~~v~vwd~~~~
                                                                               306 (349)
                 . |+. |++ | |+...
                                                        ..++...+
              T Consensus
              216 KDGEIMLWNLAAKKAMYTLSAQDEVFSLAFSPNRYWLAAATATG-----IKVFSLDPQYLVDDLRPEFAGYSKAAEPH
T 3frx A
                                                                               288 (319)
T ss_dssp
                 TTCEEEEEETTTTEEEEEEECCSCEEEEECSSSSEEEEETTE-----EEEEEETTEEEEEEECCCCTTCCGGGCCC
                 CCCEEEEECCCChhheeecCCCCEEEEEECCCCCEEEEEECCC-----ceEEeccccccCCCccccccCCCCC
T ss_pred
                 EEEEEECCCCEEEEecCCC
Q ss pred
Q Fri_Mar_04_23: 307 VWSVSWNLTGTILSSAGDDGKVRLWKATYSN 337 (349)
O Consensus
              307 i~~v~~spdg~~las~s~D~~v~iW~~~~~ 337 (349)
              +.+++|+||++|++|+||++...+

289 v----s-dg--1-sg--dg-i-vw---t-- 319 (319)
T Consensus
              289 AVSLAWSADGQTLFAGYTDNVIRVWQVMTAN 319 (319)
T 3frx A
                 EEEEECTTSSEEEEEETTSCEEEEEEEC-
T ss dssp
T ss_pred
                 eEEEEECCCCcEEEEEecCCceEEEEeecC
                         PDB SNCBI Pub Med
No 21
sjam_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-36 Score=263.71 Aligned cols=298 Identities=17% Similarity=0.250 Sum probs=0.0
                 Q ss pred
Q Fri_Mar_04_23:
               1 MQPFDSGHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSN-WELSDSWRAHDSSIVAIDWASPEYGRIIASASYD
                                                                                78 (349)
               1 -----h---v---s--d---l-t-s-D--v-iwd------h---v--v--v--v----las-s-D
O Consensus
                                                                                78 (349)
                 T Consensus
                                                                                87 (326)
               10 LRGTLEGHNGWVTSLSTSAAOPNLLVSGSRDKTLISWRLTENEOOFGVPVRSYKGHSHIVODVVVSA--DGNYAVSASWD
                                                                                87 (326)
T 3jam g
                 EEEEECCCSSCCCEEECCSSCSSEEEEECTTSCEEEEEECCSSSCSEEEEEECCCCSSCEEEEEECS--SSSEEEEEETT
T ss_dssp
T ss_pred
                 EEEEecccCcceEEEEccCCccEEEEecccCcccceehhhhccCccceEEEECC--CCCEEEEEcCC
                 Q ss pred
Q Fri_Mar_04_23:
               79 KTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLS
                                                                               158 (349)
               Q Consensus
                                                                               158 (349)
               T Consensus
                                                                               145 (326)
               88 KTLRLWNLATG-----NSEARFVGHTGDVLSVAIDAN-SSKIISASRDKTIRVWNTVGDCAYVL-----
T 3jam g
                                                                               145 (326)
 T ss dssp
                 SCEEEEETTTT-----EEEEEECCCSSCEEEEECTT--SCEEEEEETTSCEEEEESSSCEEEEE-----
                 CCEEEEECCCC------CcceEEeccCCcEEEEEEcCC--CCEEEEECCCCcEEEEe
T ss_pred
                 ccccccceeEEEEcccc-----CCcceEEecccc-eEEEEecccccceEEEEEccccccceeEEEECcccccceE
Q ss pred
O Fri Mar 04 23: 159 IPPANHLOSDFCLSWCPSR-----FSPEKLAVSALEO-ATIYORGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYOL
                                                                               230 (349)
O Consensus
                                                                               230 (349)
              T Consensus
                                                                               217 (326)
              146 ---LGHTDWVTKVRVAPKNLEDGEVDDGRITFVSAGMDKIVRSWSLNEDSY-RIEADFIGHNNYINVVQPSPDG----SL
T 3jam g
                                                                               217 (326)
                 ---CCCSSCEEEEECCCCC----CCCSCEEEEEEESSSEEEEEEC--CC-SEEEEEECCSSCEEEEEECSSS----SE
T ss dssp
                 ---eccCcEEEEEecCCcccceecCCceEEEEecCCCcEEEEecCCCc--cceeeecCCCcceEEEEECCCC----CE
T ss_pred
Q ss_pred
                 Q Fri_Mar_04_23: 231 IATGCKDGRIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDH-----
                                                                               303 (349)
              231 las-s-d--v-vwd-----
Q Consensus
                                                                       ~~~h----
                                                                               303 (349)
                 |++++.|+.|+.|++||+...
              218 AASAGKDQIYVWNLKHKSAFMNFDAKDEVFALAFSPSRFWLTAATASG------IKIYDLENEVLIDELKPEFAGYTK 290 (326)
T 3jam q
T ss dssp
                 EEEEETTSEEEEETTTTBCCCEEECSSCCCEEECSSSSEEEEECSSS-----EEEEESSSCCEEEEECCCCSSCCS
                 EEEecCCCEEEEEECCCCcEEEEeecCCCcEEEEecCCcceEEEecCCC-----EEEEECCCchhhhhhhchcccchh
T ss_pred
                 --CceEEEEECCCCCEEEEecCCCC
Q ss_pred
 Q Fri_Mar_04_23: 304 --NGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSN 337 (349)
              304 --~~i~~v~~spdg~~las~s~D~~v~iW~~~~~ 337 (349)
 Q Consensus
              ...+.+++|+||++++++|+|+++...+
291 -----1-s-dg--1-sg--dg-i-vw---t-- 326 (326)
T Consensus
              291 AQDPHAVSLAWSADGQTLFAGYTDNVIRVWQVMTAN 326 (326)
 T 3jam_g
T ss_dssp
                 SCCCCEEEEECTTSCEEEEEETTSCEEEEECCBCC
 T ss pred
                 hccCceEEEECCCCCEEEEEcCCCceEEEEEeecC
```

```
PDB"
No 22
                                               S
                                                      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=3.2e-36 Score=268.69 Aligned cols=280 Identities=15% Similarity=0.226 Sum probs=0.0
                   \texttt{CCCe---EEEEEECC-CCCEEEEEeCCCCeEEEEECCCCCCeeEeeeeccccceEEEEEEccccccEEEEEecccceEEE}
Q ss pred
Q Fri Mar 04 23:
                 \textbf{8} \hspace{0.1cm} \textbf{HDDL---VHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKL} \\
                 8 h-----v---s--d---l-t-s-D--v-iwd------h---vh---v-v-v------las-s-Dg-v-1
                                                                                       83 (349)
                |... |.+++|+| ++++|++|+.|++|+|+... ....+.+|...|++++|+| ++++|++++..|+.++
67 h-----1-sg--dg-v-vwd-------h---v-v-v-p-----l-sg--dg-i-i
T Consensus
                                                                                      140 (354)
                67 HSASIPGILALDLCPSDTNKILTGGADKNVVVFDKSSE----QILATLKGHTKKVTSVVFHP--SQDLVFSASPDATIRI
T 41q8 A
                                                                                      140 (354)
 T ss dssp
                   SCSSSCCEEEEEETTEEEEEEEETTSCEEEEETTTT----EEEEEECCCSSCCCEEECT--TSSEEEEECTTSCEEE
T ss_pred
                   cccCCCceeeeeccCccceeeeeccccceeeeecccc----eeeeeeccccceeeeeccccceee
                   eeccCcccccccceeEEEEcCCCCcEEEEEECcCCCccEEEEEecCCCcceeeeccccEEEeecCCCc
Q ss_pred
O Fri Mar 04 23:
                84 WEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPAN
                                                                                      163 (349)
                         -----p-----l----d--i-iwd---
                                                                                      163 (349)
 Q Consensus
                               +.+..+.|...|.+++|+|+ +...++++.|+..+++||+..+.....
T Consensus
                141 wd~~~--
                          _____h~~~v~~~
                                               -----l~s~~~d~~i~~d~~~~~--
                                                                                      198 (354)
                141 WSVPNA-----SCVOVVRAHESAVTGI/SI,HAT--GDYI,I/SSSDDOYWAFSDIOTGRVI/TKVTD------ET
T 41g8 A
                                                                                      198 (354)
                   EETTTT-----TT
T ss dssp
                   eeCCCC-----eeeEEEecCCCCEEEEEEcCC--CCEEEEEECCCCcEEEEecC-------CC
T ss pred
Q ss_pred
                   Q Fri Mar 04 23: 164 HLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRI
                                                                                      242 (349)
                164 ~~~~
                                        ---i----las-s-d--v-v
                                                                                      242 (349)
O Consensus
                   +...+.+++|+| ++..++++.++ +.+|+....
                                                   ..+..+.+|...|.+++|+|++
                                                                         .+|++++.|++|++
                199 ~~~~v~~~~p-
                              -----h---v--v--s---
                                                                         -~~l~s~s~d~~v~l
T 41q8 A
                199 SGCSLTCAQFHP---DGLIFGTGTMDSQIKIWDLKER---TNVANFPGHSGPITSIAFSENG----YYLATAADDSSVKL
                                                                                      268 (354)
T ss_dssp
                   TCCCEEEEECT---TSSEEEEEETTSCEEEEETTTT---EEEEEECCCCSCEEEEEECTTS----SEEEEEETTSEEEE
                   CCCcEEEEECC---CCCEEEEECCCCeEEEEECCCC---ceEEEECCCC----CEEEEECCCEEEE
T ss pred
Q ss pred
                   Q Fri_Mar_04_23: 243 FKITEK---LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTIL
                                                                                      319 (349)
Q Consensus
                243 wd-----h--i-v-spdg--1
                                                                                      319 (349)
                   ||++..
                          ..++....+.+..+|...|++++|+|+|++|
                  wd~~~
                         ----v---v
                                                               ----h---v--v--s-
T Consensus
                                                                                      340 (354)
                269 WDLRKLKNFKTLQLDNNFEVKSLIFDQSGTYLALGGTD------VQIYICKQWTEILHFTEHSGLTTGVAFGHHAKFI
T 41q8 A
                                                                                      340 (354)
T ss_dssp
                   EETTTTEEEEEECCTTCCEEEEEECTTSSEEEEEESS-----EEEEETTTTEEEEEECCSSSCEEEEECGGGSCE
T ss_pred
                   EEecCCCeEEEec
Q ss pred
Q Fri_Mar_04_23:
               320 SSAGDDGKVRLWKA 333 (349)
                320 as~s~D~~v~iW~~
                                333 (349)
O Consensus
                  ++|+.|++|+||++
                341 ~s~s~Dq~v~iw~l 354 (354)
T Consensus
                341 ASTGMDRSLKFYSL
T 41q8 A
                                354 (354)
 T ss_dssp
                   EEEETTSCEEEEEC
                   EEEECCCcEEEecC
T ss_pred
                             PDB
No 23
                                      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=6.4e-36 Score=265.60 Aligned cols=303 Identities=14% Similarity=0.180 Sum probs=0.0
                   CccCCCcCeEEEEECCCCCEEEEEECCCCCCceeEeeec------cccceEEEEECCCCCCC
Q ss pred
Q Fri_Mar_04_23:
                 2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWR-----AHDSSIVAIDWASPEYGR
                                                                                       70 (349)
                 2 -----h---y----s-d---1-t-s-D--y-iwd-------
O Consensus
                                                                    ___~h~~~v~~v~~~
                                                                                       70 (349)
                   ...+.+|...|++++|+|+|+|+|+|+|+|+.+....+.
                                                                      +|...|++++|+| +++
T Consensus
                                                                     ~qh~~~v~~~~s~--dq~
                                                                                       80 (343)
                 7 IRVLRGHQLSITCLVVTPDDSAIFSAAKDCSIIKWSVESG---RKLHVIPRAKKGAEGKPPGHSSHVLCMAISS--DGK
T 4j0w A
                                                                                       80 (343)
 T ss_dssp
                   CEEEECCSSCEEEEECTTSSEEEEEETTSCEEEEETTTC----CEEEEECCC-----CCCSCCSSCEEEEECT-TSC
                   ceEecCCCceEEEEEcCCCCEEEEECCC----cEEEEeccCccccccCCCCCCEEEEEECC--CCC
T ss_pred
0 ss pred
                   EEEEEeCCCeEEEeecCCccccccccccceeeec
Q Fri_Mar_04_23:
                71\ {\tt IIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTL}
                                                                                      150 (349)
                71 ~las~s~Dq~v~lwd~~~~~~~~~~
                                             -----v----p-----l-----d--i-iwd---
                                                                                      150 (349)
                   +|++|+.|++|++||+.+.
                                         T Consensus
                 81 ~lasgs~d~~i~iwd~~~~--
                                        -----l-s-s-D--v-iWd-----
                                                                                      148 (343)
                81 YLASGDRSKLILIWEAOSC-----OHLYTFTGHRDAVSGLAFRRG-THOLYSTSHDRSVKVWNVAENSYVETLF-
T 4j0w A
                                                                                      148 (343)
T ss_dssp
                   EEEEEETTSCEEEEETTTT-----EEEEEECCCSSCEEEEECTT-SEEEEEEEGGGTEEEEEE
T ss pred
                   EEEEecCCCEEEEEECCCC-----cccccccccccccceEEEEecC--CCEEEEecCCCCEEEee
Q ss_pred
                   Q Fri_Mar_04_23:
               151 TSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQ
                                                                                      229 (349)
Q Consensus
                151
                                                ~~~~~i
                                                        -----h---v--sp--
                                                                                      229 (349)
                             +|...+.++.+.| ++..+++++++++++|+....
                                                               ....+.+|...|.+++|+++
                T Consensus
T 4j0w A
                                                                                      204 (343)
T ss dssp
                   -----CCSSCCCEEECS--SEEEEECBTTCEEEEEETTTT---EEEEEECSSSCEEEEEEET----T
```

```
T ss_pred
                 -----CCCCccEEEEcC---CCCEEEEEcCCC----ccEEEecCCCcEEEEEcCC----C
0 ss pred
                 Q Fri_Mar_04_23: 230 LIATGCKDGRIRIFKITEKLSPLASEESL-----TNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVEL 296 (349)
              230 ~las~s~d~~v~vwd~~~~~~~~~~~
                                                                               296 (349)
              .....
                                           ----v-lw-----
T Consensus
                                                                               281 (343)
              205 HMVSGADDGSVALWGLSKKRPLALQREAHGLRGEPGLEQPFWISSVAALLNTDLVATGSHSSC---VRLWQCGEGFRQLD 281 (343)
T 4j0w A
                 EEEEEETTSCEEEEESSCSSCSEEETTTTCEESSTTCCEECCCCEEEECTTSSEEEEECSSSE---EEEEECGGGCCEE
T ss dssp
T ss_pred
                 EEEEEeCCCceEEEEECCCCcceeehhhhcCCCCcccccceEEeeecCCCCEEEEeCCCc---EEEEECCCcchhh
                 eeeccCCceEEEEECCCCCEEEEec--CCCeEEEEecccCCcEEEEEEeeccC
Q ss pred
Q Fri Mar 04 23: 297 LSEHDDHNGEVWSVSWNLTGTILSSAG--DDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
              297 -----h---i--v--spdg--las-s---D--v-iW------
                                                            349 (349)
O Consensus
                 .....|.+.|++|+||||++|+++++++++|++....-.|+..+...
                                                            336 (343)
T Consensus
              282 ----v~vafspdg~l~----w~---w
              282 LLCDIPLVGFINSLKFSSSGDFLVAGVGQEHRLGRWWRIKEARNSVCIIPLRRVP 336 (343)
T 4j0w A
                 EEEEEECCSEEEEEECSSSEEEEEEESSCTTCSSCCCTTSCCEEEEEC----
T ss dssp
T ss_pred
                 hhhcCCCCCEEEEEECCCCCEEEEEecCCCceeeEEecccccceEEEEecCCC
                           PDB NCBI
No 24
                                                 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=1.6e-35 Score=261.12 Aligned cols=260 Identities=15% Similarity=0.229 Sum probs=0.0
                 0 ss pred
Q Fri Mar 04 23:
              3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                                82 (349)
O Consensus
               3 ----h---v--s-d---l-t-s-D--v-iwd------h----h---v-v--v-----las-s-Dg-v-
                                                                                82 (349)
               T Consensus
                                                                               120 (327)
               47 DRFDGHDGPVRGIAFHPTQPIFVSGGDDYKVNVWNYKSR----KLLFSLCGHMDYVRVCTFHH--EYPWILSCSDDQTIR
T 4j87_A
                                                                               120 (327)
                 EEEECCSSCEEEEECSSSSEEEEETTSCEEEEETTTT----EEEEEECCCSSCEEEEEECS--SSSEEEEEETTSCEE
T ss dssp
T ss pred
                 EEECCCCCEEEEEECCCCCEEEEECCCC----eEEEEECCCCCCEEEEEECC--CCCEEEEECCCCCeEE
Q ss_pred
                 ReeccCcccccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCeEEEEEC
Q Fri_Mar_04_23:
              83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDA-----LEP
                                                                               142 (349)
Q Consensus
               83 lwd-----d--i-iwd-------
                                                                               142 (349)
                        + | | + . + .
T Consensus
              121 IWNWQSR-----NCIAILTGHSHYVMCAAFHPS-EDLIVSASLDQTVRVWDISGLRMKNAAPVSMSKEDQKAQAH 189 (327)
T 4j87_A
T ss dssp
                 EEETTTT-----EEEEEECCCSCEEEEECCSS-SSEEEEEETTSEEEEECHHHHHHHHSCCCCCGGGSCTTC-
T ss_pred
                 EEECCCC-----ceeeEccCCccEEEEECCC--CCEEEEECCCcEEEEEcCCceeccccccccc
                 Q ss_pred
Q Fri_Mar_04_23: 143 SDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWA
                                                                               221 (349)
Q Consensus
              221 (349)
                 T Consensus
                                                                               265 (327)
              190 NSISNDLFGSADAIVKFVLEGHDRGVNWCAFHP---TLPLILSAGDDRLVKLWRM-TASKAWEVDTCRGHFNNVSCCLFH
                                                                               265 (327)
т 4ј87_А
                 -----CCSEEEEEECCSSCEEEEECS---SSSEEEEETTSEEEEEECCSSCEEEEEECCSSCEEEEEC
T ss_dssp
                 ccccceecCCCceEEEEecCCCcEEEEECC---CCCeEEEECCCCEEEEEEe-cCCceEEEEEEC
T ss pred
                 Q ss pred
Q Fri_Mar_04_23: 222 PSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHD
                                                                               301 (349)
              222 p----las-s-d--v-vwd-----
 O Consensus
                                                                               301 (349)
                     .+|++++.|++|++||+...
T Consensus
              266 p~~----1~s~s~Dg~i~vWd~~~~
                                                                               295 (327)
              266 PHQ---ELILSASEDKTIRVWDLNRR-----TAVQTFR
T 4i87 A
                                                                               295 (327)
                 SSS---SEEEEEETTSEEEEEETTTC------CEEEEEE
 T ss dssp
T ss pred
                 CCC----CEEEEEeCCCCeEEEEECCCC------Chhhhhhh
                 CCCceEEEEECCCCCEEEEecc
Q ss pred
Q Fri Mar 04 23: 302 DHNGEVWSVSWNLTGTILSSAGDDGKVRLWKAT 334 (349)
              302 ~h~~~i~~v~~spdg~~las~s~D~~v~iW~~~
                                           334 (349)
Q Consensus
              +|...|++++|++++||+++|+++
296 ----v-v-v----
T Consensus
                                            327 (327)
              296 RANDRFWFITVHPKLNLFAAAH-DSGVMVFKLE 327 (327)
T 4i87 A
                 CSSCCEEEEECSSSSCEEEEE-TTEEEEEEC
T ss dssp
T ss_pred
                 hcCCcEEEEECCCceEEEEec-CCcEEEEEcC
                           PDB"
                                           Pub Med
No 25
                                   NCBI
->4wjs_A RSA4; ribosome assembly, ribosome biogenesis, biosynthetic protein; 1.80A {Chaetomium thermophilum}
           E-value=7.2e-36 Score=277.51 Aligned cols=287 Identities=17% Similarity=0.348 Sum probs=0.0
Q ss_pred
                 Q Fri_Mar_04_23:
               3 PFDSGHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                81 (349)
              3 ----h---v---s--d---1-t-s-D--v-iwd------h---y--v-v-----
Q Consensus
                                                                      ~las~s~Dq~v
                                                                                81 (349)
                 108 ~-l-gh---V----fsp-----lasgs-D--V-iWd--t------lgh---V--V--sp--dg--las-s-D--i
108 HRIPGHGOPILSCOPSPVSSSRLATGSGDNTARIWDTDSG----TPKFTLKGHTGWVLGVSWSP--DGKYLATCSMDTTV
                                                                               181 (485)
T 4wjs_A
                                                                               181 (485)
```

EEECCCSSCEEEEECSSCTTEEEEEETTSCEEEEETTTT----EEEEEECCCSSCEEEEEECT--TSSCEEEEETTSCE

T ss dssp

```
T ss_pred
                eeeccCcCcEEEEEccCCCCEEEEEeCCCc=---CcceEeCCCCCEEEEEECC--CCCEEEEE
                EEeeccCccccccceeEEEEcCCCCcEEEEEECc-----CCCCcEEEEEECCCCCcceeeeccccEE
0 ss pred
Q Fri_Mar_04_23:
              82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP-----AHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMK
                                                                             155 (349)
              Q Consensus
                                                                             155 (349)
              T Consensus
                                                                             244 (485)
              182 RVWDPESGKQV-----NQEFRGHAKWVLALAWQPYHLWRDG-TARLASASKDCTVRIWLVNTGRTEHVL-----
T 4wjs A
                                                                             244 (485)
                 EEEETTTTEEC----SSCBCCCSSCEEEEECCGGGCBTT-BCEEEEETTSCEEEEETTTTEEEEEE
T ss_dssp
T ss_pred
                 EEEECCCCccc-----ccccCCCcceEEEEeccccCCCC--CCEEEEEeCCCcceEEec--
                EeecCCCcccceeEEEcccCCCCceEEecCCc-eEEEEecCCccEEEE------
Q ss pred
Q Fri Mar 04 23: 156 VLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVA------ 205 (349)
                                                                             205 (349)
O Consensus
                     .+|...+.+.|.+ ...+++++++++++++|+.......
T Consensus
             314 (485)
              245 ----SGHKGSVSCVKWGG---TDLIYTGSHDRSVRVWDAVKGTLVHNFTAHGHWVNHIALSSDHVLRTAYHDHTKEV 314 (485)
T 4wjs_A
                -----CCCSSCEEEEEECT----TSEEEEEETTSCEEEEETTTTEEEEEECCCSSCEEEEEETTHHHHH
T ss_dssp
T ss pred
                 ----cCCCCceEEEEECC----CCeEEEEECCCceEEEEEcCCceEEEEecCCcceEeeEEEcCCccc
Q ss_pred
                -----EEGCCCCGeeEEEEE
Q Fri_Mar_04_23: 206 ---------------------------AKLPGHKSLIRSISWAPSIGRWYQLIATG
                                                                             234 (349)
Q Consensus
              206 -----h-~-v~-v-sp~---
                                                                       ~~~las~
                                                                             234 (349)
                                                     ..+.+|...|.+++|+|++
                            -----las-
T Consensus
                                                                             390 (485)
              315 PGTEEERRAKAKERFEKAAKIKGKVAERLVSASDDFTMYLWDPTNNGSKPVARLLGHQNKVNHVQFSPDG----TLIASA 390 (485)
T 4wjs_A
T ss dssp
                cCchhhhHHHHhhhhhhhhccCCcccEEEEEeCCCEEEEEecCCCCccceEecCCCCCEEEEEECCCC----CEEEEE
T ss_pred
Q ss_pred
Q Fri_Mar_04_23: 235 CKDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSW 312 (349)
O Consensus
              235 s~d~~v~vwd~~~~
                                         312 (349)
                                                       ..+|+...++.+..+|...|++++|
                391 s-d-i-lwd------l-h---v----spd---l-s-s-D-----i-vwd-------l-h---v-v--v-v
T Consensus
                                                                             464 (485)
              391 GWDNSTKLWNARDGKFIKNLRGHVAPVYQCAWSADSRLVVTGSKDCT-----LKVWNVRTGKLAMDLPGHEDEVYAVDW
T 4wjs_A
                                                                             464 (485)
                 ETTSCEEEEETTTCCEEEEECCCSSCEEEEEECTTSSEEEEEETTSC-----EEEEETTTTEEEEEECCCSSCEEEEE
T ss_dssp
                 T ss pred
Q ss_pred
                CCCCCEEEEecCCCeEEEEe
Q Fri_Mar_04_23: 313 NLTGTILSSAGDDGKVRLWK 332 (349)
Q Consensus
              313 spdg~~las~s~D~~v~iW~ 332 (349)
                +|||++||+|+.|++|+||+
              465 spdg~~l~s~~~D~~v~iW~
                                 484 (485)
T Consensus
T 4wjs_A
              465 AADGELVASGGKDKAVRTWR 484 (485)
T ss_dssp
                CTTSSEEEEETTCCEEEEE
                 cccceeeecc
T ss pred
                                  PDB"
No 26
                         SCOPe
                                                         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=2.2e-35 Score=258.27 Aligned_cols=243 Identities=17% Similarity=0.298 Sum_probs=0.0
                CCCeEEEEECCCCCEEEEEeCCCeEEEEECCCCCceeEeeeccccceEEEEECCCCCCEEEEEeeCCc
Q ss pred
               8 HDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEED
Q Fri Mar 04 23:
                                                                              87 (349)
               O Consensus
                                                                              87 (349)
                 ~~~v~~~s-dg~~lasg~~dg~v~iwd~~~~---------l~gh~~~V~~~~~--------l~s~s~D~~i~~wd~~
T Consensus
                                                                             132 (308)
T 4bh6_A
              61 TENEYTSLSWIGAGSHLAVGQANGLVEIYDVMKR----KCIRTLSGHIDRVACLSWN----NHVLTSGSRDHRILHRDVR
                                                                             132 (308)
                CSSCEEEEECTTSSEEEEEETTSCEEEEETTTT----EEEEEECCCSSCEEEEEE----TTEEEEEESSSCEEEEETT
T ss dssp
                 T ss pred
                Q ss pred
Q Fri Mar 04 23:
              88 PDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQS
                                                                             167 (349)
                   -----v-----p-----1-----d--i-iwd----
                                                                             167 (349)
Q Consensus
                          133 -----h----h---v--v--s-----las-s-b--v-iwd----------h---
T Consensus
                                                                             189 (308)
              133 MPDPF------FETIESHTQEVCGLKWNVA--DNKLASGGNDNVVHVYEGTSKSPILTF-------DEHKAA
T 4bh6 A
                                                                             189 (308)
                SSSSC----SEEECCCSSCEEEEEECSS-SCEEEEETTSCEEEEETTCSSCSEEE-----CCCSSC
T ss dssp
T ss_pred
                CCccc-----ceeeccCCCEEEEEEeCC--CCEEEEECCCCEEEEe-------cCCccc
Q ss_pred
                PERRECCCCCCCCERRC--CCC-PRERECCCCCCRRRERECCCCCCCPPRERECCCCCCCCCPREREC-ECCCCCCRRE
Q Fri Mar 04 23: 168 DFCLSWCPSRFSPEKLAVSA-LEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIAT--GCKDGRIRI
                                                                             242 (349)
                      242 (349)
Q Consensus
              168 ~~
                 +.+++|+|. ....+++++ .++ +++|+......
                                                  +...+.+++|+|++
              T Consensus
                                                                             259 (308)
T 4bh6_A
              190 \ \texttt{VKAMAWSPH--KRGVLATGGGTADRRLKIWNVNTSIKMSDID----SGSQICNMVWSKNT----NELVTSHGYSKYNLTL}
                                                                             259 (308)
                EERRECSS--STTEEERRECTTTCEREEEETTTTERREERE----CSSCEREERCSSS----SCREERCTTCCCERE
T ss_dssp
                EEEEEECCC--CCCeEEecCCCCCeEEEEECCCCceEEEEe----CCCcEEEEEECCCC----CeEEEeccCCCceEEE
T ss pred
                Q ss pred
Q Fri Mar 04 23: 243 FKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSA 322 (349)
```

```
Q Consensus
             243 wd~~~
                ||+...
                                                      +.+..+.+|...|++|+||||++||+|
             260 wd~~~~
T Consensus
                                     -----l~h~~v~~~s~dg~~l~s~
                                                                            293 (308)
             260 WDCNSM-----DPIAILKGHSFRVLHLTLSNDGTTVVSG
T 4bh6 A
                                                                            293 (308)
T ss dssp
                 ECSSSC-----CEEEEECCCSSCEEEEECTTSSEEEEE
                 T ss pred
Q ss pred
                cccceeeeecccc
Q Fri_Mar_04_23: 323 GDDGKVRLWKATYSN 337 (349)
Q Consensus
             323 s~D~~v~iW~~~~~
                            337 (349)
                +.|++|+||++....
T Consensus
             294 S~D~~V~~W~~~~~
                            308 (308)
             294 AGDETLRYWKLFDKP 308 (308)
T 4bh6 A
T ss_dssp
                ETTTEEEEEECCCCC
T ss_pred
                          PDB"
No 27
                                               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=5.3e-35 Score=256.22 Aligned_cols=289 Identities=18% Similarity=0.287 Sum_probs=0.0
                Q ss pred
Q Fri_Mar_04_23:
               5 DSGHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSN-WELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                             82 (349)
               5 ~~~h~~~v~~~s~-d~~~l~t~s~D~~v~iwd~~~~~~~h~~~v~~v~~v~~v~~~las~s~Dg~v
                                                                             82 (349)
Q Consensus
              T Consensus
                                                                             88 (314)
              11 LAGHNGWVTAIATSSENPDMILTASRDKTVIAWQLTREDNLYGFPKKILHGHNHFVSDVAISS--DGQFALSSSWDHTLR
T 4d6v A
                                                                             88 (314)
T ss_dssp
                ECCCSSCEEEEECCSSCTTEEEEEETTSCEEEEEECCCSSCSEEEEEECCT--TSSEEEEEETTSCEE
T ss_pred
                Q ss_pred
                Q Fri_Mar_04_23:
              83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                            162 (349)
Q Consensus
              83 lwd-----
                                   ----v----p-----l-----d--i-iwd---
                                                                            162 (349)
                         +.+..+.|...|.+++|+|+ +...+++++.|+.+++||...
                +||+.++
T Consensus
                         ----h---v----
                                         ----l~s~~~d~~i~iwd~~--
              9 LWDLNTG-----LTTKKFVGHTGDVLSVSFSAD-NRQIVSASRDRSIKLWNTL------GECKFDIVED 145 (314)
T 4d6v_A
                EEETTTT-----SCEEEEECTT--SSCEEEEETTSCEEECTT-----SCEEEEECTT
T ss_dssp
T ss pred
                Q ss_pred
                cccceeEEEccCCCCceEEecCCc-eEEEEccCCCcEEEEEEccCCCceeEEEECCCCCceEEEEEccCCCCEE
Q Fri Mar 04 23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR 241 (349)
O Consensus
             163 -----h---v-v--sp-----las-s-d--v-
                                                                            241 (349)
             217 (314)
T Consensus
              146 GHTEWVSCVRFSPNPA-LPVIISAGWDKTVKVWELSNC---KLKTTHHGHTGYLNTLAVSPDG----SLAASGGKDGITM
T 4d6v A
                CCSSCEEEEECCCSS-SCEEEEETTSCEEEEETTTT---EEEEEECCCSSCEEEEEECTTS----SEEEEEESSSEEE
T ss dssp
T ss_pred
                Q ss_pred
                Q Fri Mar_04 23: 242 IFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEH------DDHNGEVWSVS
                                                                            311 (349)
              +||+...
             218 iwd-----i-iwd----
T Consensus
                                                                      ~v~~1~
                                                                            290 (314)
              218 LWDLNEGKHLYSLDAGDVINALVFSPNRYWLCAATASS-----IKIFDLESKSLVDDLQPDFDGLSDKARKPECTSLA 290 (314)
T 4d6v A
                EEESSSSSEEEEECSSCEEEEEECSSSSEEEEEESSC-----EEEEETTTTEEEEEECCCCSSCCSSCCCCCEEEEE
T ss_dssp
T ss pred
                EEECCCCcEEEEecCCCceEEEEecCCc------EEEEEcccCceehhhccCcccccccccccccccc
                ECCCCCEEEEec
0 ss pred
Q Fri_Mar_04_23: 312 WNLTGTILSSAGDDGKVRLWKA 333 (349)
             312 ~spdg~~las~s~D~~v~iW~~
                |+|||++|++|+.|+.|+|
             291 ~s~dg~~l~sg~~dg~v~vw~~
                                  312 (314)
T Consensus
             291 WSADGQTLFAGFSDNLVRVWAV 312 (314)
T 4d6v A
                ECTTSSEEEEETTSCEEEEE
T ss dssp
                 Ecccceeeeecccceeeee
T ss pred
                         PDB'-
No. 28
                                               Pub Med
>4all_B DNA excision repair protein ERCC-8; DNA binding protein, DNA damage repair; HET: DNA; 3.31A {Homo
 sapiens}
Probab=100.00 E-value=2.4e-35 Score=268.05 Aligned_cols=296 Identities=16% Similarity=0.210 Sum_probs=0.0
                CccCCCcceEEEEECC-CCCEEEEEeCCCCcceeEeeee------cccceEEEEEECCCCCCCE
0 ss pred
Q Fri_Mar_04_23:
               2 QPFDSGHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTSNWELSDSW------RAHDSSIVAIDWASPEYGRI
                                                                             71 (349)
               +..+.+|.+.|++++|+| +|++|+||+.|++|+|||+.....
              36 -----h---V--v--sp-dg--lasgs-Dg-i-lwd--------h---V--v--p------
36 RDVERIHGGGINTLDIEPVEGRYMLSGGSDGVIVLYDLENSROSYYTCKAVCSIGRDHPDVHRYSVETVOWYPH-DTGM
T Consensus
                                                                            114 (408)
T 4a11 B
                                                                            114 (408)
                T ss dssp
 T ss_pred
                Q ss_pred
                EEEEeCCCeEEEeeccCcccccccccceeEEEEcCCCCcEEEEEECc---CCCCcEEEEEECCCCcceee
```

```
Q Fri_Mar_04_23: 72 IASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP---AHLGLKLACLGNDGILRLYDALEPSDLRSW 148 (349)
O Consensus
              T Consensus
                                                    ~--~~lasg~~d~~v~lwd~~~~~
                                                                       ~1 182 (408)
             115 FTSSSFDKTLKVWDTNTL-----QTADVFNFEETVYSHHMSPVSTK-HCLVAVGTRGPKVQLCDLKSGSCSHIL 182 (408)
T 4a11 B
                EEEEETTSEEEEEETTTT-----EEEEEEECSSCEEEEEECSSCS--CCEEEEEESSSSEEEEESSSSCCEEE
T ss_dssp
                EEEEcCCCeEEEeECCCC-----eEEEEEeccCceeeEEeccCCC--CcEEEEEECCCCcEEEE
T ss pred
                Q ss pred
Q Fri_Mar_04_23: 149 TLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAA------KLPGHKSL
                                                                          214 (349)
                                     -----h---
             247 (408)
T Consensus
             183 -----QGHRQEILAVSWSPR--YDYILATASADSRVKLWDVRRASGCLITLDQHNGKKSQAVESANTAHNGK
T 4a11 B
                                                                          247 (408)
                -----CCCCSCEEEEECSS-CTTEEEEEETTSCEEEEETTCSSCCSEECCTTTTCSCCCTTTSSCSCSSC
T ss dssp
T ss_pred
                Q ss pred
Q Fri Mar 04 23: 215 IRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEES-----LTNSNMFDNSADVDMDAQGRSDSNTEEKA
                                                                          286 (349)
             215 v--v--sp-----las-s-d--v-vwd-----
                                                                          286 (349)
Q Consensus
                |.+++|+|++
                          .+|++++.|++|++||+..+.....
T Consensus
             248 V--1-fspdg-----1-s-s-D--v-1Wd------
                                                                     ----i 316 (408)
             248 VNGLCFTSDG----LHLLTVGTDNRMRLWNSSNGENTLVNYGKVCNNSKKGLKFTVSCGCSSEFVFVPYGST-----I
T 4a11 B
                                                                          316 (408)
                EEEEEECTTS----SEEEEEETTSCEEEEETTTCCBCCCCCCCCCCCCCCCSSCCCEECCSSSCEEEEEETTE-----E
T ss_dssp
                eeEEEECCCC----CEEEEECCCCcEEEEECCCCceeeeeeccccCCcccEEEEEEcCCCccEEEEECCCE-----
T ss_pred
Q ss_pred
                CCCCCCCeeeeeccCCCceEEEEECCCCCEEEEecCCCeEEEEeccCC
Q Fri_Mar_04_23: 287 ELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYS
                                                     336 (349)
             287 -----h---i--v--spdg--las-s-D--v-iW-----
Q Consensus
                                                     336 (349)
                317 ~vwd~~~g~~~~l~gh~~~V~~v~fspdg~~l~s~s~D~~i~lW~~~~~
T Consensus
                                                     366 (408)
T 4a11 B
                                                     366 (408)
             317 AVYTVYSGEQITMLKGHYKTVDCCVFQSNFQELYSGSRDCNILAWVPSLY
                EFFETTTCCFFFFCCCSSCFFFFFFTTTFFFFFFTTSCFFFFFCC-
T ss_dssp
                EEEEeecCcChhhhhcccCcceEEEEcCCCCEEEecCCCc
T ss pred
No 29
                               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
          E-value=1.2e-35 Score=266.54 Aligned_cols=294 Identities=16% Similarity=0.196 Sum_probs=0.0
Q ss_pred
                Q Fri Mar 04 23:
              3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAH-DSSIVAIDWASPEYGR--IIASASYD-
                                                                           78 (349)
              3 ----h--v-v-s-d--l-t-s-D-v-iwd------h---v-v-v-v-----las-s-D-
O Consensus
                                                                           78 (349)
                ---v--v-fsp--dg----la-----
              15 ~~l~gH~~~V~~vafspdg~~las~s~D~tvrlWd~~~g---~~~
              15 TIFRGHEGRVRSVAIDPTGVALATGGDDGTVRVWELLTG----RQVWSVKLNGDEAVNTVRWRP--TKDTFILAAAAGED
T 5cxb B
                                                                           88 (369)
                EEECCCSSCEEEEECTTSSEEEEETTSEEEEEETTTC----CEEEEEESCTTSCEEEEEECS--CTTCCCEEEEETTE
T ss_dssp
                eEEecCCccEEEEECCCCeEEEEEccCCeEEEEEccCCe
T ss pred
                            Q ss pred
Q Fri_Mar_04_23:
              79 ----KTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVK
                                                                          115 (349)
Q Consensus
              115 (349)
                                              +.+++||....+
                                                              ....+++
T Consensus
T 5cxb B
              89 IFLMIPTHPSVTPALDQASRDILNAGFGHATNGKQQANLPPGKEPPGKWARPGTRLEDEG----VLLRITVRSTIKAIS
                                                                          163 (369)
T ss_dssp
                EEEECCCCTTCCHHHHHHHHHHTTC-------CCCEEECCCHHHHHTT----EEEEEECSSCCCEEE
T ss_pred
                ECCCCCCEEEEEeCC---CeEEEEECCCCCcceeeeccccEEEeecCCCcccceeEEeccCCCCCceEEecCCccE
Q ss_pred
Q Fri_Mar_04_23: 116 FAPAHLGLKLACLGND---GILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQAI
                                                                          192 (349)
O Consensus
             116 ~-p-----l-----i-iwd---------
                                                                          192 (349)
             225 (369)
T Consensus
             164 WHRR--GDHFATVSPSGQRSSVAIHTLSKHLTQIPF------RKLNGLAQTASFHP---LRPLFFVATQRSIR
T 5cxb B
                                                                          225 (369)
                ECTT--SSEEEEECGGGTTSCEEEEETTTTEEECCC------CCCSSCEEEEEECS---SSSEEEEEESSCEE
T ss_dssp
                T ss_pred
                Q ss pred
Q Fri_Mar_04_23: 193 IYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKIT---EKLSPLASEESLTNSNMFDN-SA 268 (349)
             Q Consensus
                                                                          268 (349)
             +|+.... +..++|...|.+++|+|++ +.+|+|++|++|++ ....+..+.......|+| ++
226 lwd------lasgs-D--i-wd-----lasgs-D--i-h---v-v-fsp---
                      .+..+.+|...|.+++|+|++
T Consensus
                                                                          298 (369)
             226 CYDLQKLE---LVKIVQPGAKWISSFDVHPGG----DNLVVGSYDKRLLWHDLDLSNRPYKTMRFHTEAIRAVRFHKGGL
T 5cxb B
                                                                          298 (369)
T ss dssp
                EEETTTTS---CSEEECCCCSSEEEEEECTTS----SEEEEEETTSCEEEEETTTCSSCSEEEECCCSSCEEEEECCCSSC
T ss_pred
                EEECcCc---eeeeccCcccEEEEECCCC----CEEEEecCCccEEEEeccccchhhhhccccccEEEEEECCCCC
Q ss pred
                cccccccccccccc---ccccccceeeeeccCCC----eEEEEEECCCCCEEEEecCCCCeEEEEe
Q Fri_Mar_04_23: 269 DVDMDAQGRSDSNTEEKA---ELQSNLQVELLSEHDDHNG----EVWSVSWNLTGTILSSAGDDGKVRLWK 332 (349)
             269 -----h----i-v--spdg--las-s-D--v-iW- 332 (349)
Q Consensus
             T Consensus
             299 PLFADASDDGSLOIFHGKVPNDOLENPTIVPVKMLKGHKVVNKLGVLDIDWHPREPWCVSAGADGTARLWM 369 (369)
T 5cxb B
```

```
T ss_dssp
                  SEEEEEETTSEEEEEEECCSSTTSCEEEEEEECCCCBTTBCEEEEECSSSSCEEEEETTSCEEEC
T ss_pred
                  CEREERCCCCEREERCCCchhhacccccceeREERccccccccccceEEEEECCCCEREERCCCCeREE
                             PDB"
                                     NCBI Pub Med
No 30
>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=2.2e-34 Score=253.85 Aligned_cols=291 Identities=14% Similarity=0.218 Sum_probs=0.0
                  EEEEEECCCCCEEEEEeCCCceEEEEECCCCCceeEeeeeccccceEEEEEEcCCCCCEEEEEeeccCccc
 Q Fri_Mar_04_23:
                12 VHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEEDPDQE
                                                                                      91 (349)
                12 v----s-d---l-t-s-D--v-iwd------h---v--v--v-----las-s-Dq-v-lwd-----
O Consensus
                                                                                      91 (349)
                  3 ~s~~~~d~~~l~s~s~D~~v~~Wd~~~~~
                                                      ~~~v~~~
                                                              -_---i~iwd----
                                                                                      75 (326)
T Consensus
                 {\tt 3} \verb| TSPGTVGSDPVILATAGYDHTVRFWQAHSG----ICTRTVQHQDSQVNALEVTP--DRSMIAAAGYQ-HIRMYDLNSNNP| \\
T 4jsn D
T ss dssp
                  ----CCSSSEEEEEETTSEEEEECTTTC----CEEEEEECTTSCCCEEECT--TSSEEEEECBS-CEEEEESSSCSC
T ss_pred
                  CCCCcCCCCCEEEEecCCCcEEEEECCCC----eEEEEecCCCCCEEEEEECC--CCCEEEecCCC-cEEEEECCCCCc
Q ss_pred
                  Q Fri Mar 04 23:
                92 ECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCL
                                                                                     171 (349)
                O Consensus
                T Consensus
                                                                                     134 (326)
T 4jsn D
                76 NP-----IISYDGVNKNIASVGFHED-GRWMYTGGEDCTARIWDLRSRNLQCQRIF-----QVNAPINCV 134 (326)
                  CC----SEEECCCCSBEEEEEECTT--SSEEEEEETTSEEEEEETTSCCSSCSEEE-----ECSSCEEEE
 T ss_dssp
T ss_pred
                   cc-----eEeccccCceeEEEEcCC--CCEEEEEcCCCceeEEEee------ccCCcEEEE
0 ss pred
                  EEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCcceeEEEECCCCCceEEEEEccCCCCEEEEEecCc-
Q Fri_Mar_04_23: 172 SWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK--
                                                                                     248 (349)
               T Consensus
                                                                                     204 (326)
T 4jsn D
                                                                                     204 (326)
 T ss dssp
                  EECT---TSSEEEEEETTSCEEEEETTTCC--EEEECSSTTSCEEEEEECTTS----SEEEEEETTSCEEEEEECCCGG
 T ss pred
                   EECC---CCCEEEEECCCCcEEEEECCCCc---eeEeccCCCcceEEEEECCCC----CEEEEEECCCCcc
Q ss_pred
                  -----EEEEE
Q FTI MAT 04 23: 249 -----LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGE-----VWSVSW
                                                                                     312 (349)
Q Consensus
                                          ~~~~~~h~~~~h~~~~
               249 -----
                                                                                     312 (349)
               T Consensus
                                                                                     278 (326)
               205 DEVTOLIPKTKIPAHTRYALOCRESPDSTILATCSADOT-----CKIWRTSNESLMTELSIKSGNPGESSRGWMWGCAF
T 4jsn_D
                                                                                     278 (326)
T ss dssp
                  GSCCCEEEEEECCCSSCEEEEECTTSSEEEEETTTE-----EEEEETTTCCEEEEEECCCSSTTSCCCCCEEEEE
                  cccccccccccccccceEEEEECCCCCEEEEecCCCe-----EEEEECCCCceeeeeeccCCCCcccceEEEEEE
T ss_pred
                  CCCCCEEEEccCCCeeeeeeccC
Q ss pred
Q Fri_Mar_04_23: 313 NLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
               Q Consensus
                                                  349 (349)
                  +|||++||+|+.|++|+||+++.+ .++.++.+|.
               279 s~d~~~l~s~s~D~~v~lWd~~~g---~~~gH~ 312 (326)
T Consensus
               279 SGDSQYIVTASSDNLARLWCVETG---EIKREYGGHQ 312 (326)
T 4jsn D
T ss_dssp
                  CTTSSEEEEETTSEEEEEETTTC---CEEEEEECCS
T ss_pred
                  CCCCCEEEEccCCCCEEEEEccCC---ceeeeecCcc
                         PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
                                                     Pub Med
Sgan_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=2.4e-35 Score=272.52 Aligned_cols=285 Identities=19% Similarity=0.252 Sum_probs=0.0
                  7 GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWR-AHDSSIVAIDWASPEYGRIIASASYDKTVKLWE
7 -h---v---s-d---l-t-s-D--v-iwd-----------h---v-----las-s-Dg-v-lwd
+|...|++++|+|++++|++|+|.|.|++||+....+.+|...|++++|+...|++++|+...|+++|+...|++|+|...|++|+|
Q Fri_Mar_04_23:
                                                                                      85 (349)
Q Consensus
                                                                                      85 (349)
T Consensus
                     ---i----s--g--latgs-dg-v-vwd------h---v--l---p-----l-s---dg-i-vwd
               173 \ \ VSTKPISAVSLSTDDMVVATGSWAGDLQVLNSQTL----QPLTQKLDSHVGKIGAIDWHPD-SNNQMISCAEDGLIKNFQ
T 5gan H
                                                                                     247 (465)
T ss_dssp
                  CCSSCCCEEECSSSSEEEEETTTEEEEEETTTC----CBCCCCTTSCSSCEEEEECCSS-SSCEEEEETTSCEEEEE
T ss_pred
                  Q ss pred
                  \verb|cccccccccceeeEEEccCCcceeeEEEeccCccceeeeccceEEEeeccCccceeeeccceEEEeeccCcccc| \\
Q Fri_Mar_04_23:
                86 EDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHL
                                                                                     165 (349)
                O Consensus
                                                                                     165 (349)
               T Consensus
                                                                                     307 (465)
               248 YSNE----EGGLRLLGDLVGHERRISDVKYHPS--GKFIGSASHDMTWRLWDASTHQELLLQ------EGHD
T 5gan H
T ss_dssp
                  ECSS----SCSEEEEEECCCSSCEEEEEETT-TTEEEEEESSSCEEEEETTTEECCCC-----CCCS
T ss pred
                  CCCC----CCcceeeeeccCCCCeeEEEECCC--CCEEEEEcCCCcEEEEEcCCCceEEEe
                  \verb|cceeEEEEcccCCCceeEeecCc-eEEEEeccCCceeEEEEcccCCcceeEEEEcccCCceeEEEEcccCCCeeEEEE
Q ss pred
 Q Fri_Mar_04_23: 166 QSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFK 244 (349)
               Q Consensus
T Consensus
               308 ~~v~~~~sp~g----~l~s~~dg~i~iwd~~~~--~~v~~~sp~g---~~l~t~s~dg~v~iwd 377 (465)
```

```
308 KGVFSLSFQC---DGSLVCSGGMDSLSMLWDIRSG---SKVMTLAGHSKPIYTVAWSPNG----YQVATGGGDGIINVWD 377 (465)
T 5gan H
T ss_dssp
                 SCEEECCBCT---TSSEEEEEETTSCBEEEETTTT---EECCBCSSCSSCCCEEEEETTT---TEEEEECSSSEEEEEC
T ss_pred
                 CCEEEEECC---CCCEEEEECCCCEEEEECCCC---ceeEEeccCCCcEEEEEECCCC----CEEEEECCCCeEEEEE
                 Q ss pred
 Q Fri_Mar_04_23: 245 ITEKLS----PLASEESLTNSNMFDNS--ADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTI
                                                                               318 (349)
Q Consensus
              245
                                                           ~~~~~~h~~~i~~v~~spdg~~
                                                                               318 (349)
                                                    ..+|+...+.+..+.|...|++++|+|+|+|
                       ----v-vwd-----h---v-s-d-
                                                                               451 (465)
T Consensus
              378 IRKRDEGQLNQILAHRNIVTQVRFSKEDGGKKLVSCGYDNL-----INVYSSDTWLKMGSLAGHTDKIISLDISNNSHF
 T 5gan_H
                                                                               451 (465)
                 CSCTTCCCSEEEECCSSCEEEEECCTTTSCCEEEEEESSSE-----EEEEETTTCCEEEEEECCSSCEEEEECCSSSSC
T ss_dssp
                 T ss_pred
Q ss_pred
                 EEEecCCCeEEEe
Q Fri_Mar_04_23: 319 LSSAGDDGKVRLWK 332 (349)
O Consensus
              319 las~s~D~~v~iW~
                             332 (349)
                 |++|+.|++|+||+
T Consensus
              452 l~s~s~dq~i~iWd 465 (465)
T 5gan H
              452 LVSGGWDRSIKLWN 465 (465)
T ss_dssp
                 EEEEETTSEEEEEC
                 EEEEeCCCeEEeCC
T ss pred
No 32
                                                 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
 4179 A
Probab=100.00 E-value=4e-34 Score=249.42 Aligned cols=247 Identities=19% Similarity=0.241 Sum probs=0.0
Q ss_pred
                 Q Fri_Mar_04_23:
               3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                                82 (349)
               82 (349)
O Consensus
                 T Consensus
                                                                               122 (301)
               49 RSIQVTETPVRAGKFIARKNWIIVGSDDFRIRVFNYNTG---EKVVDFEAHPDYIRSIAVHP--TKPYVLSGSDDLTVK
T 4j73_A
                                                                               122 (301)
T ss_dssp
                 EEEECCSSCEEEEEEGGGTEEEEEETTSEEEEEETTTC----CEEEEEECCSSCEEEEEECS--SSSEEEEEETTSCEE
                 eEecccccEEEEEeCCCCEEEEECCCC----cEEEEEeCCCCcEEEEECC--CCCEEEEECCCCCEE
T ss pred
                 EeeccCccccccccceeEEEEcCCCCcEEEEEEcCCCCcEEEEEeCCCCcceeeeccccEEEeecCCC
Q ss pred
               {\tt 83~LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA}
 Q Fri Mar 04 23:
 O Consensus
               162 (349)
                            .....+.+|...|.+++|+|... +..|++++.|++|++||+.......
                 +||+.++
T Consensus
              123 lWd-----h---v--v--p-----l-sgs-D--v-iwd-------
                                                                               181 (301)
              123 LWNWENN-----WALEQTFEGHEHFVMCVAFNPKD-PSTFASGCLDRTVKVWSLGQSTPNFTLT-----T
T 4173 A
                                                                               181 (301)
                 T ss dssp
T ss_pred
                 EEECCCC-----cchhhhcccCCCcEEEEEEcCCC-CCEEEEEECCCCcCceee------c
                 Q ss pred
Q Fri Mar 04 23:
              163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR
                                                                               241 (349)
                                       ---i-----las-s-d--v-
                                                                               241 (349)
 Q Consensus
                 ++...+..+.|... +.++++++.++ +++|+..... .+..+|...|.+++|+|+|
                                                                   ++ | ++ | +. | ++ | +
T Consensus
              253 (301)
              182 GOERGVNYVDYYPI.PD-KPYMTTASDDI.TIKTWDYOTKS---CVATI.EGHMSNVSFAVFHPTI.----PIIISGSEDGTI.K
T 4j73_A
                                                                               253 (301)
                 CCTTCCCEEEECCSTT-CCEEEEECTTSEEEEEETTTCC---EEEEEECCSSCEEEEEECSSS----SEEEEEETTSCEE
T ss dssp
T ss_pred
                 CCCCEEEEEECCC-CCEEEEECCCCCEEEEECCCC---hhhhhcCCCCCeEEEEECCCC----CEEEEECCCCeEE
Q ss_pred
                 Q Fri Mar 04 23: 242 IFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGT--IL
                                                                               319 (349)
                                                           ----h---i--v--spdg----1
              242 vwd~~~
O Consensus
                                                                               319 (349)
                 +||+.+.
                                                         254 iWd~~~
T Consensus
                                                                               287 (301)
T 4j73_A
              254 IWNSSTY-----KVEKTLNVGLERSWCIATHPTGRKNYI
                                                                               287 (301)
T ss_dssp
                 EEETTTC-----CEEEEECCSSSSEEEEEC----CCE
T ss pred
                 EEeCCCc-----eeEEecccCCcceEE
                 EEecCCCeEEE
Q ss pred
Q Fri Mar 04 23: 320 SSAGDDGKVRL 330 (349)
O Consensus
              320 as~s~D~~v~i 330 (349)
                 |+|+.|+.+.+
                     -g----
T Consensus
              288 asg~~
              288 ASGFDNGFTVL
T 4j73 A
                           298 (301)
T ss_dssp
                 REFETTEREER
T ss_pred
                 EEecCCcEEEE
                           PDB'
                                   NCBI
                                                 Pub Med
>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=1.9e-34 Score=259.85 Aligned_cols=290 Identities=12% Similarity=0.081 Sum_probs=0.0
Q ss pred
                 Q Fri Mar 04 23:
               3 PFDSGHDDLVHDVVYDFYG-RHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                               81 (349)
```

```
Q Consensus
              3 ----h---v---s-d----l-t-s-D--v-iwd-----h---v--v-v--v----las-s-Dg-v
                                                                           81 (349)
                T Consensus
                                                                           143 (383)
              67 RTASPFDRRVTSLEWHPTHPTTVAVGSKGGDIILWDYDVQNK--TSFIQGMGPGDAITGMKFNQF-NTNQLFVSSIRGAT
T 3ei3 B
                                                                           143 (383)
                EEECCCSSCEEEEECSSCTTEEEEEEBTSCEEEEETTSTTC--EEEECCCSTTCBEEEEEEETT-EEEEEEETTTEE
T ss dssp
                eccCCCCCEEEEEecCCCCCEEEEEeCCCccc--ceeEecCCCCCCEEEEEecCCC-CCCEEEEEecCCCeE
T ss pred
                EEeeccCcccccccceeEEEEcCCC---CcEEEEEECcCCCccEEEEEECCCCcceeeeccccEEEee
Q ss pred
Q Fri_Mar_04_23:
              82 KLWEEDPDQEECSGRRWNKLCTLNDSK---GSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLS
                                                                           158 (349)
Q Consensus
              82 ~lwd~~~
                                   ----v----p-----l-----d--i-iwd----
                                                                           158 (349)
             T Consensus
                                                                           201 (383)
             144 TLRDFSG----SVIQVFAKTDSWDYWYCCVDVSVS--RQMLATGDSTGRLLLLGL-DGHEIFKEK-----
T 3ei3 B
                                                                           201 (383)
T ss_dssp
                EEEETTS-----CEEEEEECCCCSSCCEEEEEETT--TTEEEEEETTSEEEEEET-TSCEEEEEE
T ss_pred
                EEEECCC-----ceEEEecCCCcccceeEEEECCC--CCEEEEEeCCCeEEEee----
Q ss_pred
                CCCCcccceeEEEcccCCCCC-ceEEecCCc-eEEEEccCCCcEEEEEccCCCCceeEEEECC-CCCCceEEEEEcc
Q Fri_Mar_04_23: 159 IPPANHLQSDFCLSWCPSRFSPE-KLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAP-SIGRWYQLIATGC
                                                                           235 (349)
Q Consensus
                            -----h---v--sp-----las-s
                                                                           235 (349)
                   T Consensus
             202 ---LHKAKVTHAEFNP---RCDWLMATSSVDATVKLWDLRNIKDKNSYIAEMPHEKPVNAAYFNPTDS---TKLLTTD
T 3ei3 B
                                                                           270 (383)
                ----CSSSCEEEEECS---SCTTEEEEEETTSEEEEEEGGGCCSTTCEEEEEECSSCEEEEEECTTTS----CEEEEEE
T ss_dssp
                T ss pred
Q ss_pred
                Q Fri Mar 04 23: 236 KDGRIRIFKITEKLSPLASE-----ESLTNSNMFDNSADVDM------DAQGRSDSNTEEKAELQSNLQVELLS
                                                                           298 (349)
O Consensus
             298 (349)
                . |+. |++ | |+....+
             271 -d--i-vwd-----i-iwd---
                                                                           344 (383)
T Consensus
             271 QRNEIRVYSSYDWSKPDQIIIHPHRQFQHLTPIKATWHPMYDLIVAGRYPDDQLLLNDKRT-----IDIYDANSGGLVH
                                                                           344 (383)
T ss_dssp
                SSSEEEEETTBTTSCSEEEECCBCCCTTSCCCCCEECSSSSEEEEECBCCTTTCTCCCC-----EEEEETTTCCEEE
                CCCCEEEEECCCCCcccceeeccccccccccceeeEEECCCCCEEEEeccCCccccccCCCc-----EEEEECCCCCEEE
T ss_pred
                ecc--CCCceEEEEECCCCCEEEEecCCCeEEEEeccc
Q ss_pred
Q Fri Mar 04 23: 299 EHD--DHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATY 335 (349)
             299 ~~~--h~~~i~~v~~spdg~~las~s~D~~v~iW~~~~
Q Consensus
                                             335 (349)
                .+. +|...+..+|+|+|+|+|+|+|+|+++.
-----v----spdg-l-s-s-d-i-iW----
                                             382 (383)
T Consensus
T 3ei3 B
             345 QLRDPNAAGIISLNKFSPTGDVLASGM-GFNILIWNRED 382 (383)
                EECBTTBCSCCCEEEECTTSSEEEEEE-TTEEEEEECC-
T ss dssp
                EEeCCCCCceeeeEECCCCCeEEEec-CCeEEEEecCC
T ss pred
No 34
                         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=5.3e-34 Score=255.64 Aligned cols=271 Identities=15% Similarity=0.216 Sum probs=0.0
                CCccCCCcCeEEEEECC--CCCEEEEECC------CCeEEEEECCCCCCceeEeeeeccccceEEEEECCCCCCCEE
Q ss pred
Q Fri_Mar_04_23:
               1 MQPFDSGHDDLVHDVVYDF--YGRHVATCSS-----DQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRII
                                                                           72 (349)
              1 -----h---v--s--d---l-t-s-----D--v-iwd------h---v--v--v--v-----l
                                                                           72 (349)
                T Consensus
                                                                           78 (368)
               3 M-LRYHMQGFSGYGVQYSPFFDNRLAVAAGSNFGLVGNGKLFILEIDRS-GRIVEVNSFL-TQDCLFDLAWNES-HENQV
T 3w15 A
                {\tt C-EEEECTT-EEEEEEECSSCTTEEEEEEEEGGTSSCEEEEEEECTT-CCEEEEEEEE-ESSCEEEEEECTT-CTTEE}
T ss_dssp
                T ss pred
                EEEeCCCeEEEeeccCccccccccceeEEEECCCCcEEEEEECc-CCCcEEEEEECCCCCcceeeecc
0 ss pred
Q Fri_Mar_04_23:
              73 ASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP-AHLGLKLACLGNDGILRLYDALEPSDLRSWTLT
                                                                           151 (349)
              145 (368)
T Consensus
              79 LVAQGDGTLRLFDTTFKEFP-----IAIFKEHEREVFSCNWNLVN--RQNFLSSSWDGSIKIWSPLRKQSLMTL---
T 3w15 A
                                                                           145 (368)
                EEEETTSEEEEEETTSCSSC-----SEEEECCSSCEEEEECSSS-SSCEEEEETTSCEEEECTTCSSCSEEE---
T ss dssp
                EEECCCCcEEEEECCCCCC-----ceeehhccCcEEEEECCCC--CCEEEEecCCCceeeee-
T ss pred
                Q ss pred
Q Fri Mar 04 23: 152 SEMKVLSIPPANH------LQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLH
                                                                          203 (349)
                                                                           203 (349)
                                            ...+.+++|+|. .+..+++++++++|+......
             T Consensus
                                                                          213 (368)
             146 -----TPRPLEITKMVDPLNAIILKKKSFTGISKNRNCVYQAQFSPH--DQNLVLSCSGNSYASLFDIRLPSGKN 213 (368)
T 3w15 A
                -----CCCCHHHHHHSCTTGGGSCC-----CCEEEEEECSS-CTTEEEEEETTSEEEEETTSCTTSS
T ss dssp
T ss_pred
                Q ss_pred
                Q Fri_Mar_04_23: 204 VAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKIT----EKLSPLASEESLTNSNMFDNSADVDMDAQGRS
                                                                           278 (349)
             204 ~~~~h~~~v~~v~~sp~~~~~las~s~d~~v~vwd~~~~~~~
Q Consensus
                                                                           278 (349)
                ~~~v~~~~sp~~~--~lasgs~D~~i~lWd~~~~~~
T Consensus
T 3w15 A
             214 QNNFLVHSGLEALTCDFNKYRP---YVVATGGVDNAIRIWDIRMLNKNPG-----
                                                                           260 (368)
T ss dssp
```

```
T ss_pred
                  cceeEecCCcceEEecCCCC---CEEEEecCCCcEEEEECCcccCcC------
                  ccccccccccccee----eeec-cCCcceEEEEECCC-CCEEEEeccCCceEE
 0 ss pred
 Q Fri_Mar_04_23: 279 DSNTEEKAELQSNLQVE----LLSEH-DDHNGEVWSVSWNLT-GTILSSAGDDGKVRLWKATYSNEFK------ 340 (349)
               279 ~~~~~~~~~~~~~~~~~h~~i~~v~~spd-g~~las~s~D~~v~iW~~~~~~~~~~~~~~~~~
               T Consensus
                                                                                ~~~ 324 (368)
               261 -----QLHNSSCINEIPNAHGLAIRKVTWSPHHSNILMSASYDMTCRIWRDLSNDGAKETYKTNSTDAT 324 (368)
 T 3w15 A
                     -----CEEEEETTSSSSCEEEEECSSCTTEEEEEETTSCEEEEECTTC-----CCTTTSTT
 T ss dssp
 T ss_pred
                      Q ss pred
                  --EEEEeeccC
 Q Fri_Mar_04_23: 341 -- CMSVITAQQ 349 (349)
 O Consensus
                     .
----H-
 T Consensus
               325 ~~
                            335 (368)
 T 3w15_A
               325 KGSIFNFTQHS 335 (368)
 T ss_dssp
                  TTEEEEECCCS
 T ss_pred
                  ccccchhhcCc
 No 35
                                                   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=1.7e-33 Score=246.07 Aligned_cols=295 Identities=17% Similarity=0.269 Sum_probs=0.0
 Q ss pred
                  Q Fri_Mar_04_23:
                1 MOPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                    80 (349)
                1 -----h---v--s-d---l-t-s-D--v-iwd------h---v--h---v---h---v--las-s-Dg-
                T Consensus
                                                                                    88 (312)
 T 4ery A
                                                                                    88 (312)
 T ss dssp
                  EEEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEETTTC---CEEEEECCCSSCEEEEECT-TSSEEEEEETTSE
 T ss pred
                  EEEEcccCCceeEEEEccccceEEEeecccc----ceeeeeccccceeEEEecc--cccEEEEecccc
 Q ss_pred
                  EEReeccCccccccccccceeereeccCcceeereeccccceeeeeccceeeeccceeeeccc
 Q Fri Mar 04 23:
                81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                   160 (349)
                81 v~lwd~~~~d~i~iwd~~~
 Q Consensus
                                                                                    160 (349)
                                +.+..+.|...+.++|+|+|+ +...++++.|+.|++||+.+......
                  |++||+.++
 T Consensus
                89 v~vwd~~~~~
                                        145 (312)
 T 4ery_A
                89 I.KTWDVSSG-----KCI.KTI.KGHSNYVFCCNFNPO--SNI.TVSGSFDESVRTWDVKTGKCI.KTI.-----
                                                                                   145 (312)
 T ss dssp
                  EEEEETTTC-----CEEEEEECCSSCEEEEEECSS-SSEEEEEETTSCEEEEETTTCCEEEEE
                  EEEEECCCC-----eeEEEEeCCCCceEEEEECCC--CCEEEEecCCCceeeec-----
 T ss_pred
 Q ss_pred
                  CCcccceeEEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCceeEEEEEccCCCCceEEEEEccCCCC
 Q Fri_Mar_04_23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGR
                                                                                   239 (349)
 Q Consensus
               161 ~~~~~
                            -----h---v--y--y--sp-----las-s-d--
                                                                                    239 (349)
               T Consensus
               T 4ery A
                                                                                   215 (312)
 T ss_dssp
                  -CCCSSCEEEEECT---TSSEEEEEETTSCEEEEETTTCC--EEEEECCSSCCCEEEEEECTTS----SEEEEEETTTE
 T ss_pred
                  -cccccceeeeecc---ccceeeeecccc--eeeeeecccc---ceeeeecccc
 Q ss pred
                  Q Fri_Mar_04_23: 240 IRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTIL 319 (349)
               240\ v-vwd------h--i-v--spdg--1\quad 319\ (349)
 O Consensus
               T Consensus
               216 LKLWDYSKG-KCLKTYTGHKNEKYCIFANFSVTGGKWIVSGSEDNLVYIWNLQTKEIVQKLQGHTDVVISTACHPTENII
 T 4ery A
                                                                                   294 (312)
                  {\tt EEEEETTT-EEEEEECSSCCSSSCCCEEEECSSSCEEEECCTTSCEEEEETTTCCEEEEECCCSSCEEEEEECSSSSEE}
 T ss_dssp
 T ss_pred
                  EEEecCCCC-cEEEEEecCCCCcEEEEEEEccCCEEEEEEccCCceeeeeccCCCcceEEccCCCCCEE
                  EEecC--CCeEEEEeccc
 Q ss pred
 Q Fri_Mar_04_23: 320 SSAGD--DGKVRLWKATY
                                  335 (349)
               320 as~s~--D~~v~iW~~~~
 Q Consensus
                                  335 (349)
               ++++. |++|+|+.+.
295 ~s~~~d~i~~W~~~~
 T Consensus
                                  312 (312)
               295 ASAALENDKTIKLWKSDC 312 (312)
 T 4ery A
 T ss_dssp
                  EEEECTTTCCEEEEECCC
 T ss pred
                  EEeeccCCCeEEEeeccC
                                              Pub Med
                           PDB™
PROTEIN DATA BANK
 No 36
->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=252.09 Aligned cols=294 Identities=15% Similarity=0.236 Sum probs=0.0
                  Q ss pred
                3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
 Q Fri_Mar_04_23:
                                                                                    82 (349)
                Q Consensus
 T Consensus
```

```
58 RVISGHLGWVRCIAVEPGNOWFVTGSADRTIKIWDLASG----KLKLSLTGHISTVRGVIVST--RSPYLFSCGEDKQVK 131 (374)
 T 4yvd A
 T ss_dssp
                          ERECCCSSCEREEECTTSSEEREETTSCEREETTTC----CEREEECCCSSCEREERCS--SSSEREERETTSCER
 T ss_pred
                          EEECCCCCEEEEECCCCCEEEEECCCC----ceEEEEcCcCceeEEEECC--CCCEEEEEECCCeEE
                          \texttt{E}eecc\texttt{C}cccccccee\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{E}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{C}\texttt{e}\texttt{e}\texttt{e}\texttt{e}\texttt{e}\texttt{e}\texttt{C}\texttt{C}\texttt{C}\texttt{C}}
 Q ss pred
 Q Fri_Mar_04_23:
                       83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                                                                         162 (349)
                                                                                                                         162 (349)
 Q Consensus
                       83 lwd-----d--i-iwd-----
                                     +||+.+.
                      132 iwd~~~---
                                                                                                                         187 (374)
 T Consensus
                      132 CWDLEYN-----KVIRHYHGHLSAVYGLDLHPT-IDVLVTCSRDSTARIWDVRTKASVHTLS-----
 T 4yvd_A
                                                                                                                         187 (374)
                           EEETTTT-----EEEEECCCCSSCEEEEEECSS-SSEEEEEETTSEEEEEETTTCCEEEEEE
 T ss_dssp
 T ss_pred
                           Q ss_pred
                          cccceeEEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCceeEEEEEccCCCcceEEEEE
 Q Fri_Mar_04_23:
                      163 \  \  NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRRAM (Compared to the compact of th
                                                                                                                         241 (349)
 O Consensus
                      241 (349)
                           .+...+..|+| ++...+++..+ +..+|+.... ....+..+|+|+|+
                                                                                                      .+|++++.++ |+
                           256 (374)
 T Consensus
                      188 GHTNAVATVRCQA---AEPQIITGSHDTIRLWDLVAG---KTRVTLTNHKKSVRAVVLHPRH----YTFASGSPDN-IK
 T 4yvd A
                                                                                                                         256 (374)
                           CCSSCEEEEECS---SSSCEEEEETTSCEEEEETTTT---EEEEEECCCSSCCCEEEECTTS---SEEEEECSSC-EE
 T ss_dssp
                           CCCccEEEEECC---CCCEEEEEECCCeEEEEECCCC---eEEEEecCCCcEEEEEECCCC----CEEEEecCCc-EE
 T ss pred
                          Q ss pred
 Q Fri_Mar_04_23: 242 IFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDH------NGEVWSVS
                                                                                                                         311 (349)
 Q Consensus
                          +||+...
                                                                              ..+++...+..+
                      T Consensus
                                                                                                                         329 (374)
                      257 QWKFPDGSFIQNLSGHNAIINTLTVNSDG-VLVSGADNGT-----MHLWDWRTGYNFQRVHAAVQPGSLDSESGIFACA
 T 4yvd A
                                                                                                                         329 (374)
 T ss_dssp
                           EEETTTTEEEEEECCCCSCEEEEEECTTC-EEEEEETTSC-----EEEEETTTCCEEEEECC------CCCEEEEE
                           EEECCCCcEEeecccCcceeEEEEECCCC-EEEEccCCCe-----EEEEECCCCeeeeeeecccCcccccCCccEEEE
 T ss pred
                          ECCCCCEEEEccCCCeEEEEE
 Q ss pred
 Q Fri_Mar_04_23: 312 WNLTGTILSSAGDDGKVRLWKATYSNEFKCMSV
                                                                   344 (349)
                      312 ~spdg~~las~s~D~~v~iW~~~~~~~
 Q Consensus
                                                                   344 (349)
                          T Consensus
                      330 FDQSESRLLTAEADKTIKVYREDDTATEETHPV 362 (374)
 T 4yvd_A
 T ss_dssp
                          ECTTSCEEEEETTSCEEEEEC-----
                          ECCCCCEEEEecCCCeEEEEECCCCcccCCCcc
 T ss pred
                                         PDB"
                                                                            Pub Med
□ >5ams_ā SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=3.5e-34 Score=262.13 Aligned_cols=285 Identities=16% Similarity=0.143 Sum_probs=0.0
                           5 DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEY-GRIIASASYDKTVKL
5 ~~~h~~~v~~~~s-d~~~l~t-s~D~~v~iwd~~~~~~~~~h~~~v~~v~~v~~~~~~~las~s-Dg-v~l
 Q Fri_Mar_04_23:
                                                                                                                          83 (349)
 Q Consensus
                                                                                                                          83 (349)
                          ---h---v----s--g--l-s---dg-i-vwd------
                                                                                    ----p-----i----dg-i-i
 T Consensus
                                                                                                                         181 (431)
                      105 LTGYGESVISCSFTSEGGFLVTADMSGKVLVHMGQKGGAQWKLASQMQEVEE-IVWLKTHP--TIARTFAFGATDGSVWC
 T 5ams A
                                                                                                                         181 (431)
 T ss_dssp
                          ECCCSSCREEEECTTSSEEEEETTSCEEEEEEEGGGTEEEEEECCSSC-EEEEECS--SSTTEEEEETTCCEEE
 T ss_pred
                           eeccC--cccccccceeEEEEcC--CCCcEEEEEEC----cCCCcEEEEEECCCCcceeeecccE
 Q ss pred
 Q Fri_Mar_04_23:
                       84 WEEDP--DOEECSGRRWNKLCTLND--SKGSLYSVKFA----PAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEM 154 (349)
 O Consensus
                       154 (349)
                      T Consensus
                      182 YOINEODG-----SLEOLMSGFVHOODCSMGEFINTDKGEN-TLELVTCSLDSTIVAWNCFTGOOLFKI-----
                                                                                                                         244 (431)
 T 5ams A
                           EEECTTTC-----CEEEEEEECCCSSCEEEEEESCSSCSS--CCEEEEEETTSCEEEEETTTCCEEEEE-----
 T ss_dssp
                          EEeeCCCC-----ceEEEEeccCCCCceEEEEEecccCCC--CCEEEEEECCCCeEEEEE
 T ss_pred
                          EEeecCCC----cccceeEEEEcc-----cCCCCCceEEecCc-eEEEEecc-CCcEEEEEEcc------CCC
 Q ss pred
                      155 KVLSIPPA----NHLQSDFCLSWCP-----SRFSPEKLAVSALEQ-AIIYQRGK-DGKLHVAAKLP------GHK
 Q Fri_Mar_04_23:
                                                                                                                         212 (349)
 Q Consensus
                      155
                                   -_____h~
                                                                                                                         212 (349)
                                T Consensus
                                                                                                                         311 (431)
                      245 -----TQAEIKGLEAPWISLSLAPETLTKGN--SGVVACGSNNGLLAVINCNNGG--AILHLSTVIELKPEQDELD
 T 5ams A
                                                                                                                         311 (431)
 T ss dssp
                          -----CGGGTTTCCCCEEEEEECTTTTTSC---TTEEEEEETTSEEEEEEGGGTS---EEEEEEESCCCCSSSCGG
                           -----cCcccCCcCCEEEEEECCcccCCC---CCEEEEEcCCCCeEEEEECCCCC---cEEEEEeeeecccccC
 T ss_pred
                          Q ss pred
 Q Fri Mar 04 23:
                      {\tt 213~SLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQS}
                                                                                                                         290 (349)
                      213 ~~v~~v~~sp~~~~~las~s~d~~v~vwd~~~~-
 Q Consensus
                                                                                                                         290 (349)
                      T Consensus
 T 5ams A
 T ss dssp
                          GCEEEEEETTT----TEEEEEETTSEEEEEETTTTEEEEEE-ECSSCEEEEEETT--EEEEEETTSC-----EEEEE
                          CCEEEEECCCC----CEEEEECCCCEEEEECCCceEEEEE-cCCCCEEEEEECCC--EEEEEECCC------EEEEE
 T ss pred
 Q ss pred
                          CCCCeeeeeccCCCceEEEEEC-----CCCCEEEEecCCCeEEEEeccc
```

```
Q Fri_Mar_04_23: 291 NLQVELLSEHDDHNGEVWSVSWN------LTGTILSSAGDDGKVRLWKATY 335 (349)
O Consensus
               291 ~~~~~h~~i~~v~~s-----pdg~~las~s~D~~v~iW~~~~
                                                              335 (349)
               T Consensus
                                                              431 (431)
               379 ARTGQEKFVCVGHNMGVLDFILLHPVANTGTEQKRKVITAGDEGVSLVFEVPN 431 (431)
T 5ams A
                  \tt TTTCCEEEEECCCSSCEEEEEEECCCCSSCCCCEEEEEEETTSCEEEEEECC
T ss_dssp
                  CCCCGEEEEECCCCGGEEEEEeccccGCCCCCGEEEEECCCGEEEEECCC
T ss pred
                           SCOPe PDB<sup>™</sup> PROTEIN DATA BANK
No 38
🗌 >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=1.9e-33 Score=247.04 Aligned cols=246 Identities=19% Similarity=0.387 Sum probs=0.0
                  Q ss_pred
Q Fri_Mar_04_23:
                5 DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                                     84 (349)
O Consensus
                5 ---h---v---s-d---l-t-s-D--v-iwd------h---v-v--v--v-----las-s-Dq-v-lw
                                                                                     84 (349)
                  T Consensus
                                                                                    134 (318)
T 4ggc_A
                \textbf{63} \ \texttt{MEQPGEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQQ----KRLRNMTSHSARVGSLSWN----SYILSSGSRSGHIHHH}
                                                                                    134 (318)
                  CCSTTCCEEEEECTTSSEEEEEETTSEEEEETTTT----EEEEEEECCSSCEEEEEE----TTEEEEEETTSEEEEE
T ss_dssp
                  T ss pred
                  eccCccccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEECCCCC----cceeeecccEEEeecC
Q ss pred
Q Fri_Mar_04_23:
                85 EEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPS----DLRSWTLTSEMKVLSIP
                                                                                    160 (349)
                                     ----v-----p------l-----d--i-iwd------
                85 d~~~~~~
                                                                                    160 (349)
                               135 d-----h---v--l--spd-g--las-s-D--v-wd-------
T Consensus
                                                                                    192 (318)
               135 DVRVAEHH-----VATLSGHSQEVCGLRWAPD-GRHLASGGNDNLVNVWPSAPGEGGWVPLQTF-----
T 4ggc A
                                                                                    192 (318)
 T ss dssp
                  ETTSSSCE-----EEEEECCSSCEEEEEECTT--SSEEEEEETTSCEEEEESSCBTTBSCCSEEE------
T ss_pred
                  ecccccc-----eeeecCCCCCEeEEEECCC--CCEEEEEeCCCCcCcccceee------
                  CCcccceeEEEEccCCCCCceEEec--CCc-eEEEEecCCCcEEEEEEccCCCCceeEEEECc-
Q ss pred
Q Fri Mar 04 23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSA--LEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC--
                                                                                    235 (349)
 Q Consensus
                    235 (349)
                   ..|...+.+++|+|. ....++++++ .++ +++|+..... .+..+..| ..+..++|+|+|+
               193 ---h---v---p------l-s---s-D--i-1wd-------v----sp-----sp------l------
T Consensus
                                                                                    261 (318)
               193 -TOHOGAVKAVAWCPW--OSNVLATGGGTSDRHTRIWNVCSGA---CLSAVDAH-SOVCSILWSPHY----KELISGHGF
T 4ggc_A
                                                                                    261 (318)
T ss dssp
                  -CCCCSCEEEEECTT--STTEEEEEECTTTCEEEEEETTTCC---EEEEEECS-SCEEEEEEETTT----TEEEEEECT
                  -eccccceEEEEccc--cccEEEEecccccccEEEEEccccc--EeEEeccc-CceeEEEECccc---CeEEEEEcc
T ss_pred
Q ss_pred
                  Q Fri Mar 04 23: 236 KDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLT
                                                                                    315 (349)
O Consensus
               236 ~d~~v~vwd~~~~
                                                                    ----h---i--v--spd
                                                                                    315 (349)
                  . | + . | ++ | | + . . .
                                                                  +.+..+.+|...|++|+|+|
               262 ~d~~i~iwd~~~
                                                                  -----h---v--l--spd
               262 AONOLVIWKYPTM-----AKVAELKGHTSRVLSLTMSPD
T 4ggc A
                                                                                    295 (318)
T ss_dssp
                  TTCCEEEEETTTC------CEEEEECCCSSCEEEEEECTT
T ss pred
                  CCEEEEcCCCeEEEEcccCC
Q ss pred
 Q Fri_Mar_04_23: 316 GTILSSAGDDGKVRLWKATYSN 337 (349)
Q Consensus
               316 g~~las~s~D~~v~iW~~~~~
                                     337 (349)
                  | ++ | | +++. | ++ | + | | ++....
               296 g--1-s-s-D--v-1W-----
T Consensus
                                     317 (318)
               296 GATVASAAADETLRLWRCFELD
T 4ggc_A
                                     317 (318)
T ss_dssp
                  SSCEEEETTTEEEEECCSCCC
T ss_pred
                  CCeEEEecCCccEEEEecccC
                           PDB<sup>IN</sup>
PROTEIN DATA BANK
                                     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=1.3e-33 Score=256.04 Aligned cols=279 Identities=18% Similarity=0.323 Sum probs=0.0
                  Q ss pred
Q Fri_Mar_04_23:
                7 \ \ \mathsf{GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEE
                                                                                     86 (349)
Q Consensus
                7 ~h~~~v~~~s~d~~l~t~s~D~~v~iwd~~~~~~~h~~~v~~v~~v~~~~~las~s~Dq~v~lwd~
                                                                                     86 (349)
                  ---v--l--s--g--l-sgs-dg-v-iw------h---v--l-----l-s---d--i-iwd-
T Consensus
T 41q9 A
               109 PSNKDVTSLDWNSEGTLLATGSYDGFARIWTKDGN-----LASTLGQHKGPIFALKWNK--KGNFILSAGVDKTTIIWDA
                                                                                    181 (400)
T ss_dssp
                  CSSCCEEEEECTTSSEEEEEETTSEEEEEETTSC----EEEEEEECSSCEEEEECS--SSSEEEEEETTSCEEEEET
T ss_pred
                  CCCCcEEEEECCCCCEEEEECCCc----EEEEeccCCccEEEEEECC--CCCEEEEEeCCCceEEEE
Q ss_pred
                  cCccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCCcceEEEEE
 Q Fri_Mar_04_23:
                87 DPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQ
                                                                                    166 (349)
 Q Consensus
                166 (349)
                          +...+..|...+..+..|.+ +...++++..|+..+++|++....+..+
                                           ~~___~h~~
T Consensus
               182 ~~~~~~~~~~~~~
                                                                                    236 (400)
               182 HTG-----EAKQQFPFHSAPALDVDWQS--NNTFASCSTDMCIHVCKLGQDRPIKTF-----QGHTN
T 41q9 A
                                                                                    236 (400)
 T ss_dssp
                  TTT-----EEEEEECCCSSCEEEEEESS--SSEEEEEETTSCEEEEETTCSSCSEEE------CCCSS
 T ss_pred
                  CCC-----ccceeccCCCCcEEEEecC---CCeEEEECCCCEEEEEECCCccceee------cCCcc
```

```
Q ss pred
                ceeEEEccCCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEECCCCCCce-----EEEEEcC
Q Fri Mar 04 23: 167 SDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQ------LIATGCK
                                                                           236 (349)
O Consensus
             236 (349)
             {\tt 237~EVNALKWDP---TGNLLASCSDDMTLKIWSMKQDN---CVHDLQAHNKEIYTIKWSPTG----PGTNNPNANLMLASASF}
T 4lg9 A
                                                                           306 (400)
T ss_dssp
                CEEEEECT---TSSEEEEEETTSEEEEEETTCSS---CSEEEECCSSCEEEEECSCS----TTSSSTTSCCCEEEEET
T ss_pred
                ceeeeecc---ccceeeeeeccc---eeeehhhcccceeeeeeccc---ccccccceeeeeecc
Q ss_pred
                Q Fri_Mar_04_23: 237 DGRIR:FKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNL
                                                                           314 (349)
O Consensus
             237 d--y-ywd-----h---i--y--sp
                                                                           314 (349)
             ..+|+...+.+.+|.. |.+++|+|
T Consensus
                                                                           379 (400)
                                                                   ~-v~~v~~s~
             307 DSTVRLWDVDRGICIHTMTKHQEPVYSVAFSPDGRYLASGSFDKC-----VHIWNTQTGALVHSYRGTGG-IFEVCWNA
T 41g9_A
                                                                           379 (400)
                TSCEEEEETTTEEEEEECCCCSCEEEEEECTTSSEEEEEETTSE-----EEEEETTTCCEEEEEECSSC-EEEEEECT
T ss_dssp
T ss pred
                CCCEEEECCCCCEEEEECCCCCEEEEEECCCCC-----EEEEECCCCC-EEEEECCCC-
Q ss pred
                CCCEEEecCCCeEEEecc
Q Fri_Mar_04_23: 315 TGTILSSAGDDGKVRLWKAT 334 (349)
             315 dg~~las~s~D~~v~iW~~~
Q Consensus
                                334 (349)
             +|+++++.|+.|+||++.
380 ~g~~l~~~~dg~v~vwd~~
T Consensus
                                399 (400)
             380 AGDKVGASASDGSVCVLDLR
T 41q9 A
                                399 (400)
                TSSEEEEETTSCEEEEECC
T ss_dssp
T ss_pred
                CCCEEEEeCCCcEEEEEcc
                         PDB<sup>™</sup>
PROTEIN DATA BANK
No. 40
                                 NCBI
                                         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=2.4e-34 Score=264.17 Aligned_cols=304 Identities=17% Similarity=0.181 Sum_probs=0.0
Q ss pred
                Q Fri_Mar_04_23:
              2 QPFDSGHDDLVHDVVYDFY------D
Q Consensus
              2 ~~~~~h~~~v~~~~s~d--------------l~t~s~D~~v~iwd~~~------
                                                                            41 (349)
                                +++|+||+.|++|++||+..
                ..++.+|.+.|++++|+|+
              T Consensus
                                                                           104 (451)
              25 OSFTRVGENNLTCISCFOPVLNKYTFEESSNGDKNKGRLFAYTVSKDLOLTKYDITDFSKRPKKLKYAKGGAKYIPTSKH 104 (451)
T 4j0x A
                EEEEECSSSCEEEEEECC------CCEEEEEETTSEEEEEECCCTTSCCEEEEEECCGGGCC---
T ss_dssp
T ss_pred
                Q ss pred
                42 TSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLN--DSKGSLYSVKFAPA
                                                                           119 (349)
O Fri Mar 04 23:
              O Consensus
                                                                           119 (349)
                T Consensus
             105 ---EYENTTEGHYDEILTVAASP-DGKYVVTGGRDRKLIVWSTESL-----SPVKVIPTKDRRGEVLSLAFRKN
T 4j0x A
                                                                           169 (451)
                -----CCCSSCCSCEEEEECT-TSSEEEEETTTSEEEEETTTT-----EEEEEEECCCTTCCEEEEEECTT
T ss_dssp
                ---eeeEEeccCCccEEEEECC--CCCEEEEecCCCeEEEEECCCC-----eEEEEEecCCCCccEEEEEecC
T ss pred
Q ss_pred
                CCCCEEEEECCCCeEEEEECCCCCcceeeeccccEEEeccCCCccceEEEECccCCCCceEEecCCc-eEEEEccC
Q Fri_Mar_04_23: 120 HLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGK
                                                                           198 (349)
                ----l----d--i-iwd-----
Q Consensus
             120
                                                                           198 (349)
                  +..|++++.|+.|++||+.+...+..+.
                                                         ---~-l~~~~d~~i~iwd~~~
                231 (451)
T 4j0x A
             170 --SDOLYASCADFKIRTYSINOFSOLEILY------GHHDIVEDISALA---MERCVTVGARDRTAMLWKIPD
                                                                           231 (451)
T ss dssp
                --SSEEEEEETTSEEEEEETTTTEEEEEEE------CCSSCCCEEECCS--SSEEEEECBTTCEEEEEEGGG
T ss_pred
                --CCEEEEECCCEEEEECCCCCEEEEEC------CCCCCeEEEEECC---CCCEEEEECCCCeEEEEECCCC
                CCCEEEEE.....ccCCCCceeEEEEcCCCCCceEEEEec
Q ss_pred
Q Fri_Mar_04_23: 199 DGKLHVAAK-------LPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKIT
                                                                           246 (349)
             199 -----h---y--y--sp-----las-s-d--y-vwd--
Q Consensus
                                                                           246 (349)
                                             +..|...|.+++|+|+
                                                            .+|++++.|+.|++||+.
                                                         -----l----dg-i-iwd--
             232
                                                                           306 (451)
T Consensus
             232 ETRLTFRGGDEPQKLLRRWMKENAKEGEDGEVKYPDESEAPLFFCEGSIDVVSMVDD-----FHFITGSDNGNICLWSLA
                                                                           306 (451)
T 4j0x_A
                TEEEEEECCCCHHHHHHHHTTC-------CCCCCCEEEEEEETT----TEEEEEETTSCEEEEETT
T ss dssp
                CceeeecCCCcceeEEecCCccEEEecCCccCCCCCEEEEEeCCC-----CEEEEEeCCC
T ss pred
                Q ss pred
Q Fri Mar 04 23:
             247 EKLSPL-----ASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNL
                                                                           292 (349)
O Consensus
             292 (349)
                -----v-iw---
T Consensus
             307
                                                                           380 (451)
T 4j0x A
             307 KKKPIFTERIAHGILPEPSFNDISGETDEELRKRQLQGKKLLQPFWITSLYAIPYSNVFISGSWSGS-----LKVWKIS
                                                                           380 (451)
                CSSCSEEETTTTCBC-----EEEEEEC
T ss_dssp
                CCCeeeEEeccCceeccCcceEEEEcCCCcccCCCcceEEEEEecCCce
T ss pred
                cc----eeeeeccCCcceEEEEEECCCC------CEEEEecCCCeEEEEEecc--cCCcEEEEEEeeccC
Q ss pred
Q Fri Mar 04_23: 293 QV---ELLSEHDDHNGEVWSVSWNLTG-----TILSSAGDDGKVRLWKAT--YSNEFKCMSVITAQQ 349 (349)
             293 ~~---
                     -----h---i--v--spdg-----las-s-D--v-iW-----
                                                                    349 (349)
Q Consensus
             T Consensus
```

```
T 4j0x_A
             381 DNLRSFELLGELSGAKGVVTKIQVVESGKHGKEKFRILASIAKEHRLGRWIANVSGARNGIYSAVIDQTG 450 (451)
T ss_dssp
                TTSSCEREERETTCCSERREERERC----CEERREERESSCTTCCCCSCCTTCCCEREERERC--
T ss pred
                CCCcceEEEEEcCCCccEEEEEECCCCcccccccEEEEecCCCEEEEEecccccCceEEEEe
                        SCOPe POEM PROTEIN DATA BANK
                                                  Pub Med
                                         NCBI
>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=5.6e-34 Score=254.84 Aligned_cols=296 Identities=13% Similarity=0.183 Sum probs=0.0
                0 ss pred
Q Fri Mar 04 23:
             3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                            82 (349)
               82 (349)
O Consensus
               77 (372)
T Consensus
T 1k8k C
               2 AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKS--GNKWVQVHELKEHNGQVTGVDWAP--DSNRIVTCGTDRNAY
                                                                            77 (372)
                CEESCSSCCEEEECTTSSEEEEECSSSEEEEEEE--TTEEEEEEEECCSSCEEEEEET--TTTEEEEETTSCEE
T ss dssp
                ccccCCcceEEEECCCCCEEEEEcCCCCEEEEEcc--CCCcceeeeccCCCCcEEEEECC--CCCEEEECCCCEEE
T ss pred
Q ss_pred
                ReeccCcccccccccceeEEEEcCCCCcEEEEEECcCCCCEEEEEEeCCCeEEEEECCCCcceeeeccccEEEeecCCC
Q Fri_Mar_04_23:
              83 LWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                            162 (349)
Q Consensus
              162 (349)
                T Consensus
                                                                            139 (372)
              78 VWTLKGRTW------KPTLVILRINRAARCVRWAPN-EKKFAVGSGSRVISICYFEQEN------DWWVCKHIKK
T 1k8k C
                                                                            139 (372)
T ss dssp
                EEEEETTEE-----TEEEEECCCCSCEEEEECTT-SSEEEEEETTSSEEEEEETTT-----TEEEEEEECT
                T ss pred
Q ss_pred
                cccceeEEEEccCCCCceEEecCCc-eEEEEecCC------CcEEEEEEccCCCCceeEEEECCCCCC
Q Fri_Mar_04_23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKD------GKLHVAAKLPGHKSLIRSISWAPSIGR
                                                                           226 (349)
             163 -----h---y--y--y--sp----
O Consensus
                                                                            226 (349)
                .+...+..+|+| ++...+++...+ +...+|+....
                          T Consensus
                ~~~~i~~~
                                                                            214 (372)
              140 PIRSTVLSLDWHP---NSVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMFESSSSCGWVHGVCFSANG--
T 1k8k_C
                                                                            214 (372)
T ss_dssp
                TCCSCEEEEECT---TSSEEEEEETTSCEEEEECCCTTTSCCCCCBTTBSCCCTTCEEEECCCSSCEEEEECSSS-
T ss pred
                Q ss pred
 Q Fri_Mar_04_23: 227 WYQLIATGCKDGRIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQ------
 Q Consensus
             227 ----las-s-d--v-vwd-----
                                                     ----- 293 (349)
             T Consensus
                                                                           285 (372)
             215 -- SRVAWVSHDSTVCLADADKKMAVATLASETLPLLAVTFITESSLVAAGHDCF------PVLFTYDSAAGKLSFGGRL 285 (372)
T 1k8k C
                --SEEEEEETTTEEEEEGGGTTEEEEECCSSCCEEEEEEETTEEEEETTSS-----CEEEEEETTTTEEEECCCC
T ss dssp
T ss_pred
                 --CEEEEEecCCeEEEEecCCCceEEEeecCCCCeEEEeecCCc
                -----ceeeeccCCCceEEEEECC---CCCEEEEeccCCCceEEEEecc
Q ss pred
Q Fri Mar 04 23: 294 -------VELLSEHDDHNGEVWSVSWNL---TGTILSSAGDDGKVRLWKAT 334 (349)
                   -----h---i--v--sp----dg--las-s-D--v-iW--
                                                                        334 (349)
 Q Consensus
             360 (372)
T Consensus
              286 DVPKQSSQRGLTARERFQNLDKKASSEGSAAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVR
T 1k8k C
                                                                        360 (372)
                CCC-----CHHHHHHHHCCCCC-----CCCSSSSSSCEEEEEEESTTTSCSEEEEEEEHH
T ss dssp
T ss_pred
                PDE NCBI Pub Med
No 42
>4zoy_A SQT1; chaperone, ribosome biogenesis, WD40-repeat; 1.50A (Chaetomium thermophilum) PDB: 4zn4_A 4zoz_A
 Probab=100.00 E-value=1.5e-33 Score=260.99 Aligned_cols=311 Identities=19% Similarity=0.179 Sum_probs=0.0
Q ss_pred
                CCccCCCcceEEEEECCC-CCEEEEEeCCC------eEEEEECCCCCcce------eEeeeec
Q Fri_Mar_04_23:
              1 MOPFDSGHDDLVHDVVYDFY-GRHVATCSSDQ-----HIKVFKLDKDTSNW------ELSDSWR
                                                                            52 (349)
               1 ~~~~~h~~~v~~~~s~d~~~~l~t~s~D~~~~~v~iwd~~~~~~~~~
Q Consensus
                                                                            52 (349)
                ....+.+|.+.|++++|+|+++|+.|+ +|+||+|
               7 ----l--H----V-----s----l-s---dg------i-vw
                                                                            86 (491)
               7 SIAYFDGHKDSVFAIAQHPLYPNIVATGGSEGDADDAPGKGYVLDISAAAGRPVLPPSYNSDPSSAPQQNTSLNPIFEID
T 4zoy A
                                                                            86 (491)
T ss_dssp
                CSEEECCCSSCEEEEECSSCTTEEEEEEESCSSTTCCEEEEEEEGGGC------CBCCCSEEEC
                T ss pred
Q ss pred
                cccceEEEEEcCCCCCEEEEEecCCceEEEeeccCcccc------
Q Fri_Mar_04_23:
              53 AHDSSIVAIDWASPEYGRIIASASYDKTVKLWEEDPDQEE-----
                                                                            92 (349)
                                                                            92 (349)
O Consensus
              53 ~h~~~v~~v~~v~las~s~Dq~v~lwd~~~~~~
                +|...|++++|+|+ ++++|++++.|+.|++||+.+...
-h~~v~~~~~1~s~~dg~v~iwd~~~~~~~~
T Consensus
T 4zoy A
              87 GHTDSINALTFTLP-RGDFLVSGGMDGRMRVYAVSVPQNGALAQFKFLAESQETEEINWFAPCPSPDHPNTIALGASDGS
                                                                            165 (491)
T ss_dssp
                CCSSCEEEEECTT-TCCEEEEEETTCCEEEEEEECCTTTTCCEEEEEEECCSSSCEEEEECCCTTSTTEEEEEETTSC
T ss_pred
                Q ss pred
                  ------ccccceeEEEEcCCCCcEEEEECcCCCccEEEEEecCCCeEEEEE
 Q Fri_Mar_04_23:
              93 -----LEPSDLRSW 148 (349)
 O Consensus
              93 -----v----v-----p------l-----d--i-iwd------- 148 (349)
                         . .+.+..+|...|.+++|+|+|+ +..|++++.|+.|++||+
```

```
T Consensus
            166 VWVFTLDASDPSNP----VQIVQSYFLHTGPCTAGAWSPD--GLLLATVSEDESLHVYDVFGVAASKSLVTDNGQTVVSL 239 (491)
T 4zoy_A
T ss dssp
               EEEEEECC----CC----EEEEEEECCCSSCEEEEEECTT--SSEEEEEETTSCEEEEETTSHHHHTTCCCTTSSEEEEE
               EEEEEccCCCccc---eEEeeecccCcceeEEEEcCC--CCEEEEEeCCCcEEEEe
T ss pred
Q ss_pred
               eccccerreecCCCccccceerrercccCCCccerrecCCc-errecCC-------
Q Consensus
            149 ----- 199 (349)
            T Consensus
            T 4zoy A
T ss dssp
               T ss_pred
               -----CcEEEEEEccCCCCceeEEEECCCCCceEEEEEccCCCCEEEEEeccccccc-----ccccccccc-
Q ss_pred
Q Fri_Mar_04_23: 200 -----GKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEE-----SLTNSNMFDN-- 266 (349)
            O Consensus
                                                                 ~~~-- 266 (349)
T Consensus
                                                                      385 (491)
            310 QQTTSHQAGTILASLQIQSDNIESLAFSPSA----PILAAGSTDGSIAVFDTSRSFALRRHLRGAHAEDPVVKVEFVKSP 385 (491)
T 4zoy A
               -----CTTCEEEEECCSSSCEEEEEECSSS----SEEEEEETTSCEEEEEETTTTTTEEEEEETTTTTTSCEEEEEECSSC cccccccceEeeeccCCCCceEEEEECCCC----CeEEEECCCCeeeeEEecCCccceeeEEEEecccc
T ss_dssp
T ss pred
               ----ccccccccccccccccccccccee-----eeeccCCc----eEEE
Q ss pred
Q Fri_Mar_04_23: 267 ----SADVDMDAQGRSDSNTEEKAELQSNLQVEL-----LSEHDDHNG----EVWS
                                                                     309 (349)
                    -----i--
O Consensus
            267 ----~
                                                                      309 (349)
                ++.+.+.+..+..
                                                       +..+.+|..
                                                                . | ++
            386 ----1-iwd------i
                                                                      459 (491)
T Consensus
                                                                 ~~v~~
T 4zoy_A
            386 PNAAMAGWLLTSCGMDGV-----VRRWDLRGGTAGPGTLPHMQHLQQQRQQQQEGAAPSGLVKEWKGHRSGQEGGGVLG 459 (491)
               T ss dssp
T ss_pred
               EEECCCCCEEEEecCCCceEEEEecccCCc
Q ss pred
Q Fri Mar 04 23: 310 VSWNLTGTILSSAGDDGKVRLWKATYSNE 338 (349)
            310 v~~spdg~~las~s~D~~v~iW~~~~~~
Q Consensus
              ++|+|||++|++|+.|++|+||++....
            T Consensus
T 4zoy A
               EECTTTSSEEEEEETTSCEEEEECCCCCC
T ss dssp
T ss_pred
               EEECCCCCeEEEeecCceEeeeccccc
No 43
                      PDB NCBI
                                           Pub Med
                                      >5ams_A SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}
Probab=100.00 E-value=1.2e-33 Score=258.47 Aligned_cols=301 Identities=15% Similarity=0.115 Sum_probs=0.0
               CCCCCCCCEEEEEECCCCCEEEEEeCCCCCEEEEEEC--CCCCCGeeEeeeccccceEEEEEECCCCCCCEEEEEeCC
Q ss_pred
Q Fri_Mar_04_23:
            1 MOPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKL--DKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYD
                                                                      78 (349)
             1 ------h---v---s-d---l-t-s-D--v-iwd-_-----h---v--h---v--v---las-s-D
Q Consensus
                                                                      78 (349)
             T Consensus
                                                                      130 (431)
             57 SLTYFDKHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSHSQPP----KFAGTLTGYGESVISCSFTS--EGGFLVTADMS
T 5ams_A
               CSEEECCCSSCCCCEEECSSSSEEECCTTSCEEEEESSSSC----CEEEEECCCSSCEEEEEECT--TSSEEEEEETT
T ss_dssp
               T ss pred
Q ss_pred
               Ceeeeeccccccccccceeeeecccceee
Q Fri Mar 04 23:
             79 KTVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE--PSDLRSWTLTSEMKV 156 (349)
            O Consensus
T Consensus
            131 GKVLVHMGQK-----GGAQWKLASQMQEVEEIVWLKTHPTI-ARTFAFGATDGSVWCYQINEQDGSLEQLMS----- 196 (431)
T 5ams A
T ss_dssp
               SCEEEEEEG-----GGTEEEEEEECCSSCEEEEEECSSS-TTEEEEEETTCCEEEEEECTTTCCEEEEE
               CCEEEEECCC-----CceeEEEeeecCCCCCEEEEEecCCC-CCEEEEEeeCCCCceEEEEe
T ss_pred
Q ss_pred
               eecCCCc--ccceeEEEc----ccCCCCceEEecCCc-eEEEEecCCceEEEEEcc----CCCCceeEEEECC-
Q Fri Mar 04 23: 157 LSIPPAN--HLQSDFCLSWC----PSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLP----GHKSLIRSISWAP- 222 (349)
            O Consensus
                                                                     222 (349)
T Consensus
                                                                     264 (431)
            197 -----GFVHQQDCSMGEFINTDKGE---NTLELVTCSLDSTIVAWNCFTGQ---QLFKITQAELKGLEAPWISLSLAPE 264 (431)
T 5ams_A
               ----ECCCSSCEEEEEESCSSCS---SCCEEEEEETTSCEEEEETTTCC--EEEEECGGGTTTCCCCEEEEEEECT
T ss_dssp
T ss pred
               Q ss pred
Q Fri_Mar_04_23: 223 ----SIGRWYQLIATGCKDGRIRIFKITE-K--LSPLA------SEESLTNSNMFDNSADVDMDAQGRSDSNTEEK
                                                                     285 (349)
            223 -----las-s-d--v-vwd------
            T Consensus
            265 TLTKGNS----GVVACGSNNGLLAVINCNNGGAILHLSTVIELKPEQDELDASIESISWSSKFSLMAIGLVCGE----- 334 (431)
T 5ams A
               TTTTSCT----TEEEEEETTSEEEEEEGGGTSEEEEEESCCCCSSSCGGGGCEEEEEETTTTEEEEEETTSE-----
T ss dssp
               cccCCC----CEEEEEcCCCeEEEEEEcCCCceEEEEEeeeecccccccCCcEEEEEEcCCCceEEEEEcCCCc-----
T ss pred
```

```
Q ss pred
                  CCCCCCCeeeeeccCCCceEEEEECCCCCEEEEeccCCCeEEEEeccCCCcEEEEEeeccC
Q Fri_Mar_04_23: 286 AELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVITAQO
                                                                      349 (349)
O Consensus
               286 -----h---i--v--spdg--las-s-D--v-iW------
                                                                       349 (349)
                  335 i~iwd~~~~~v~~v
T Consensus
               335 ILLYDTSAWRVRHKF-VLEDSVTKLMFDND--DLFASCINGKVYQFNARTG---QEKFVCVGHN
T 5ams A
                                                                       392 (431)
T ss_dssp
                  ERREETTTTEERREE-ECSSCREEERRTT--EEERRETTSCREEERTTTC---CERREECCCS
                  EEEEECCCceEEEEE-cCCCCEEEEEEeCC--EEEEEeCCCeEEEEECCCC---cEeEEEeCCC
T ss_pred
                            PDB<sup>™</sup>
PROTEIN DATA BANK
                                     NCBI
                                              Pub Med
>5cvl_A WD repeat-containing protein 48; UAF1, USP, deubiquitinase, DUB, protein BI; 3.00A (Homo sapiens) PDB:
 5cvn A
 Probab=100.00 E-value=4.9e-34 Score=271.51 Aligned_cols=300 Identities=15% Similarity=0.167 Sum_probs=0.0
                  Q Fri Mar 04 23:
                2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                    81 (349)
O Consensus
                2 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v--v-----las-s-Dg-v
                                                                                    81 (349)
                  T Consensus
                  ------h----V--l--spdg--latg--dg-I-iwd------h-----h----V--l--s---dg--l-sgs-Dg-I
                                                                                   114 (598)
                38 DEVEKYNRNGVNALQLDPALNRLFTAGRDSIIRIWSVNQH-KQDPYIASMEHHTDWVNDIVLCC--NGKTLISASSDTTV
T 5cvl A
                                                                                   114 (598)
T ss_dssp
                  CSCCCSBSSCEEEEEETTTTEEEEEETTSCEEEEECSSC-CSCCEEEEEECCCSSCEEEEEEG--GGTEEEEEETTSCE
T ss_pred
                  Q ss_pred
                  EEeeccCcccccccceeEEEEcCCCCcEEEEEEcCcCcccEEEEEecCcCccceeeeccccEEEeecCC
 Q Fri Mar 04 23:
                82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP
                                                                                   161 (349)
O Consensus
                161 (349)
                           ++||+.++
T Consensus
               115 ~vwd~~~~---
                                                                                   179 (598)
T 5cvl A
               115 KVWNAHKG------FCMSTLRTHKDYVKALAYAKD--KELVASAGLDRQIFLWDVNTLTALTASNNTVTTSSL--- 179 (598)
T ss dssp
                  EEEETTTT-----EEEEEECCCSSCEEEEEETT-TTEEEEEEEHHHHHSCSSSCCCCCCEEE---
T ss pred
                  EEEECCCC-----ceeeEecCCCceEEEEEcCC--CCEEEEEeCCCeEEEEECCCcccccCCCccceec----
Q ss pred
                  \texttt{CcccceeEEEEcccCCCcceEEeccCc-eEEEEeccCCcceeEEEEccCCCcceeEEEEccCCCCc}
Q Fri_Mar_04_23:
               240 (349)
 Q Consensus
               162
                                         ---i-----las-s-d--v
                                                                                   240 (349)
                                                                        .+|++++.|+.|
                  ..+...+.|+| ++..+++.++ +..+|+.... .+..+|...|.+++|+|+|
T Consensus
               249 (598)
               180 SGNKDSIYSLAMNQ--LGTIIVSGSTEKVLRVWDPRTCA---KLMKLKGHTDNVKALLLNRDG----TQCLSGSSDGTI
T 5cvl A
                                                                                   249 (598)
                  CCCCSCEEEEECT---TSSCEEEEETTSSEEEECTTTCC--EEEEECCCSSCEEEEEECTTS---SEEEEEETTSEE
 T ss_dssp
                  CCCCCCEEEEECC---CCCEEEEECCCCEEEEecCCCc---eeEEEeCCCCCEEEEEeCCCC----CEEEEEeCCCEE
 T ss_pred
Q ss pred
                  Q Fri Mar 04 23: 241 RIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGT-
                                                                                   317 (349)
               241 ~vwd~~
                                                                    ~~h~~~i~~v~~spdg~-
O Consensus
                                                                                   317 (349)
               T Consensus
                                                                                   323 (598)
T 5cvl A
                                                                                   323 (598)
                  EEEETTTTEEEEEEECCSSCEEEEEECTTSCEEEEEETTCE-----EEEEESSSTTCEEEEEECCSSSS
T ss dssp
                  EEEECCCCceEEEEecCCCCEEEEEECCCCCEEEEECCCCC
T ss pred
Q ss_pred
                  --EEEEecCCCeEEEEeccc
Q Fri_Mar_04_23: 318 --ILSSAGDDGKVRLWKATY
                                    335 (349)
               318 --~las~s~D~~v~iW~~~~
Q Consensus
                                    335 (349)
                    + | ++++. | +. | ++ | ++..
               324 ~~~l~s~s~dg~I~iwd~~~
               324 PPAIWVATTKSTVNKWTLKG 343 (598)
T 5cvl A
T ss dssp
                  CCEEEEESSSCEEEECTT
T ss pred
                  CCEEEEECCC
No 45
                                                    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=9.6e-34 Score=256.97 Aligned_cols=245 Identities=18% Similarity=0.301 Sum_probs=0.0
                  Q ss pred
                7 GHDDLVHDVVYDFY-GRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGR-IIASASYDKTVKLW
7 ~h~~v~~~s-d-~~l-t-s-D~v~iwd~~~~~~h~~~v~v~~v~~~~~-las-s-Dq-v-lw
Q Fri_Mar_04_23:
                                                                                    84 (349)
                                                                                    84 (349)
O Consensus
                  188 (401)
T 4psw B
               116 EHEEEITRARYMPODPNIVATINGOGTTFLYSRS-E----GLOSTLKFHKDNGYALSFST--LVKGRLLSGSDDHTVALW
                                                                                   188 (401)
T ss dssp
                  EESSCEEEEEETTEEEEEEEETTSCEEEETT-T----EEEEEECCCCSCCEEEECS--SSTTEEEEECTTSCEEEE
T ss_pred
                  CCCCcEEEEECCCCCEEEEEcCCCCEEEEECC-C----CCCceECCCCCEEEEEeCC--CCCCeEEEE
Q ss_pred
                  eccCc----cccccccceeEEEEcc-CCCcEEEEEECc-CCCCcEEEEEecCCceEEEEE
 Q Fri_Mar_04_23:
                85 EEDPD----QEECSGRRWNKLCTLND-SKGSLYSVKFAP-AHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLS
                                                                                   158 (349)
O Consensus
                85 d-----d--i-iwd------
                                                                                   158 (349)
                              +..+.+ |...|.+++|+| + +..|++++.|+.|++||+++|...+...
                  1+..+
                           -----h---v--v
                                                 ----l-s---dg-i-iwd-----
T Consensus
               189 d~~
                                                                                   248 (401)
               189 EVGSGGDPTKP------VRTWNDLHSDIINDNKWHNFN--KDLFGTVSEDSLLKINDVRANNTTIDTV------
 T 4psw_B
                                                                                   248 (401)
 T ss dssp
                  ECSSSSCCSSC-----SEEESSSCSSCEEEEEECSSC-TTEEEEEETTSEEEEEETTCSSCEEEEE-----
                  ECCCCCcccc----ceEecCCCCeEeEEEEcCc--CCEEEEEECCCcEEEEe-----
 T ss_pred
```

```
Q ss_pred
                 CCCCcccceeEEEEcccCCCCCc=eEEecCCc=eEEEEcCCCcEEEEEEccCCCcceeEEEECCCCCCceEEEEEcc
Q Fri Mar 04 23: 159 IPPANHLQSDFCLSWCPSRFSPEK-LAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCK
                                                                                236 (349)
O Consensus
              159
                                          ----i-----las-s-
                                                                                236 (349)
                    .+...+..+|+| ++... +++++.++ +..+|+..... .+..+..+|...|.+++|+|+|+...
                 ____~v~~v~~v~~~l~tg~dg~i~iwd~~~~~h~~v~~v~~v~~p~~~l~s~~~l~s~~~
T Consensus
                                                                                316 (401)
              249 ----KCPQPFNTLAFSH---HSSNLLAAAGMDSYVYLYDLRNMKE--PLHHMSGHEDAVNNLEFSTHVD---GVVVSSGS
T 4psw_B
                                                                                316 (401)
                 ----ECSSCEEEEECS---SCSSEEEEEETTSCEEEEETTCTTS--CSEEECCCSSCEEEEEECSSST---TEEEEEET
T ss_dssp
                 ----cccccceeeecc---ccceeeeeccccc--cceeeeccccc--ceeeeeccccc--ceeeeecccc--ceeeeecc
T ss pred
Q ss_pred
                 Q Fri_Mar_04_23: 237 DGRIRIFKITE-----KLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLOVELLSEHDD
                                                                                302 (349)
              237 d~~v~vwd~~~----
O Consensus
                                                                                302 (349)
                 |+.|++||+..
T Consensus
              317 dg~v~iwd~~~~
                                                                                350 (401)
              317 DNRLMMWDLKQIGAEQTPDDAEDGVP-----ELIMVHAG
T 4psw_B
                                                                               350 (401)
T ss_dssp
                 TSCEEEEEGGGTTCCCCHHHHTTCCT-----TEEEEECC
T ss_pred
                 CCceEEEEECCCCC-EEEEecCCCeEEEEeccCC
Q ss_pred
 Q Fri Mar 04 23:
              303 HNGEVWSVSWNLTGT-ILSSAGDDGKVRLWKATYS
                                             336 (349)
              303 h---i--v--spdg---las-s-D--v-iW-----
                                             336 (349)
 Q Consensus
              |...|++++|+|+++++++++|+.|+||+++...
351 h~~v~~~~~l~s~s~dg~v~iw~~~~
T Consensus
                                             385 (401)
              351 HRSSVNDFDLNPQIPWLVASAEEENILQVWKCSHS
T 4psw B
                                             385 (401)
                 CSSCEEEEECSSSTTEEEEEETTSEEEEEECTT
T ss dssp
                 cccceeeeeccccceeeeeccc
T ss pred
                   SCOPe PROTEIN DATA BANK
No 46
                                                          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=4.4e-33 Score=254.16 Aligned cols=247 Identities=19% Similarity=0.381 Sum probs=0.0
                 Q ss pred
 Q Fri Mar 04 23:
                5 DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                                84 (349)
O Consensus
                84 (349)
              T Consensus
                                                                                214 (420)
              143 MEQPGEYISSVAWIKEGNYLAVGTSSAEVQLWDVQQQ----KRLRNMTSHSARVGSLSWN----SYILSSGSRSGHIHHH
T 4gga_A
                                                                                214 (420)
                 CCSTTCCEEEEECTTSSEEEEETTSCEEEEETTTT---EEEEEECCCSSCEEEEEE---TTEEEEEETTSEEEEE
T ss_dssp
T ss pred
                 eccCccccccceeEEEEcCCCCcEEEEEECCCCCcEEEEEeCCCc----cceeeecccEEEeecC
0 ss pred
Q Fri_Mar_04_23:
               85 EEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPS----DLRSWTLTSEMKVLSIP
                                                                                160 (349)
                      -----v-----p-----l----d--i-iwd-------
                                                                                160 (349)
                 |+....
              215 d-----h---v--lasgs-d--v-iwd------
T Consensus
                                                                               272 (420)
              215 DVRVAEH-----HVATLSGHSQEVCGLRWAPD--GRHLASGGNDNLVNVWPSAPGEGGWVPLQTF------
T 4qqa A
                                                                               272 (420)
                 ETTSSSC-----EEEEEECCSSCEEEEEECTT--SSEEEEEETTSCEEEEESSCCSSCSCCSEEE------
T ss_dssp
                 ECCCCCc----ceeeeccccceeeeeccc--cceeeeeeccc--cceeeee
 T ss pred
                 CCcccceeEEEEcccCCCCceEEec--CCc-eEEEEecCCCcEEEEEEccCCCCceeEEEEEc--
Q ss_pred
Q Fri Mar 04 23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSA--LEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC--
                                                                               235 (349)
                                          ---i----las-s--
                                                                                235 (349)
                  ..|...+..++|+|. ....+++++ .++ +.+|+.... ..+..+..|. .|.+++|+|++
              341 (420)
T Consensus
              273 -TOHOGAVKAVAWCPW--QSNVLATGGGTSDRHIRIWNVCSG---ACLSAVDAHS-QVCSILWSPHY----KELISGHGF 341 (420)
T 4gga_A
                 -CCCSSCEEEEECTT--CTTEEEEEECTTTCEEEEEETTTT---EEEEEEECSS-CEEEEEEETTT----TEEEEEECT
T ss dssp
                 T ss_pred
Q ss_pred
                 Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLT
                                                                               315 (349)
              236 ~d~~v~vwd~~~
                                                                ----h---i--v--spd
Q Consensus
                                                                               315 (349)
                 .|+.|++||+...
                                                              +.+..+.+|...|.+++|+||
T Consensus
              342 ~d~~i~iwd~~
                                                              ----h---V----
                                                                           ~spd
              342 AQNQLVIWKYPTM-----AKVAELKGHTSRVLSLTMSPD
T 4qqa A
                                                                               375 (420)
T ss dssp
                 TTCCEEEEETTTC------CEEEEECCCSSCEEEEECTT
T ss_pred
                 CCCeEEEECCCc-----CEEEEECCCCccEEEEECCC
Q ss pred
                 CCEEEecCCCeEEEeccCCCc
Q Fri_Mar_04_23: 316 GTILSSAGDDGKVRLWKATYSNE 338 (349)
O Consensus
              316 g-~las~s~D~~v~iW~~~~~
                                    338 (349)
                 Ī++|++|+.|++|+||++....
              376 g~~l~s~s~D~~v~iW~~~
T Consensus
                                    398 (420)
              376 GATVASAAADETLRLWRCFELDP 398 (420)
T 4gga_A
T ss dssp
                 SSCEEEETTTEEEEECCSCSSC
T ss_pred
                 CCEEEECCCCCEEEECCCCCC
No 47
                           PDB
                                   NCBI
                                            Pub Med
>3sfz_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=1.4e-33 Score=289.59 Aligned_cols=294 Identities=19% Similarity=0.271 Sum_probs=0.0
Q ss pred
                2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
O Fri Mar 04 23:
                                                                          81 (349)
              2 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v----las-s-Dg-v
Q Consensus
                                                                          81 (349)
             T Consensus
                                                                          681 (1249)
T 3sfz A
                                                                          681 (1249)
                SEEECCCSSCEEEEECTTSSEEEEEETTSCEEEEETTTC----CEEEEECCCSSCEEEEECT--TSSEEEEEETTSEE
T ss dssp
                eeEeeCCCCcEEEEEECCCCEEEEEECCCC=---CEEEEEecCCCCEEEEEEcc--CCCEEEEEECCCCE
T ss pred
                Q ss_pred
Q Fri Mar 04 23:
              82 KLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP
                                                                         161 (349)
                           -----v----v----p-----l----d--i-iwd---
Q Consensus
              82 ~lwd~~~~~
                                                                          161 (349)
                       +.+.++.+|...|.+++|+|+..+..+++++.|++|++||+.++.....
                ++||+.++
                         T Consensus
                                                                          739 (1249)
T 3sfz A
             682 KIWDSATG-----KLVHTYDEHSEQVNCCHFTNKSNHLLLATGSNDFFLKLWDLNQKECRNTM------
                                                                         739 (1249)
                EEEETTTC-----CEEEEEECCSSCEEEEEECSSSSCCEEEEEETTSCEEEEETTSSSEEEEE-----
T ss_dssp
                EEEECCCC-----eEEEEECCCCCEEEEEEEeCCCceEEEEeccCCceEEee-----
T ss pred
                CcccceeEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEE-----
Q ss pred
Q Fri_Mar_04_23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVA------
                                                                         205 (349)
             162 -----
                                                                          205 (349)
Q Consensus
                        .+|...+.++|+| ++..++++.++ +++|+.....
             740 --h---v----sp---dg--1-s-s-dg-v-vwd--------v----s-dg--1-
T Consensus
                                                                          816 (1249)
             740 FGHTNSVNHCRFSP---DDELLASCSADGTLRLWDVRSANERKSINVKRFFLSSEDPPEDVEVIVKCCSWSADGDKIIVA
T 3sfz A
                                                                          816 (1249)
T ss_dssp
                CCCSSCEEEEECS---STTEEEEEESSSEEEEEGGGTEEEEEECCCC------CCCCCBCCCCBCTTSSEEEEE
T ss_pred
                Q ss_pred
                -----EccCCCceeEEEECCCCCC
Q Fri_Mar_04_23:
             206 -----AKLPGHKSLIRSISWAPSIGR
                                                                          226 (349)
O Consensus
             206 -----h~~v~~v~~sp~~~
                                                                          226 (349)
                                                        ..+.+|...|.+++|+|++
             817 ----i---d------i----s----l-----d--v-lwd------
                                                          -----h----V---v--spdg--
T Consensus
                                                                          894 (1249)
T 3sfz A
             817 AKNKVLLFDIHTSGLLAEIHTGHHSTIQYCDFSPYDHLAVIALSQYCVELWNIDSRLKVADCRGHLSWVHGVMFSPDG--
                                                                          894 (1249)
                ETTEEEEEETTTCCEEEEECSSSCCCEEEECSSTTEEEECSSSCEEEEETTTTEEEEEECCCSSCEEEEECTTS--
T ss_dssp
                T ss pred
Q ss pred
                Q Fri_Mar_04_23: 227 WYQLIATGCKDGRIRIFKIT-----EKLSPLASEESLTNSNMFDNS
                                                                         267 (349)
             227 ~~~las~s~d~~v~vwd~~-----
Q Consensus
                                                                          267 (349)
                 .+|++++.|++|++||+.
                                   ----sp
T Consensus
             895 --~~1~s~s~D~~i~vWd~~~~~
                                                                          972 (1249)
             895 --SSFLTASDDOTIRVWETKKVCKNSAIVLKOEIDVVFOENETMVLAVDNIRGLOLIAGKTGOIDYLPEAOVSCCCLSPH
T 3sfz A
                                                                         972 (1249)
                --SEEEBEBTTSCEEEEEHHHHHSCCSSSEEEEEEEEEETTBEEEEEEESSSSEEEEEEESSCCEEEECCSCEEEEECTT
T ss dssp
                T ss pred
                Q ss pred
Q Fri_Mar_04_23: 268 ADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYS 336 (349)
Q Consensus
             268 ~~~
                    T Consensus
T 3sfz A
T ss dssp
                SSEEEEETTSC----CEEEETTTTSCEEECCCSSCCCCEEECSSSCEEEECSSBEEEEETTT
                T ss pred
                                        Pub Med
No 48
                       PDB™ SMDB
PROTEIN DATA BANK NCBI
Scvo_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=8.1e-34 Score=272.31 Aligned_cols=300 Identities=15% Similarity=0.166 Sum_probs=0.0
                Q ss_pred
Q Fri_Mar_04_23:
              2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                          81 (349)
              2 -----h---v---s-d---las-s-Dg-v
Q Consensus
                                                                          81 (349)
               +..+.+|.+.|++++|+|++++|++|+.|+.|+.|+.||+...
              23 ~~~~gH~~V~lafspdg~Latgs~Dg~I~iWd~~~~~1~h~~V~l~sp-dg~Lasgs~Dg~I
23 DEVEKYNRNGVNALQLDPALNRLFTAGRDSIIRIWSVNQH-KQDPYIASMEHHTDWVNDIVLCC--NGKTLISASSDTTV
T Consensus
                                                                          99 (677)
T 5cvo A
                                                                          99 (677)
                CSCCCSBSSCEEEEETTTTEEEEEETTSCEEEEECSSC-CSCCEEEEECCCSSCEEEEECS--TTCCEEEEETTSCE
T ss dssp
                cccccccceEEEEEeCCCCEEEEEECCCC-CCceEEEEecCCCCCeEEEEEcc--CCCEEEEEECcCeE
T ss pred
Q ss_pred
                EEeeccCccccccccceeEEEEcCCCCcEEEEEEcCCCCcEEEEEEcCCCCcceeeeccccEEEeecCC
Q Fri_Mar_04_23:
              82 KLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP 161 (349)
             O Consensus
T Consensus
             100 KVWNAHKG------FCMSTLRTHKDYVKALAYAKD--KELVASAGLDRQIFLWDVNTLTALTASNNTVTTSSL---
T 5cvo A
                                                                          164 (677)
T ss_dssp
                EEEETTTT-----EEEEEECCCSSCCCEEEETT-TTEEEEECTTSCEEEEEHHHHHCSCCSSCCCCCEEE----
                EEEECCCC-----eEeEEECCCCccEEEEEEeCC--CCEEEEEECCCCccccccCCcccccccccCcccceeee----
T ss_pred
                \texttt{CcccceeEEEEcccCCCCceEEeccCc-eEEEEeccCCcceEEEEEcccCCCceeEEEEEcccCCCc}
Q ss_pred
Q Fri_Mar_04_23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI 240 (349)
O Consensus
             162 ------las-s-d-v 240 (349)
```

```
..+...+.++|+| ++...+++++.++ +.+|+... ..+..+.+|...|..+++|+|++ ...+|+++...|
165 -----V-l--spdg--Lasgs-dg-I-iwD--t--------1-h---V-l--spdg-----L-sgs-Dg-I 234 (677)
T Consensus
              165 SGNKDSIYSLAMNQ---LGTIIVSGSTEKVLRVWDPRTC---AKLMKLKGHTDNVKALLLNRDG----TQCLSGSSDGTI
T 5cvo A
                                                                              234 (677)
                 CCCCSCEEEEECT---TSCCEEEEETTSSEEEEETTTT---EEEEEECCCSSCEEEEEECTTS----SEEEEEETTSEE
T ss dssp
                 eCCCCCEEEEEcC---CCCEEEEEeCCCEEEEeeCCCC---EEEEEEcCCC----CEEEEEecCCEE
 T ss_pred
                 Q ss pred
Q Fri_Mar_04_23: 241 RIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGT-
                                                                              317 (349)
              241 ~vwd~~~--~h~~i~v~spdq~-
                                                                               317 (349)
Q Consensus
                 ++||+...
              235 -iwd-----i-----h---V-l--spdg--l-sgs-dg------V-vwdl-------l-----V-l--spdg--
235 RLWSLGOORCIATYRVHDEGVWALOVNDAFTHYYSGGRDRK-----TYCTDLRNPDIRVLICEEKAPVLKMELDRSADP
T Consensus
T 5cvo A
                                                                              308 (677)
                 EEEETTTTEEEEEEECCSSCEEEEEECTTSCEEEEEETTCE-----EEEEESSCTTCEEEEEECCSSSS
T ss dssp
                 EEEECCCCceEEEEeccCCCceEEEEEcccccc
T ss pred
Q ss pred
                 --EEEEecCCCeEEEEeccc
Q Fri_Mar_04_23: 318 --ILSSAGDDGKVRLWKATY 335 (349)
              318 --~las~s~D~~v~iW~~~~
Q Consensus
                                 335 (349)
                  +|++++.|+.|++|++..
              309 ~~~L~s~s~Dg~I~iwd~~~
T Consensus
                                 328 (677)
              309 PPAIWVATTKSTVNKWTLKG
T 5cvo A
                                 328 (677)
T ss_dssp
                 CSEEEEESSSCEEEEECTT
                 CEEEEEECCCEEEEECCC
T ss_pred
                          PDB"
PROTEIN DATA BANK
                                   NCBI
                                                 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=8.4e-35 Score=261.05 Aligned_cols=293 Identities=16% Similarity=0.239 Sum_probs=0.0
                 CCccCCCcceEEEEECCCCCEEEEEeCCCceEEEEECCCCCcceeEeeeccccceEEEEECCCCCCEEEEEeCCCe
Q Fri Mar 04 23:
               1 \ \texttt{MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT}
                                                                               80 (349)
               1 -----h---V----s-d---l-t-s-D--V-iwd-----h---V--V---V-----las-s-Dg-
Q Consensus
                                                                               80 (349)
                 78 (377)
T Consensus
T 3dwl C
               3 TSQVLHILPKPSYEHAFNSQRTEFVTTTATNQVELYEQD--GNGWKHARTFSDHDKIVTCVDWAP--KSNRIVTCSQDRN
                                                                               78 (377)
T ss_dssp
                 CEREEECSSCSCCECSSSSEECCCSSSCBCEEEEE--TTEEEECCCBCCCSSCEEEEECT--TTCCEEEEETTSS
                 cceeccCCCcEEEEECCCCCeEEEEECCCCEEEEEECC--CCCcceEEEEccC--CCCEEEEEecCCe
T ss_pred
                 EEEeeccCccccccceeEEEEccCCCcEEEEEEccCCCceEEEEEccCCCc---cceeeecccEEEe
Q ss_pred
Q Fri_Mar_04_23:
              81 VKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPS---DLRSWTLTSEMKVL
                                                                              157 (349)
O Consensus
               157 (349)
                 T Consensus
               79 v~vwd~~~----
T 3dwl C
               79 AYVYEKRP-----DGTWKQTLVLLRLNRAATFVRWSPN-EDKFAVGSGARVISVCYFEQENDWWVSKHL----- 141 (377)
                 EEEC-----CCCCEEECCCCSSCEEEECCTT-SSCCEEEESSSCEEECCC----CCCCEEE-----
T ss dssp
                 EEEEEccC-----CCcceeeEEeccCCcceEEEEECCC--CCEEEEEECCCcchhhhhhhc-----
T ss pred
                 Q ss pred
              158 SIPPAN-HLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDG------KLHVAAKLPGHKSLIRSISW
Q Fri_Mar_04_23:
                                                                               220 (349)
 Q Consensus
              158
                                    ~~~~~~~h~~~V~~V~~
                                                                               220 (349)
                   T Consensus
              213 (377)
              142 ----KRPLRSTILSLDWHP---NNVLLAAGCADRKAYVLSAYVRDVDAKPEASVWGSRLPFNTVCAEY-PSGGWVHAVGF
T 3dwl C
                                                                               213 (377)
T ss dssp
                 ----CSSCCSCEEEEECT---TSSEEEEEESSSCEEEEECCSSCC-CCCSCSSCSCCCEEEEEECC-CCSSSEEEEE
                 T ss_pred
                 Q ss pred
Q Fri Mar 04 23: 221 APSIGRWYQLIATGCKDGRIRIFKITE----K-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQV
                                                                               294 (349)
              221 sp-----las-s-d--v-vwd------
O Consensus
                                                                               294 (349)
              T Consensus
                                                                               282 (377)
              214 SPSG---NALAYAGHDSSVTIAYPSAPEOPPRALITVKLSOLPLRSLLWANESAIVAAGYNYS-----PILLOGNES
T 3dwl C
                                                                              282 (377)
                 CTTS----SCEEEETTTEEC-CEECSTTSCEEECCCEECSSSCEEEEEEETTEEEEEESSSS-----EEEECCC-
T ss dssp
                 CCCC----CEEEEEeCCCeEEEEECCCCccchhhheeecCCCCceEEEEEcCCcceEEEEcCCc-----EEEEEeCCC
T ss_pred
Q ss_pred
                 Q Fri Mar 04 23: 295 ------ELLSEHDDHNGEVWSVSWNLTGT----I
                                                                              318 (349)
Q Consensus
              295 -----h~~i~v~spdg~---
                                                                               318 (349)
                                                        ....+.+|...|++|+|+|+++
              283 GWAHTROLDAGTSKTSFTHTGNTGEGREEEGPVSFTALRSTFRNMDLKGSSQSISSLPTVHQNMIATLRPYAGTPGNITA 362 (377)
T 3dwl C
T ss dssp
                 T ss_pred
                 EEEecCCCeEEEec
Q ss_pred
 Q Fri_Mar_04_23: 319 LSSAGDDGKVRLWKA 333 (349)
 Q Consensus
              319 las~s~D~~v~iW~~ 333 (349)
                 |+||+.|++|+||++
              363 l~s~s~Dg~v~iW~~ 377 (377)
T Consensus
              363 FTSSGTDGRVVLWTL 377 (377)
 T 3dwl C
T ss_dssp
                 EEEEETTSEEEEECC
 T ss pred
                 EEEecCCceEEEEeC
```

```
PDB'
 No 50
                                                      NCBI Pub Med
           PRE-mRNA-splicing factor PRP5; spliceosome, U2/U5/U6, lariat, RNA binding protein-RNA compl; HET: GDP
 ADP; 3.60A {Schizosaccharomyces pombe 972h-}
 Probab=100.00 E-value=1.9e-34 Score=267.13 Aligned cols=286 Identities=17% Similarity=0.263 Sum probs=0.0
                           Q ss pred
 Q Fri_Mar_04_23:
                        3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                        ....+.+|...|++++|+| ++++|++|+.|+.|+
                                                                                        ---v--l--s---l-s---dg-v-
 T Consensus
                                                                                                                          230 (473)
 т 3јb9 К
                      157 RVISGHLGWVRCVDVEPGNQWFCTGAGDRTIKIWDLASG----VLKLTLTGHIATVRGLAVSP--RHPYLFSCGEDKMVK
                                                                                                                          230 (473)
 T ss dssp
                           EEEECCSSCBCCCEECTTSSEEECCBTTSEEEEEETTTC----CEEEEEECCSSCEEEEEECS--SSSBEEEEETTSCEE
 T ss_pred
                           EEECCCCCCEEEEEccCCCEEEEEccCCC----EEEEEEcCCCCCEEEEEec--CCCEEEEEecCCCCeE
                           EeeccCcccccccceeEEEEcCCCccEEEEEECcCCCcEEEEEEcCCCCcceeeeccccEEEeecCCC
 Q ss_pred
 O Fri Mar 04 23:
                       83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                                                                          162 (349)
                                                                ---p----l----d--i-iwd---
                                                                                                                          162 (349)
 Q Consensus
                                                +..+.+|...|.+++|+|+ +..|++++.|+.|++||+.+.....+.
                           + | | + . + + . .
 T Consensus
                      231 vwd~~~~~--
                                                                    -----l----dg-i-iwd--------
                                                                                                                          286 (473)
                      231 CWDLETNKV-----TRHYHGHLSGVYALKLHPT--LDVLVTAGRDAVARVWDMRTRONVHVLS-----
 T 3jb9 K
                                                                                                                          286 (473)
                           CCBTTTTBC-----CCBCCCCCSCEEEEECSS-SSCEEEEETTTEEEEEEETTTTEEEEEEE
 T ss dssp
                           EEECCCCeE-----EEEEcCCCCCEEEEEEeCC--CCEEEEEECCCCcEeEEEe-----
 T ss pred
 Q ss_pred
                           Q Fri Mar 04 23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR
                                                                                                                          241 (349)
                      163 ~~~~
                                                           ----i-----las-s-d--v-
 O Consensus
                                                                                                                          241 (349)
                           .+...+.++|+| ++..++++.++ +..+|+....
                                                                         ..+..+..|...|.+++|+|+
                                                                                                         .+|++++.| .|+
                                           ---~-l~~~~dg~i~vwd~~~~--
 T 3jb9_K
                      287 GHKSTVASLAVOE---FDPOVVTGSMDSTIRLWDLAAG---KTLTTLTHHKKTVRALSLHPDE----FTFASGSSD-NIK
                                                                                                                          355 (473)
 T ss dssp
                           CCSSCEEEEECS---SSSCEEEEETTSCCEEEETTTT---EEEEECCCCSSCCCCCCCCCTTT----SCRCCCCSS-CEE
                           CCCCCEEEEEcc---CCCEEEEEcCCC---cEEEEEcCCC---cEEEE
 T ss pred
 Q ss pred
                           Q Fri_Mar_04_23: 242 IFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD------HNGEVWSVS
                                                                                                                          311 (349)
 Q Consensus
                      242 vwd-----h---i--v-
                                                                                                                          311 (349)
                           +||+...
                                                                                ..+|+...+.+..+..
                                                                                                              |...|++++
                                     -----v-iwd-
 T Consensus
                      356 iwd~~~
                           HWKFPEGAFMGNFEGHNAIVNTLSINSDN-VMFSGADNGS-----MCFWDWKSGHKYQELQSVVQPGSLDSEAGIFASS
 т 3јb9 К
 T ss_dssp
                           ECCSTTCCCCEEECCCCSCBCCCEECSSS-EEEEBTTSC-----EEEEETTTCCCCEEECCCCTTCCTTTCCEEEEE
 T ss_pred
                           ECCCCCEEEEecCCCeEEEEecccC
 Q ss pred
 Q Fri_Mar_04_23: 312 WNLTGTILSSAGDDGKVRLWKATYS 336 (349)
                      312 ~spdg~~las~s~D~~v~iW~~~~~
 O Consensus
                                                          336 (349)
                          |+|+|++|++|+.||.|+||++...
-s--g--l-s---dg-v-iw-----
 T Consensus
                                                          453 (473)
 T 3jb9 K
                      429 FDKTGLRLITCEADKSVKIYKQVDN
                                                          453 (473)
 T ss_dssp
                           ECSSSCEEEEETTTEEEEECCSS
                           ECCCCCEEEEeCCCC
 T ss_pred
                                          PDB'
                                                      NCBI
 No 51
                                                                            Pub Med
3dm0_A Maltose-binding periplasmic protein fused with RA; MBP RACK1A, receptor for activiated protein C-kinase
 1, beta propeller WD40 repeat; HET: GLC; 2.40A {Escherichia coli}
 Probab=100.00 E-value=6.3e-33 Score=268.73 Aligned cols=295 Identities=17% Similarity=0.275 Sum probs=0.0
                           CccCCCcCeEEEEECCC-CCEEEEEeCCCeEEEEECCCCCc-eeEeeeeccccceEEEEECCCCCCEEEEEeCCC
 Q ss_pred
 Q Fri Mar 04 23:
                        {\tt 2~QPFDSGHDDLVHDVVYDFY-GRHVATCSSDQHIKVFKLDKDTSN-WELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKD}
                                                                                                                           79 (349)
                        2 -----h---v---s-d----l-t-s-D--v-iwd-------h---v--v--v--v-----las-s-Dg
 O Consensus
                                                                                                                           79 (349)
                           +..+.+|.+.|++++++|+||+|.+|+|...+...+.+|...+++|...+++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...+|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...+|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...+|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...++|...+
 T Consensus
                                                                                                                          452 (694)
 T 3dm0 A
                      375 KGTMRAHTDMVTAIATPIDNADIIVSASRDKSIILWKLTKDDKAYGVAQRRLTGHSHFVEDVVLSS--DGQFALSGSWDG
                                                                                                                          452 (694)
 T ss_dssp
                           EEEEECCSSCEEEEECCTTCCSEEEEEETTSEEEEEECCCSTTCSCEEEEEECCSSCEEEEEECT--TSSEEEEEETTS
                           T ss_pred
 0 ss pred
                           eEEEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCceEEEEeccCccceeeecccEEEeec
 Q Fri_Mar_04_23:
                       {\tt 80 \ TVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSI}
                                                                                                                          159 (349)
                       80
                           ~v~lwd~~~
                                                           ----v----p-----l-----d--i-iwd------
                                                                                                                          159 (349)
                           . | ++ | | + . ++
                                                 ..+..+.+|...|.+++|+|+ +..|++++.|++|++||+...
 T Consensus
                      453 ~i~iwd~~~---
                                               511 (694)
                      453 ELRLWDLAAG-----VSTRRFVGHTKDVLSVAFSLD--NROIVSASRDRTIKLWNTLGE-----CKYTISE
 T 3dm0 A
                                                                                                                          511 (694)
 T ss_dssp
                           EEEEEETTTT-----EEEEEEECCSSCEEEEEECTT-SSCEEEEETTSCEEEECTTSC-----EEEEECS
 T ss pred
                           Q ss_pred
                           CCCcccceeEEEEcccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEEECCCCCCceEEEEEEccCCC
 Q Fri_Mar_04_23:
                      160 PPANHLOSDFCLSWCPSRFSPEKLAVSALEQ-AIIYORGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDG
                                                                                                                          238 (349)
                                              -----h---v--sp---
 Q Consensus
                      160
                                                                                                            ~~~las~s~d~
                                                                                                                          238 (349)
 T Consensus
                                             -----l~s~s~d~~i~vwd~~~~~h~~~v~~~s~~g-
                      512 GGEGHRDWYSCVRESPNTL-OPTIVSASWDKTVKVWNLSNCK---LRSTLAGHTGYVSTVAVSPDG----SLCASGGKDG
 T 3dm0 A
                                                                                                                          583 (694)
 T ss dssp
                           STTSCSSCEEEEECSCSS-SCEEEEETTSCEEEEETTTCC---EEEEECCCSSCEEEEECTTS----SEEEEEETTS
```

```
T ss_pred
                         0 ss pred
 Q Fri_Mar_04_23: 239 RIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGE------ 306 (349)
                     239 ~v~vwd~~~~
                                                                                      ----h----
                                                                                                                   306 (349)
                         . | ++ | | +...
                                                                             ..+++...+.+..+..+..
                     T Consensus
                                                                                                                   656 (694)
                     584 VVLLWDLAEGKKLYSLEANSVIHALCFSPNRYWLCAATEHG-----IKIWDLESKSIVEDLKVDLKAEAEKADNSGPA 656 (694)
 T 3dm0 A
                         BCEEETTTTEEEECCBCSSCEEEEECSSSSEEEEETTE-----EEEEETTTTEEEEEECCCCC-----
 T ss dssp
 T ss_pred
                         eEEEEECCCCceeEeecCCCcEEEEEEcCCCeEEEEEcCCe-----EEEEECCCCchheeeccccccccCCcccc
                         -----EEEEEECCCCCEEEEecCCCceEEEecc
 Q ss pred
 Q Fri Mar 04 23: 307 ------VWSVSWNLTGTILSSAGDDGKVRLWKAT 334 (349)
                     307 ----i~~v~~spdg~~las~s~D~~v~iW~~~ 334 (349)
 O Consensus
                                |.+++|+|||++|+.|++|+.
 T Consensus
                     657 ~~~~~
                                   ~~~~spdg~~l~sgs~Dg~i~iW~i~ 692 (694)
                     657 ATKRKVIYCTSLNWSADGSTLFSGYTDGVIRVWGIG 692 (694)
 T 3dm0 A
                         ----CCCCEEEEECTTSSEEEEEETTSEEEEEC-
 T ss_dssp
 T ss pred
                         ccccceeEeEEECCCCCEEEEEcCCCeEEEEeec
                                       PDB"
 No 52
                                                                        Pub Med
>2hes X YDR267CP; beta-propeller, WD40 repeat, biosynthetic protein; 1.70A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.5e-32 Score=241.04 Aligned_cols=301 Identities=19% Similarity=0.274 Sum_probs=0.0
                         CCCCCCCARRERECCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCCARRERECCCCCCARRERECCCCCCARRERECCCCCCARRERCCCCCCARRERECCCCCCARRERCCARRERCCCCCCARRERCCARRERCCCCCCARRERCCARRECCCCCCARRERCCARRECCCCCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCARRECCA
 Q ss_pred
 Q Fri_Mar_04_23:
                       3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                                                                    82 (349)
                       3 ----h---v--s-d---l-t-s-D--v-iwd-----h---v--v--v--v----las-s-Dq-v-
 O Consensus
                                                                                                                    82 (349)
                         83 (330)
 T 2hes X
                       8 KSLKLYKEKIWSFDFSOG--ILATGSTDRKIKLVSVKYDDFTLIDVLDETAHKKAIRSVAWRP--HTSLLAAGSFDSTVS
                                                                                                                    83 (330)
 T ss dssp
                         EEEECCSSCEEEEEETT--EEEEEESSSCEEEEECSSSCCEEEEEECTTCCCSCEEEEEECT--TSSEEEEEETTSCEE
                         eeecCCCccEEEEeccCC--eEEEEecCCcEEEEeecCCceeEeeeeeecccCCeEEEEEcc--CCCEEEE
 T ss pred
 Q ss pred
                         EeeccCcccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCc----CcceeeecccEEEee
 Q Fri_Mar_04_23:
                      83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP----SDLRSWTLTSEMKVLS
                                                                                                                   158 (349)
 Q Consensus
                      83 lwd------v----v-----p-----l----d--i-iwd-------
                                                                                                                   158 (349)
                         ~_-~~l~~~~dg~i~iwd~~~~~
 T Consensus
                                                                                                                   149 (330)
                      84 IWAKEESADR--TFEMDLLAIIEGHENEVKGVAWSND--GYYLATCSRDKSVWIWETDESGEEYECISVL------
 T 2hes X
 T ss_dssp
                         EEEC-----CCCEEEEEC----CEEEEEECTT--SCEEEEEETTSCEEEEECCTTCCCCEEEEEE
 T ss_pred
                         Q ss pred
 Q Fri_Mar_04_23: 159 IPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKD 237 (349)
                     159 -----h---v--v--sp-----las-s-d 237 (349)
 O Consensus
                           220 (330)
 T Consensus
                     150 ---~v~~~v
                                                                                     ~~~v~~~
                                                                                                 ----l----d
                     150 ---QEHSQDVKHVIWHP---SEALLASSSYDDTVRIWKD-YDDDWECVAVLNGHEGTVWSSDFDKTEGV--FRLCSGSDD
 T 2hes X
                                                                                                                   220 (330)
 T ss_dssp
                       ---CCCSSCEEEEEECS---SSSEEEEEETTSCEEEEEE-ETTEEEEEEECCCSSCEEEEEECCSSSS--CEEEEEETT
                         ---cccCCceeEEECC---CCCEEEEEecCCCCEEEEec-CCCCceeeEEeccCCCc--eEEEEecCC
 T ss_pred
                         Q ss pred
 Q Fri_Mar_04_23: 238 GRIRIFKITE------KLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE---LLSEHDDH 303 (349)
                     238 ~~v~vwd~~~----
                                                                                                                  303 (349)
                    T Consensus
                                                                                                                   293 (330)
                    221 STVRVWKYMGDDEDDOOEWVCEAILPDVHKROVYNVAWGFNG-LIASVGADGV-----LAVYEEVDGEWKVFAKRALCH
 T 2hes X
                                                                                                                   293 (330)
                         SCEEEEEEEECTTSCEEEEEEECCSCCSSCEEEEEECTTS-----EEEEEEETTEEEEEEEESCTT
 T ss dssp
                         CEEEEEecCCccccccceeeeeecCcCCcceEEEEECCCC-eEEEEcCCCE------EEEEEcCCCceeeeeecccc
 T ss pred
                         C-ceEEEEECC--CCCEEEEecCCCeEEEEeccCCC
 Q ss pred
 Q Fri_Mar_04_23: 304 N-GEVWSVSWNL--TGTILSSAGDDGKVRLWKATYSN 337 (349)
                     304 ~-~i~~v~~sp--dg~~las~s~D~~v~iW~~~~~ 337 (349)
 Q Consensus
                         T Consensus
                                                                   330 (330)
                     294 GVYEINVVKWLELNGKTILATGGDDGIVNFWSLEKAA 330 (330)
 T 2hes X
                         TTSCEEEEEC----CCEEEEETTSEEEEEEC----
 T ss dssp
                         CccceeEEeccCCCcEEEEccCCCC
 T ss pred
 No 53
                                                                        Pub Med
>3gre_A Serine/threonine-protein kinase VPS15; seven-bladed propeller, WD repeat, scaffold protein, ATP- binding,
 endosome, golgi apparatus; 1.80A {Saccharomyces cerevisiae}
                E-value=5.9e-34 Score=260.85 Aligned cols=288 Identities=12% Similarity=0.046 Sum probs=0.0
 Q ss_pred
                         Q Fri_Mar_04_23:
                      3 PFDSGH-DDLVHDVVYDFYGR-HVATCSSDOHIKVFKLDKDTSNWELSDSWR-AHDSSIVAIDWASPEYGRIIASASYDK
                                                                                                                    79 (349)
                      3 ----h---v--v---s-d----l-t-s-D--v-iwd--------h---v--v--v--v----las-s-Dg
 Q Consensus
                                                                                                                    79 (349)
                         T Consensus
                      56 ATLMENEPNSITSSAVSPGETPYLITGSDOGVIKIWNI.KETIVGEVYSSSLTYDCSSTVTOITMIP--NFDAFAVSSKDG
 T 3gre A
                                                                                                                   133 (437)
 T ss dssp
                         EEECTTTTSCEEEEEECSSSCEEEEEETTSEEEEEEHHHHHHTTCCCSCSEEEECSSCEEEEECT--TSSEEEEEETTS
```

```
T ss_pred
                             EEEccccCCEEEEECCCCCEEEEEcCCCeEEEEECCccccccchhhhccCCCCEEEEEEeC--CCCEEEEEeCCC
                             eEEEeecc-----CccccccccceeEEEEc--CCCC--cEEEEEECc--CCCCcEEEEEECCCC
 0 ss pred
 Q Fri_Mar_04_23:
                         80 TVKLWEED-----PDQEECSGRRWNKLCTLN-DSKG-SLYSVKFAP-AHLGLKLACLGNDGILRLYDALEP
                                                                                                                                       142 (349)
 Q Consensus
                         80 ~v~lwd~~-----d~~i~iwd~~~
                                                                                                                                       142 (349)
                                                 . | ++ | | +.
                        134 ~v~iwd~~~~~
                                                                                                    ----l----dg-i-iwd----
 T Consensus
                                                                                                                                       202 (437)
                        134 QIIVLKVNHYQQESEVKFLN------CECIRKINLKNFGKNEYAVRMRAFVNEE--KSLLVALTNLSRVIIFDIRTL
 T 3gre A
                                                                                                                                       202 (437)
                             EEEEEEEEEEETTEEEEEE....EEEEEEEEGGGGSSCCCEEEEEEECSS.CEEEEEETTSEEEEEETTTC
 T ss_dssp
 T ss_pred
                             eEEEEEcccccccccccc-----cceeEEEeeCCCCCcceEEEEEeCCCC--ceEEEEEeCCCeEEEEECCCC
                             CcceeeeccccEEEeecCCC--cccceeEEEEcccCCCCceEEecCCc-eEEEEecCCccEEEEEEcc-CCCCceeEE
 Q ss pred
 Q Fri Mar 04 23: 143 SDLRSWTLTSEMKVLSIPPA--NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLP-GHKSLIRSI 218 (349)
                        143 -----
                                                                                             ---i----v--v 218 (349)
 O Consensus
                                                   . .+...+.++|+| ++..++++++++|+....
 T Consensus
                        203 -----l-s---dg-i-iwd------
                                                                                                                                       263 (437)
                        203 ERLOTI-----ENSPRHGAVSSICIDE--ECCVLILGTTRGTIDIWDIRFN---VLIRSWSFGDHAPITHV
 T 3gre_A
                                                                                                                                       263 (437)
                             CEEEEE-----ECCGGGCCEEEEECT--TSCEEEEEETTTC-EEEEEEBCTTCEEEEE
 T ss_dssp
 T ss pred
                             CEEEEe-----ccCCCCCceEEEEECC---CCCEEEEECCCC---CceEEEecCCCCeeEE
 Q ss_pred
                             219 --sp-----las-s-d--v-vwd------
 Q Consensus
                                                                                                                                       267 (349)
                                              .+|++++.|+.|++||+.....
                        264 ~
                                   ----d--i-vwd------
 T Consensus
                                ~p
                        264 EVCQFYGKNS----VIVVGGSSKTFLTIWNFVKGHCQYAFINSDEQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVSN 339 (437)
 T 3gre A
 T ss dssp
                             EECTTTCTTE----EEEEEESTTEEEEEETTTTEEEEEEESSSSCCCGGGGSCBCSSGGGCCCCCCSGGGGCCEEEET
                             EEeeccCCcc---eEEEEccCCCeEEEEecCCceeeeEeecccCccceeeccccchheeEecccCCCcceEEEEecC
 T ss_pred
 Q ss_pred
 O Consensus
                        268 ~~~~~
                                                                       ~~~----h~~~i~~v 310 (349)
                             +...+.+..+..
 T Consensus
                        340 \sim 1 \sim s \sim dg \sim ---i \sim i w d \sim --- \sim f s \sim --- \sim f s \sim --- \sim 
                                                                                                                          ~h~~~v~~1
                                                                                                                                       413 (437)
                        340 DKILLTDEATSS-----IVMFSLNELSSSKAVISPSRFSDVFIPTQVTANLTMLLRKMKRTSTHSVDDSLYHHDIINSI
 T 3gre_A
                                                                                                                                       413 (437)
                             TEEEEEEGGGTE-----EEEEETTCGGGCEEEECC--CCCEEEEEEEETTEEEEEECC--------CCCEEEE
 T ss_dssp
                             CCEEEECCCCCE-----EEEEECCCCccceEeccCCccceeecccCCCccEEEEeccCchhccccchhcCcCeEEEE
 T ss pred
 Q ss_pred
                             EECC--CCCEEEEecCCCeEEEEe
 Q Fri_Mar_04_23: 311 SWNL--TGTILSSAGDDGKVRLWK 332 (349)
 O Consensus
                        311 ~~sp--dg~~las~s~D~~v~iW~ 332 (349)
                            +|+| +|++|+.|++|+|+
                        414 ~~s~~~~1~s~~~dg~v~iW~ 437 (437)
 T Consensus
                        414 STCEVDETPLLVACDNSGLIGIFQ 437 (437)
 T 3gre A
 T ss_dssp
                             EEEESSSSEEEEEETTSCEEEEC
                             EEEecCCCcEEEEccCCceEEEec
 T ss pred
                                              PDB"
 No 54
                                                                                    Pub Med
>4nsx A U3 small nucleolar RNA-associated protein 21; ribosome biogenesis, UTPB complex, 90S preribosome, small
 SU processome, protein binding; HET: FLC; 2.10A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.1e-32 Score=266.36 Aligned_cols=315 Identities=13% Similarity=0.140 Sum_probs=0.0
                             Q ss pred
                          5 DSGHDDLVHDVVYDFYGR-HVATCSSDQHIKVFKLDKDTSNWELSDSWRA-H---DSSIVAIDWASPEYGRIIASASYDK
 Q Fri Mar 04 23:
                                                                                                                                        79 (349)
 O Consensus
                          5 ---h---v--s-d----l-t-s-D--v-iwd--------h-----v--v--v--v-----las-s-Dq
                                                                                                                                        79 (349)
                             +.+|...|.+++|+|+ +|++++|++|++|++| ....+.+| ...|.++.|+| ++++|++++|++++|
                        244 -----dg-1-vwd-----h-----h----v----h-----1-s---d-
 T Consensus
                                                                                                                                       317 (684)
 T 4nsx_A
                        244 IKIPQSRISSLSFRTDGSSHLSVGTSSGDLIFYDLDRR----SRIHVLKNIHRESYGGVTQATFLN--GQPIIVTSGGDN
                                                                                                                                       317 (684)
                             EECTTCCEEEEEECCSSSCEEEEEETTSCEEEEETTTT----EEEEEETTSSCGGGTSCSEEEECT--TSSEEEEECSSS
 T ss dssp
                             EECCCCcEEEEECCCCCcEEEEECCCC----cceEEEecccCCCCCCeeEEEEC--CCCEEEEecCCC
 T ss pred
                             eEEEeeccCcccccc---ceeEEEEccCCCcEEEEEEccCCccEEEEEEccccccc
 Q ss pred
 Q Fri Mar 04 23:
                         80 TVKLWEEDPDQEECSGRR---WNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDA------ 139 (349)
                                                                     ----v----p-----l-----d--i-iwd------ 139 (349)
 Q Consensus
                                                         .+.+..+.|...|.+++|+|... +..++++.|+.+++||+
                        T Consensus
                                                                                                                                       396 (684)
                        318 SLKEYVFDPSLSQGSGDVVVQPPRYLRSRGGHSQPPSYIAFADSQ-SHFMLSASKDRSLWSFSLRKDAQSQEMSQRLHKK 396 (684)
 T 4nsx A
                             EEEEEECCC-----CCCEEEEEEECCSSCEEEEEECCTT-SCEEEEEETTSCEEEEECSTTCCEEECBCC----
 T ss dssp
                             cEEEEEeCCCCccccccCCCcceeEeecCCCCcEEEEEeCCC-CCEEEEEeCCCcceeEeEcccccccchhcccchhc
 T ss pred
 Q ss_pred
                             Q Fri Mar 04 23: 140 ------LEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPE
                                                                                                                                      181 (349)
                        140 -----
 Q Consensus
                                                                                                                                       181 (349)
                        T Consensus
                                                                                                                                       473 (684)
                        397 QDGGRVGGSTIKSKFPEIVALAIENARIGEWENIITAHKDEKFARTWDMRNKRVGRWTFDTTDDGFVKSVAMSQ---CGN
 T 4nsx_A
                                                                                                                                       473 (684)
 T ss_dssp
                             -----CCCCCEEEEECSTTTTTSCCEEEEETTCSEEEEEETTTTEEEEEEECSSSCCEEEEEECT---TSC
 T ss pred
                             cccccccccccccccccccccceEEeecCCccceEEEecCCccceeEeecCCCccEEEEEEeC---CCC
                             ceEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEECCCCCceEEEEEcCCCCCEEEEEecCc--cccccccc
 Q ss pred
 Q Fri Mar 04 23: 182 KLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK--LSPLASEESL 258 (349)
```

```
Q Consensus
                .++++..++ +.+|+..... ....+..+|...|.++|+|++ ..+|+++|+.|+.|++||+... ...+...
T Consensus
             474 ~l~q~dq~i~v~d~~~~~h~~v~l~~s~~~l~s~~dq~v~~wd~~~~~~
                                                                         545 (684)
             474 FGFIGSSNGSITIYNMQSGI---LRKKYKLHKRAVTGISLDGMN----RKMVSCGLDGIVGFYDFNKSTLLGKLKLD-AP
T 4nsx A
                                                                         545 (684)
                EEEEEETTSEEEEEETTTCC---EEEEEECCSSCEEEEEECTTS----CEEEEEEETTSEEEEEEESSSCCEEEEEECS-SC
T ss dssp
                T ss pred
                Q ss pred
Q Fri_Mar_04_23: 259 TNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNE
                                                                         338 (349)
Q Consensus
                                             ~~~h~~~i~~v~~spdg~~las~s~D~~v~iW~~
                                                                         338 (349)
             T Consensus
                                                                         619 (684)
             546 ITAMVYHRSSDLFALALDDLS-----IVVIDAVTQRVVRQLWGHSNRITAFDFSPEGRWIVSASLDSTIRTWDLPTGGC
T 4nsx A
                                                                         619 (684)
T ss_dssp
                EEEEEEETTTTEEEEEETTSC-----EEEEETTTTEEEEEECCCSSCEEEEEECTTSSEEEEEETTTEE
T ss_pred
                Q ss_pred
                REFER
Q Fri_Mar_04_23: 339 FKCMS
                     343 (349)
Q Consensus
             339 ~~~~
                     343 (349)
             620 ~~~~
T Consensus
                     624 (684)
T 4nsx_A
             620 IDGII
                     624 (684)
T ss_dssp
                EFFER
T ss pred
                eeEEE
No 55
                                              Pub Med
>4e54_B DNA 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=2.4e-34 Score=263.45 Aligned_cols=297 Identities=12% Similarity=0.122 Sum_probs=0.0
                CCcccCCcceEEEEECCCC-CEEEEEeCCCeEEEEECCCCCceeEeeeec--cccceEEEEEEcCCCCCEEEEEeC
Q ss_pred
Q Fri_Mar_04_23:
              1 MOPFDSGHDDLVHDVVYDFYG-RHVATCSSDOHIKVFKLDKDTSNWELSDSWR--AHDSSIVAIDWASPEYGRIIASASY
                                                                          77 (349)
              Q Consensus
                                                                  ~~~las~s~
                                                                          77 (349)
                                              ....+. +|...|++++|+|. ++.+|++++.
                +...+.+|.+.|++++|+|+| ++|++|+.|++|+|||+...
T Consensus
             185 (435)
             111 ILQKAAPFDRRATSLAWHPTHPSTVAVGSKGGDIMLWNFGIK----DKPTFIKGIGAGGSITGLKFNPL-NTNQFYASSM
T 4e54 B
                SCCEEEECSSCEEEEECSSCTTCEEEEETTSCEEEECSSCC----SCCEEECCCSSSCCCCEEEECSS-CTTEEEEECS
T ss_dssp
T ss pred
                Q ss_pred
                CCeEEEeeccCcccccccceeEEEEcCCCCcEEEEEEcCCCCcEEEEEEcCCCCcceeeeccccEEEe
Q Fri Mar 04 23:
             78 DKTVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVL 157 (349)
              78 Dq~v~lwd~~~~~d~i~iwd~~~~~
O Consensus
                                                                         157 (349)
             246 (435)
T Consensus
             186 EGTTRLQDFK-----GNILRVFASSDTINIWFCSLDVSAS-SRMVVTGDNVGNVILLNM-DGKELWNL------
T 4e54 B
T ss_dssp
                SSCEEEETT-----SCEEEEECCSSCSCCCCCEEETT--TTEEEEECSSSBEEEEES-SSCBCCCS-----
                CCeEEEECC-----CCceeeeccCCccCcceEEEEcCC--CCEEEEEcCCC-CcceEEEe-----
T ss_pred
Q ss_pred
                ecCCCcccceeEEEEccCCCCC-ceEEecCCc-eEEEEecCCccEEEEEEccCCCCceeEEEEEC
Q Fri Mar_04 23: 158 SIPPANHLQSDFCLSWCPSRFSPE-KLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC
                                                                         235 (349)
             158 ------h---y--y--sp------las-s
Q Consensus
                                                                         235 (349)
             T Consensus
                                                                         315 (435)
             247 ----RMHKKKYTHVALNP---CCDWFLATASVDQTVKIWDLRQVRGKASFLYSLPHRHPVNAACFSPDG---ARLLTTD
T 4e54 B
                ---BCCSSCEEEEECT--TCSSEEEEEETTSBCCEEETTTCCSSSCCSBCCBCSSCEEECCBCTTS---SEEEEEE
T ss_dssp
T ss pred
                0 ss pred
                Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPLASEESLTN-----SNMFDNSADVDMDAQ------GRSDSNTEEKAELQSNLQV
                                                                         294 (349)
             388 (435)
T Consensus
             316 QKSEIRVYSASQW-DCPLGLIPHPHRHFQHLTPIKAAWHPRYNLIVVGRYPDPNFKSCTPYELRT-----IDVFDGNSG
T 4e54 B
                                                                         388 (435)
                SSSCEEEEESSS-SSEEEECCCCCCCSSSCCCBCEECSSSCEEEECCCCTTSCCSSTTCCCC-----EEEECSSSC
T ss dssp
                T ss pred
                eeeeeccC-CCceEEEE-EECCCCCEEEEecCCCceEE
Q ss pred
Q Fri Mar 04 23: 295 ELLSEHDD-HNGEVWSV-SWNLTGTILSSAGDDGKVRLWKATYSNEFK 340 (349)
                T Consensus
T 4e54 B
             389 KMMCQLYDPESSGISSLNEFNPMGDTLASAM-GYHILIWSQQEARTRK 435 (435)
                CEEEEECCSSCCCCCEEEECTTSSCEEEEC-SSEEEECCCC----
T ss dssp
T ss pred
                No 56
                                              Pub Med
>3i2n A WD repeat-containing protein 92; WD40 repeats, structural genomics, structural genomic consortium, SGC,
 apoptosis, transcription; 1.95A {Homo sapiens}
Probab=100.00 E-value=3.9e-33 Score=249.08 Aligned cols=298 Identities=12% Similarity=0.191 Sum probs=0.0
Q ss pred
                CCccCCCcceEEEEECCCCC-EEEEEeC---CCeEEEEECCCCCceeEeeeccccceEEEEEECCCCCC---CEEE
```

```
Q Fri_Mar_04_23:
               1 MQPFDSGHDDLVHDVVYDFYGR-HVATCSS---DQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYG---RIIA
                                                                              73 (349)
O Consensus
               1 -----h---v---s-d----l-t-s----D--v-iwd------h---v--v--v--v-------la
                +..+.+|..|.+++|+|+..+|++|+..|++|+||+...+.+...+..|...|.+++|++ ++ ++||
T Consensus
                                                                               84 (357)
              10 IAHIQKGFNYTVFDCKWVPCSAKFVTMGNFARGTGVIQLYEIQ--HGDLKLLREIE-KAKPIKCGTFGA--TSLQQRYLA
T 3i2n A
                 EEEEEECSSCEEEEECTTSSEEEEEC--CCCEEEEEEEC--SSSEEEEEEE-ESSCEEEECTT--CCTTTCCEE
T ss_dssp
                 hhhhhcccceeEEEEccCCcceeEEeeecCCCcEEEEEcc--CCcceeeeec-cCCCceEEEecc--CCCCCEEE
T ss pred
                 EEECCCeEEEeeccCccccccccceeEEEEcCCCcEEEEE------ECcCCCCeEEEEEeCCCCccee
Q ss pred
Q Fri_Mar_04_23:
               74 SASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVK-----FAPAHLGLKLACLGNDGILRLYDALEPSDLRS 147 (349)
               85 sqs~D~v~iWd~~~~~~l~qH~~~V~~v~~~~~~s~~~~~l~s~s~D~v~lWd~~~~~~~
                                                                              151 (357)
T Consensus
T 3i2n A
               85 TGDFGGNLHIWNLEAPEMP------VYSVKGHKEIINAIDGIGGLGIGEG-APEIVTGSRDGTVKVWDPRQKDD--- 151 (357)
                 EEETTSCEEEECTTSCSSC----SEEECCCSSCEEEEEEESGGGCC-C--CCEEEEEETTSCEEECTTSCSS---
T ss dssp
T ss_pred
                 EECCCCEEEEecCCCCcce-----eEEEcCCccceEeeeccCcccCCC--CCEEEEEeCCCccEEEEECCCCCC---
                 eecccEEEeecCCcccceeEEEEc----ccCCCCcceEEecCc-eEEEEeccCcCcEEEEEEcc
Q ss pred
Q Fri Mar 04_23: 148 WTLTSEMKVLSIPPANHLQSDFCLSWC----PSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAP
                                                                              222 (349)
                                -----i-----h---v--v--sp
Q Consensus
                                                                              222 (349)
              | 152 -----PVANMEPVQGENKRDCWTVAFGNAYNQ--EERVVCAGYDNGDIKLFDLRNM---ALRWETNIKNGVCSLEFDR
T Consensus
                                                                              219 (357)
T 3i2n A
                                                                              219 (357)
                 ----CSEECCCTTSCCCCEEEEEECCCC----CCCEEEEEETTSEEEEEETTTT----EEEEEEECSSCEEEEEESC
T ss_dssp
                 ----ceeEecccCCcceeEEEEeeeeCC---CCCEEEEEecCCeEEEEECCC----cEEEeecCCccEEEEEecC
T ss_pred
Q ss_pred
                Q Fri_Mar_04_23: 223 ---SIGRWYQLIATGCKDGRIRIFKITEKLSPL------ASEESLTNSNMFDNSAD-VDMDAQGRSDSNTEEKAELQS
                                                                              290 (349)
              223 ---~-las~s~d~~v~vwd~~~~~~~
Q Consensus
                                                                              290 (349)
              T 3i2n A
              220 KDISM----NKLVATSLEGKFHVFDMRTQ-HPTKGFASVSEKAHKSTVWQVRHLPQNRELFLTAGGAGG-----LHLWK
                                                                              288 (357)
                 SSSSC----CEEEEEESTTEEEEEEEEE-ETTTEEEEEEEECCSSCEEEEEEETTEEEEEEETTSE-----EEEEE
T ss_dssp
                 CCCCc---ceEEEEcCCCcEEEEECCCC-ccCccceeeeccCCcCceEEEECCCCc-----EEEEe
T ss pred
                           -----ceeeeccCCCceEEEEECCCCCEEE-EecCCCceEEEEecccCCcE
Q ss pred
 Q Fri_Mar_04_23: 291 NLQ------VELLSEHDDHNGEVWSVSWNLTGTILS-SAGDDGKVRLWKATYSNEF 339 (349)
              Q Consensus
T Consensus
T 3i2n_A
              289 YEYPIQRSKKDSEGIEMGVAGSVSLLQNVTLSTQPISSLDWSPDKRGLCVCSSFDQTVRVLIVTKLNKI 357 (357)
T ss_dssp
                 EECCSCC--CCTTSCCCCCCEEEEEEEECCSSCEEEEEECSSSTTEEEEEETTSEEEEEECC----
T ss_pred
                 CCCcccccCCCcceeecccceeheeeccCCCeeEEEECCCCCEEEEEeecCcEEEEEEeecCC
                         PDB™
PROTEIN DATA BANK
                                 NCBI Pub Med
>3sfz_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=3.1e-33 Score=287.08 Aligned_cols=303 Identities=21% Similarity=0.338 Sum_probs=0.0
                 Q Fri_Mar_04_23:
               5 DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                               84 (349)
               Q Consensus
                                                                               84 (349)
              653 l--h---V--v-fspdg--las-s-d--v-vWd---g-----h---v----------l-sgs-d--i---W
T Consensus
              653 IKAHEDEVLCCAFSSDDSYIATCSADKKVKIWDSATG----KLVHTYDEHSEQVNCCHFTNKSNHLLLATGSNDFFLKLW
T 3sfz A
                                                                              728 (1249)
T ss_dssp
                 ECCCSSCEEEEECTTSSEEEEEETTSEEEEEETTTC----CEEEEEECCSSCEEEEEECSSSSCCEEEEETTSCEEEE
T ss_pred
                 eccCcccccccceeEEEEcCCCCcEEEEEECCCCCcEEEEEECCCC------
Q ss_pred
 Q Fri_Mar_04_23:
              85 EEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP------
                                                                              142 (349)
               85 d~~~~d~i~iwd~~~~
Q Consensus
                                                                              142 (349)
                       +.+..+.|.+.|.++|+|+ +..++++.|++|++||+..+
              729 d-----h---v----spd--g--l-s-s-dg-v-vwd-----
                                                                              797 (1249)
T Consensus
T 3sfz_A
              729 DLNQK-----ECRNTMFGHTNSVNHCRFSPD--DELLASCSADGTLRLWDVRSANERKSINVKRFFLSSEDPPEDV
                                                                              797 (1249)
                 ETTSS-----SEEEEECCCSSCEEEEECSS-TTEEEEEEESSSEEEEEGGGTEEEEEECCCCC------CC
 T ss_dssp
                 T ss_pred
Q ss pred
                 ------CcceeeecccEEEee
Q Fri_Mar_04_23: 143 -----SDLRSWTLTSEMKVLS 158 (349)
T Consensus
              798 ---v---s-dg--l-----i---d---v-lwd------
                                                                              877 (1249)
              798 EVIVKCCSWSADGDKIIVAAKNKVLLFDIHTSGLLAEIHTGHHSTIOYCDFSPYDHLAVIALSOYCVELWNIDSRLKVAD
T 3sfz A
                                                                              877 (1249)
 T ss dssp
                 \tt CCCBCCCCBCTTSSEEEEEETTEEEEEETTTCCEEEEEECSSSSCCCEEEECSSTTEEEEECSSSCEEEEETTTTEEEEE
T ss_pred
                 Q ss_pred
                 cccccceeEEEEccccccccceEEecccc-eEEEEeccc------
159 ------ 199 (349)
Q Consensus
                  .+|...+.++|+| ++..++++++++++++|+....
              T Consensus
                                                                              952 (1249)
T 3sfz_A
              878 C--RGHLSWVHGVMFSP---DGSSFLTASDDQTIRVWETKKVCKNSAIVLKQEIDVVFQENETMVLAVDNIRGLQLIAGK 952 (1249)
```

```
T ss_dssp
               E--CCCSSCEEEEECT---TSSEEEEEETTSCEEEEEHHHHHSCCSSSEEEEEEEETTEEEEEEESSSSEEEEEE
T ss_pred
               -----CcEEEEEEccCCCceeEEEEEccCCCCceeEEEE
Q ss_pred
Q Fri_Mar_04_23: 200 ------GKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR
                                                                          241 (349)
            200 -----h---y--y--sp-----las-s-d--y-
Q Consensus
                                                                          241 (349)
                                          T Consensus
             953
             953 TGQIDYLPEAQVSCCCLSPHLEYVAFGDEGAIKIIELPNNRVFSSGVGHKKAVRHIQFTADG----KTLISSSEDSVIQ 1028 (1249)
T 3sfz A
               SCCEEECCSCEEEEECTTSSEEEEEETTSCCEEEETTTTSCEEECCCCSSCCCCEEECSSS----SCEEECSSSBEE
T ss_dssp
T ss pred
               cceEeeccccEEEEECCCCcEEEEEcCCCcEEEEEcCCCcEEeeecCccCceEEEEcCCC----CEEEEEECCCCeEE
               Q ss pred
T Consensus
            1029 VWNWQTGDYVFLQAHQETVKDFRLLQDSRLLSWSFDGTVKVWNVITGRIERDFTCHQGTVLSCAISSDATKFSSTSADKT 1108 (1249)
T 3sfz A
               EEETTTTEEECCBCCSSCEEEEEECSSSEEEEEETTTTCCCEEEECCSSCCCCEEECSSSSCEEECCSSC
T ss dssp
               EEECCCCcEEEeecCCCceEEEEccCCcEEEEECCCCCEEEEECCCCCEEEEECCCCC
T ss pred
               Q ss pred
Q Fri Mar 04 23: 280 SNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSN 337 (349)
            280 -----h---i--v--spdg--las-s-D--v-iW----- 337 (349)
Q Consensus
                    T Consensus
            1109 -----v~lWd~~~~~l~~h~~~v~~v~fs~dg~~lasgs~Dg~i~lWd~~~g~ 1160 (1249)
            1109 -----AKTWSFDLLSPLHELKGHNGCVRCSAFSLDGILLATGDDNGEIRIWNVSDGO 1160 (1249)
T 3sfz A
               -----CCEECSSSSCSBCCCCCSSCEEEEECSSSSEEEEEETTSCCCEEESSSC
T ss dssp
               ----EEEEECCCCceeEEecCCCCCEEEEEEccccc
T ss pred
                        PDB STOCK Pub Med
No 58
      The anaphase-promoting complex chain R; ubiquitination, cell cycle, APC/C; 4.30A {Homo sapiens}
Probab=100.00 E-value=2.2e-32 Score=246.77 Aligned_cols=244 Identities=17% Similarity=0.295 Sum_probs=0.0
Q ss pred
               CcCeEEEEECCCCCEEEEEeCCCceEEEEecccccceEeeeccccceEEEEEccccccEEEEEeccccc
Q Fri_Mar_04_23:
              8 HDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEED
                                                                           87 (349)
Q Consensus
              8 h---v---s-d---l-t-s-D--v-iwd------h---v--v--v-----las-s-Dq-v-lwd--
                                                                           87 (349)
               201 (386)
             130 TENEYTSLSWIGAGSHLAVGQANGLVEIYDVMKR----KCIRTLSGHIDRVACLSWN----NHVLTSGSRDHRILHRDVR
T 5a31 R
                                                                          201 (386)
T ss dssp
               CSSCREEEEECTTSSEREEETTTSCREEEETTTT----EEEEEECCCSSCEEEEEE----TTEEEEEESSSCEEEEETT
T ss pred
               CCCCEEEEEcCCCCEEEEEeCCCC----eEEEEecCCCccEEEEEcC----CCEEEEEeCCCceEEEEECC
               Q ss_pred
Q Fri_Mar_04_23:
             88\ \ \texttt{PDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQS}
                                                                          167 (349)
Q Consensus
             88 -----v----v----p-----1----d--i-iwd-------
                                                                          167 (349)
                    258 (386)
T Consensus
             202 MPDPF------FETIESHTQEVCGLKWNVA--DNKLASGGNDNVVHVYEGTSKSPILTF------------DEHKAA
T 5a31_R
                                                                          258 (386)
               SSSSC-----SEEECCCSSCEEEEECSS-SSEEEEETTSCEEEEETTCSSCSEEE------CCCSSC
T ss_dssp
               CCcce-----eEEEcCcCCCEEEEEECCC--CCEEEEEeCCCCEEEEE------ccccc
T ss pred
               eeEEEEcccCCCCceEEec--CCc-eEEEEecCCCcEEEEEEccCCCcceeEEEECcCCCCceEEEE--EcCCCCEEE
Q ss pred
Q Fri Mar_04_23: 168 DFCLSWCPSRFSPEKLAVSA--LEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIAT--GCKDGRIRI
O Consensus
             168 ------h---v--v--sp------las---s-d--v-v
                                                                          242 (349)
               +.+++|+|. ....+++++ .++ +.+|+..... +...+.+++|+|++
                                                           ..|++ |+.|+.|++
             259 v--l--sp-----ll-sg-g--d--i-iwd--------v----s-----l----g--d--i-i
T Consensus
                                                                          328 (386)
             259 VKAMAWSPH--KRGVLATGGGTADRRLKIWNVNTSIKMSDID----SGSQICNMVWSKNT----NELVTSHGYSKYNLTL
T 5a31 R
                                                                          328 (386)
               EEEEEECSS--STTEEEEEECTTTCEEEEEETTTTEEEEEE----CSSCEEEEECSSS----SCEEEEECTTCCCEEE
T ss dssp
                eEEEEECCC--CCCEEEEeCCCCCCEEEEEECCCCCEeEEEc----CCCCEEEEEEeCCC----CEEEEEEccCCCcEEE
T ss pred
               Q ss pred
Q Fri Mar 04 23: 243 FKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSA
                                                                          322 (349)
                                                                          322 (349)
            243 wd~
                                                         ---h---i--v--spdg--las-
Q Consensus
                                                     +.+..+.+|...|.+++|+|+|++|++|
T Consensus
            329 wd~~~~
                                                  ----h---v--l--spdg--l-s-
                                                                          362 (386)
            329 WDCNSM------DPIAILKGHSFRVLHLTLSNDGTTVVSG
T 5a31 R
                                                                          362 (386)
               T ss dssp
T ss pred
Q ss_pred
               cCCCeEEEEecccCCc
Q Fri Mar 04 23: 323 GDDGKVRLWKATYSNE 338 (349)
Q Consensus
            323 s~D~~v~iW~~~~~
                            338 (349)
               +.|++|++|++....
                            378 (386)
             363 ~~d~~i~iw~~~~~
T Consensus
            363 AGDETLRYWKLFDVSV
T 5a31_R
                            378 (386)
T ss_dssp
               ETTTEEEEEECCCCCS
T ss pred
               eCCCCEEEEECCCCch
                       PDB"
                                NCBI
```

```
3mmy_A MRNA export factor; mRNA export, nuclear protein; HET: MES; 1.65A {Homo sapiens} PDB: 4owr_A
 Probab=100.00 E-value=3.6e-33 Score=250.24 Aliqned cols=273 Identities=15% Similarity=0.234 Sum probs=0.0
                             CCccCCCcCeEEEEECCCC---CEEEEEECCCCEEEEEECCCCCceeEeeeeccccceEEEEEECCCCCCCEEEEEEC
 Q ss pred
 Q Fri_Mar_04_23:
                        1 MQPFDSGHDDLVHDVVYDFYG---RHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASY
                                                                                                                                    77 (349)
                        Q Consensus
                                                                                                                                    77 (349)
 T Consensus
                                                                                                                                   106 (368)
 T 3mmy A
                                                                                                                                   106 (368)
                             CEECSSCCSSCEEEEEECCTTSSSEEEEEEETTSEEEEEEECTTSC--EEEEEEECSSCEEEEEECT--TSSEEEEEET
 T ss dssp
 T ss_pred
                             eeeecCCCCCCEEEEEeCCCCCCCEEEEEecCCCCEEEEEecCCCceEEEEEcC--CCCEEEEEcC
                            CCeEEEeeccCcccccccceeEEEEcCCCCcEEEEEEcCCCCceEEEEecCCCcc
 Q ss pred
 Q Fri Mar 04 23:
                        78 DKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSD----- 144 (349)
                        O Consensus
 T Consensus
                        107 D--v-iWd-----h---v--v--v----l-s-s-d--i-iWd-----
                                                                                                                                   176 (368)
                       107 DKTAKMWDLSSN-----QAIQIAQHDAPVKTIHWIKAPNYSCVMTGSWDKTLKFWDTRSSNPMMVLQLPERCYCA 176 (368)
 T 3mmy_A
                             TSEEEEETTTT----EEEEEECSSCEEEEEECSSCEEEEEETTSEEEEECSSCSEEEECSSCEEEE
 T ss_dssp
 T ss pred
                             CCCEEEEECCCC-----cEEEeccCCCcEeEEEEecCCCCEEEEEecCCCceeEEEccCcceeEE
 Q ss_pred
                             Q Fri_Mar_04_23: 145 -----LRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPE----KLAVSALEQ-AIIYQRGKDGKLHV 204 (349)
                        145 ------
                                                                                                                                   204 (349)
 Q Consensus
                                                     +..|.+....+.++++.| ++. .++++..++ +..+|+......
                                                                                        ---~a~gs~dg~v~iw~~~
 T 3mmy_A
                        177 DVIYPMAVVATAERGLIVYQLENQPSEFRRIESPLKHQHRCVAIFK---DKQNKPTGFALGSIEGRVAIHYINPPNPAKD 253 (368)
 T ss dssp
                             ERETTEEEREGGGCEERECSSSCEREECCCSCSSCEREEERE---CTTSCEREERERTTSERERESSCSCHHHH
                             T ss_pred
 Q ss_pred
                            EEEccCCCC---
                                            Q Fri_Mar_04_23: 205 AAKLPGHKS-----LIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDM 272 (349)
 O Consensus
                        272 (349)
                            ...+..|.. .|++++|+|++ .+||+++.|++|+||+..+
                        254 ~~~~h~~~~~V~~vafspdg---~lasgs~D~~v~lWd~~~
 T Consensus
                                                                                                                                   305 (368)
 T 3mmy_A
                        SEEEECSEEC----CCCEEECCEEEEECTTT----CCEEEEETTSCEEEEETTTT------
 T ss_dssp
                             CEEEeecCCCCCCCCCCeeEEEEEECCCC----CeEEEecCCCEEEEEECccc------
 T ss pred
 Q ss_pred
                             CCCCCCCCCCCCCCCCCCCCeeeeeccCCCceEEEEECCCCCEEEEecC-C--CeEEEEeccCCCCEE
 Q Fri_Mar_04_23: 273 DAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGD-D--GKVRLWKATYSNEFK 340 (349)
 O Consensus
                       354 (368)
 T Consensus
 T 3mmy_A
                        306 -----TKLKTSEQLDQPISACCFNHNGNIFAYASSYDWSKGHEFYNPQKKNYIF 354 (368)
                             -----EEEEECCCCSSCEEEEECTTSSCEEEEECCCSTTCGGGCCTTSCCEEE
 T ss dssp
                             T ss pred
                                           PDE NCBI
 No 60
                                                                        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=1.8e-32 Score=245.71 Aligned_cols=305 Identities=15% Similarity=0.118 Sum_probs=0.0
                             Q ss pred
                        1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
 Q Fri Mar 04 23:
                                                                                                                                     80 (349)
 O Consensus
                          1 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v----las-s-Dg-
                                                                                                                                    80 (349)
                             \dots + \dots + | 
                          7 ~~~1~h~~v~~~~s~~~~1~~~~d~~i~iw~~~~~~v~~~~v~~~~v~~~~~dq~
 T Consensus
                                                                                                                                    82 (381)
 T 4zox_A
                          7 SLTYFDKHTDSVFAIGHHPNLPLVCTGGGDNLAHLWTSH--SQPPKFAGTLTGYGESVISCSFTS--EGGFLVTADMSGK
                                                                                                                                    82 (381)
                             T ss dssp
                             eEEEEecCCCCEEEEEcCCCCEEEEEcCC--CCCceeeeeecccCCceEEEEEcC--CCCEEEEEECCCCC
 T ss pred
                            Q ss pred
 Q Fri Mar 04 23:
                        81 VKLWEEDPDQEE-----CSGRR-----WNKLCTLND-SKGSLYSVKFAP-
                                                                                                                                   118 (349)
                         81 v~lwd~~~~~
 Q Consensus
                                                                                                                                   118 (349)
                         T Consensus
                                                                                                                                   162 (381)
                         83 VLVHMGOKGGAOWKLASOMOEVEEIVWLKTHPTIARTFAFGATDGSVWCYOINEODGSLEOLMSGFVHOODCSMGEFINT
                                                                                                                                   162 (381)
 T 4zox A
                             EEEEEEEGGGTEEEEEEECSSCEEEEEECSSSTTEEEEEETTSCEEEEEECTTTCCEEEEEEECCCSSCEEEEEECT
 T ss dssp
                             EEEEeCCCCCcceeccccCCCCeEEEEECCCCceEEEEEcCCCcEEEEEecCCCcchhhhccccccCCCeEEEEEecc
 T ss pred
 Q ss_pred
                            ----CCCCcEEEEEeCCCeEEEEECCCCcceeeecccEEEeecCCCcccceeEEEEcccCCCC------CceEecC
 Q Fri Mar 04 23: 119 ----EKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSP-----EKLAVSAL
                                                                                                                                   188 (349)
                        Q Consensus
                                                                                                                                   188 (349)
                                 + +..++++.|+.|++||+.+....
                                                                                        ++...+.++|+| ++
                        T Consensus
 T 4zox_A
                        163 DKGEN--TLELVTCSLDSTIVAWNCFTGQQLFKITQAEIK------GLEAPWISLSLAP---ETLTKGNSGVVACGSN
                                                                                                                                   229 (381)
                             TSCTT--CCEEEEEETTSCEEEEETTTTEEEEEEECGGGTT-----TCCCCEEEEEECC---GGGTTTCTTEEEEEET
 T ss_dssp
                             ccCCC--CCEEEEEeCCCEEEEEEccCCceeEEeccccc------CCCCcEEEEEECC---CCcccCCCcEEEEECC
 T ss pred
                             Cc-eEEEEecC-CCCEEEEEEcc--CCC----CceeEEEECCCCCCceEEEEEcCCCCCEEEEEecCc--cccccccc
 Q ss pred
 Q Fri Mar 04 23: 189 EQ-AIIYQRGK-DGKLHVAAKLP--GHK----SLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK--LSPLASEESL 258 (349)
```

```
Q Consensus
              T Consensus
                                                                             304 (381)
              230 NGLLAVINCNNGGAILHLSTVIELKPEQDELDASIESISWSSKF----SLMAIGLVCGEILLYDTSAWRVRHKFV-LEDS 304 (381)
T 4zox A
                 TSEEEEEETTTTTEEEEEEECCCCTTSCGGGGCEEEEEETTT----TEEEEEEETTSEEEEEEETTTCCEEEEEE-CSSC
T ss dssp
                 \texttt{CCEEEEEecCCCceeeeeeccccccccCcCceeeeeec-cCCc}
T ss pred
                 Q ss pred
Q Fri_Mar_04_23: 259 TNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWN------LTGTILSSAGDDGKVRL
                                                                              330 (349)
Q Consensus
                                            -----h---i--v--s-----pdg--las-s-D--v-i
                                                                              330 (349)
              T Consensus
                                                                             376 (381)
              305 VTKLMFD--NDDLFASCINGK-----VYQFNARTGQEKFVCVGHNMGVLDFILLHPVANTGTEQKRKVITAGDEGVSLV
T 4zox A
                                                                             376 (381)
T ss_dssp
                 EEEEEEE--TTEEEEEETTSC-----EEEEETTTCCEEEEECCCSSCEEEEEEECCSSCCSCCCEEEEEETTSCEEE
T ss_pred
                 EEEEEEe--CCeEEEEeCCCE-----EEEEECCCCCEEEEEecCCCCEEEEEecccccccCCCccEEEEccCCCEEEE
Q ss_pred
                 Eeccc
Q Fri_Mar_04_23: 331 WKATY
                      335 (349)
              331 W~~~~
Q Consensus
                      335 (349)
                 |+++.
              377 w~~~~
T Consensus
                      381 (381)
T 4zox_A
              377 FEVPN
                      381 (381)
T ss_dssp
                 EEECC
T ss pred
                 EecCC
No 61
                                               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=8.9e-34 Score=265.99 Aligned_cols=281 Identities=13% Similarity=0.107 Sum_probs=0.0
                 Q ss_pred
Q Fri_Mar_04_23:
               5 DSGHDDLVHDVVYDF-----YGRHVATCSSDOHIKVFKLDKDTS-----NWELSDSWRAHDSSIVAIDWASPEYG
                                                                              69 (349)
Q Consensus
               5 ~~h~~v~~~s~----d~~1-t-s-D~-v-iwd~~~~~h~~v~-v~-
                                                                              69 (349)
                 +.+|.+.|++++|+| ++.+|++|+|||+..... . ....+.+|...|++++|++
T Consensus
              277 (524)
              203 IVHSFGEVWDLKWHEGCHAPHLVGCLSFVSQEGTINFLEIIDNATDVHVFKMCEK--PSLTLSLADSLITTFDFLS---P 277 (524)
T 2j04_B
T ss_dssp
                 EEECCCSEEEEECSSCCCSSSSCEEEEEETTSCEEEEECCCCSSSSSEEECCCS--CSEEECCTTTCEEEEEESS---S
T ss pred
                 EEecCCceeeeEECcCCCCCccCEEEEEecCCcEEEEEecCCcCCcceeEecc--ceEEEECCCCceEEEEecC---C
Q ss_pred
                 CEEEEEeCCCeEEEeeccCcccccccccceeeEEEcCCCCcEEEEEECCCC-CcEEEEEeCCCCeeee
Q Fri Mar 04 23:
              70 RIIASASYDKTVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHL-GLKLACLGNDGILRLYDALEPSDLRSW 148 (349)
O Consensus
              148 (349)
              349 (524)
T Consensus
              278 TTVVCGFKNGFVAEFDLTDPEVP-----SFYDQVHDSYILSVSTAYSDFEDTVVSTVAVDGYFYIFNPKDIATTKTT 349 (524)
T 2j04 B
                 SEEEEEETTSEEEEETTBCSSC-----SEEEECSSSCEEEEEEECCTTSCCEEEEEETTSEEEEECGGGHHHHCEE
T ss dssp
T ss_pred
                 CeEEEEecCCceeEEEEccCCcc-----cEEEeccCCceeeEEEEccCccceEEEEecCcccccee
                 Q ss_pred
 Q Fri Mar_04 23: 149 TLTSEMKVLSIPPANHLQ--SDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIG
                                                                             225 (349)
              149 -----h--v--y--sp---
Q Consensus
              T Consensus
                                                                              409 (524)
              350 V-----SRFRGSNLVPVVYCP--QIYSYIYSDGASSLRAVPSRAAF---AVHPLVSRETTITAIGVSRLH-
Т 2ј04_В
                                                                              409 (524)
                 E-----EECSCCSCCCEEEET---TTTEEEEECSSSEEEEEETTCTT---CCEEEEECSSCEEEEECSSC-
T ss_dssp
T ss pred
                 e-----eeecCCCcceEECC---CCceEEEecCCCCEEEEecccc---cceeEecCCCceEEEEecCCC-
                 0 ss pred
Q Fri_Mar_04_23: 226 RWYQLIATGCKDGRIRIFKITEKLSPLASE-----ESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSN------L 292 (349)
              226 ~~~~las~s~d~~v~vwd~~~~~~~
              T Consensus
              410 --- PMVLAGSADGSLIITNAARRLLHGIKNSSATQKSLRLWKWDYSIKDDK------YRIDSSYEVYPLTV 471 (524)
T 2j04 B
                 ---CBCEEEETTTEEECCBSCSSTTTCC-----CCCCEEEECBCCSSSCE-------EEECCCCCCC-
T ss dssp
                 ---CeEEEEeCCCEEEEEecchhhhccccCCcccceEEEEEEEcCCCCc------eEeccCccccCC
 T ss pred
                 cceeeeccCCceEEEEECCC---CCEEEEecCCCeEEEEeccCC
Q ss pred
Q Fri Mar 04 23: 293 QVELLSEHDDHNGEVWSVSWNLT---GTILSSAGDDGKVRLWKATYS 336 (349)
              293 -----h---i--v--spd---g--las-s-D--v-iW-----
                                                     336 (349)
              ...+..+.|...|++|+|+| |++||+|+||+||||++...
472 -----h---V--v--sp----g--lasg--dg-vrl-----
T Consensus
                                                    518 (524)
т 2ј04_В
              472 NDVSKAKIDAHGINITCTKWNETSAGGKCYAFSNSAGLLTLEYLSLE 518 (524)
                 -----CCCSCCCEEECCSTTTTTEEEEECTTSEEEEECSCC
T ss dssp
T ss pred
                 CCCcceeEcCccceEEEEecCcccceEEEEecCcc
No 62
                                                Pub Med
                                           □ >3v11_A 265 proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A {Saccharomyces
 cerevisiae} PDB: 3acp _A
 Probab=100.00 E-value=1.5e-32 Score=250.15 Aligned cols=294 Identities=11% Similarity=0.115 Sum probs=0.0
Q ss_pred
```

```
Q Fri_Mar_04_23:
               5 DSGHDDLVHDVVYDFYGR-HVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKL
                                                                              83 (349)
O Consensus
               5 ---h---v--s-d---l-t-s-D--v-iwd------h---v--v--v--v---las-s-Dq-v-l
                T Consensus
                                                            ----l-s---d--i-i
                                                                             165 (420)
              92 KMLKRADYTAVDTAKLQMRRFILGTTEGDIKVLDSNFN----LQREIDQAHVSEITKLKFFP--SGEALISSSQDMQLKI
T 3vll A
                 TTSCSCCEEEEEECTSSCEEEEETTSCEEEECTTSC----EEEEETTSSSSCEEEEEECT--TSSEEEEEETTSEEEE
T ss_dssp
                 ccccCCceEEEEccCCcceEEEEcCCCcEEEEECCCC----ceeeeeccccCceeEEEEeC--CCCEEEEEeCCCcEEE
T ss pred
                 Q ss pred
Q Fri_Mar_04_23:
               84 WEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPAN
                                                                             163 (349)
              224 (420)
T Consensus
T 3vll A
              166 WSVKDGSN-----PRTLIGHRATVTDIAIIDR-GRNVLSASLDGTIRLWECGTGTTIHTFNRKE-----N 224 (420)
                 EETTTCCC-----BEEECCSSCEEEEEETT-TTEEEEEETTTCEEEEEETTTTEEEEEECBTT------B
T ss dssp
T ss_pred
                 EeCCCCc-----hhhhhcCcccEEEEEcCC--CCEEEEEcCCCcEEEEEeccC-------CCEEEEE
                 ccceeEEEEcc-----cCCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEEC
Q ss pred
Q Fri Mar 04 23: 164 HLQSDFCLSWCP-----SRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWA
                                                                             221 (349)
Q Consensus
                                                                             221 (349)
              T Consensus
                                                                             299 (420)
              225 PHDGVNSIALFVGTDRQLHEISTSKKNNLEFGTY---GKYVIAGHVSGVITVHNVFSKEQTI--QLPSKFTCSCNSLTVD
T 3v11 A
                                                                             299 (420)
                 TTCCEEEEEEECCCSSCGGGCCCCCTTCSSCT---TEEEEEEETTSCEEEEETTTCCEEE--EECCTTSSCEEEEEEC
T ss_dssp
                 T ss_pred
Q ss_pred
                Q Fri Mar 04 23: 222 P-SIGRWYQLIATGCKDGRIRIFKITEKLSPLASE----ESLTNSNMFDNSADVDMDAQGRSDSNTEEK----AELQSNL
                                                                             292 (349)
              222 p-----las-s-d--v-vwd------
Q Consensus
                                                                             292 (349)
                  300 GNNA----NYIYAGYENGMLAQWDLRSPECPVGEFLINEGTPINNVYFA-AGALFVSSGFDTSIK-LDIISDPESERPAI
T 3vl1_A
                                                                             373 (420)
                 SSCT----TEREFEETTSEFFEETTCTTSCSEFFEETTSCEFFEEEE-TTEEFFEETTTEEEE-EFFECCTTCCSCEF
T ss_dssp
                 CCCC----CEEEEECCCCCEEEEecCCCCCchheecccCCCceeEEEEC-CCCEEEEEeCCCCCE-EEEecCcccccc
T ss pred
                 cceeeeccCCcceEEEEECCCCCE---EEEecCCCeEEEEecccC
Q ss pred
 Q Fri_Mar_04_23: 293 QVELLSEHDDHNGEVWSVSWNLTGTI---LSSAGDDGKVRLWKATYS 336 (349)
              293 ~~~~~h~~i~v~~spdg~~--las~s~D~v~iW~~~~
.....+|...|++++|+|+++. |++++.|+.|++|++.++
374 ~~~~~v~~~v~~~~l~~~dg-i-iw~~~p
Q Consensus
                                                     336 (349)
T Consensus
              374 EFETPTFLVSNDDAVSQFCYVSDDESNGEVLEVGKNNFCALYNLSNP 420 (420)
T 3vll A
T ss_dssp
                 CTTSCEEECCSSCCCCEEEEECCSSSSCEEEEETTTEEEEEESCC-
T ss_pred
                 cccCchhhccCCCCceeeEEcCCCCcceEEEEcCCCCeEEEEeCCCC
                         PDB<sup>™</sup>
PROTEIN DATA BANK
                                  Pub Med
>409d_B RIK1-associated factor 1; propeller, heterochromatin formation, DOS2, transcript regulation; 2.00A
 {Schizosaccharomyces pombe}
Probab=100.00 E-value=4e-32 Score=247.42 Aligned cols=289 Identities=13% Similarity=0.142 Sum probs=0.0
                 cccCCcceEEEEECCCCCEEEEEeCCC------eEEEEECCCCCceeEeeeecccc------eEEEEEE
 Q Fri_Mar_04_23:
              3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQ------HIKVFKLDKDTSNWELSDSWRAHDS-----SIVAIDWA
                                                                              64 (349)
               3 ~~~~h~~~v~~~s~d~~1~t~s~D~~~~~v~iwd~~~~~~h~~~~~h~~~~~~~v~~v~~v~~~
Q Consensus
                                                                              64 (349)
              .|.+++|+
T Consensus
              24 KHFNETSGDTVCVAYNPLCEKFALGSTAQDGAYNRLGNLWIGDFHSE----TIQSLESHYKLNQVGEKEYSTISDLCFS
T 409d B
                                                                              98 (428)
T ss_dssp
                 EEECCCSSCEEEEECTTSSEEEEECCCTTCCCSSCSEEEEETTTT----EEEECCCCEEECTTSCEEECCEEEEEC
T ss_pred
                 Q ss_pred
 Q Fri_Mar_04_23:
              65 SPEYGRIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPA-----
                                                                             119 (349)
Q Consensus
               119 (349)
              | ++++|++++.|+.|++||+.+ ....+|+|+|+|
99 -----d-v-iw-----
                                                          ~~1~~~~d~~i~~
T Consensus
                                                                             166 (428)
T 409d_B
              99 K--GNLFLYTGAFDNAVKVWDMEG------NLCGIFNAPTDYIHKLALSDDDLLAVACKNGYGYLLSTDNSTGEIL 166 (428)
 T ss_dssp
                 T--TSSEEEEEETTSCEEEEETTS-----CEEEEECCCCSCEEEEEECTTCCEE
                 C--CCCEEEEEeCCCCeEEEEecCCC------CEEEeecCCCCceEEEEEECCCcEEEEEEecCCCCCEE
T ss_pred
                 -----CCCCEEEEEC------CCeEEEEECCCCcceeeeccccEEEeecCCCccc
Q ss pred
Q Fri_Mar_04_23: 120 ------HLGLKLACLGN------DGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHL 165 (349)
              120 -----d~i~iwd~~~~~~
                                  +.+..++.++. ++.|++||+.+...+..+
                                 -----l--g----s-s-d--i-i-d-------
T Consensus
                                                                             233 (428)
              167 TSANLIYPEALEKGYSASLIEFSNFLGRSSDKVIIGYDSFHTSNNRGCLALFDASTASFVOKF-----NTAD
T 4o9d B
                                                                             233 (428)
 T ss dssp
                 EEEEECCHHHHHTTCEEEEEEECTTTTSCCEEEEEEECTTC--CCCEEEEEETTTTEEEEEC-----SSCS
 T ss_pred
                 eceeecCcccccCCcceEEEeccCCCCcEEEEEcccCccCCCCEEEEEECCCCceeeee---
                Q ss pred
Q Fri_Mar_04_23: 166 QSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFK 244 (349)
              166 -----h--v-v-vsp----las-s-d-v-vwd 244 (349)
Q Consensus
              T Consensus
              234 EAFTSLYMHPS--QVGFVASSNTLSNGRVYYL-DTRMYKVCLNFTTTQKDINHATISNSG----ILVTSSGTDNQTFVWD 306 (428)
 T 4o9d B
```

```
T ss_dssp
                   CEEEEEECTT--CSEEEEEECSSSEEEEE-ETTTTEEEEEEEECSSSEEEEECTTS----CEEEEEETTSEEEEE
T ss_pred
                   Q ss_pred
                   Q Fri_Mar_04_23: 245 ITEKLSPLASEESL------TNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE-LLSEHDDHNG
                                                                                      305 (349)
               245 -----h--
 Q Consensus
                                                                                      305 (349)
                                            ..... | ++++...+.+..+..
                                   ----dg----i-iwd----
                307
T Consensus
                                                                                      380 (428)
                307 SRKPDKPLSLLKHGKTKMIHFDGANEEEVDAGINMAQWQPKGNLFVTGGSDGI-----VKVWDLRLNNPFIQNFTEMNS
T 4o9d B
                                                                                      380 (428)
                   TTSTTSCSEEEECCSCCC-------CCCCEEEECTTSSCEEEECTTSS-----EEEECTTSSCEEEEEEECSS
 T ss_dssp
                   CCCCcceeEeeccCccccccccccccCCceEEEEECCCCCEEEEecCCCc-----EEEEEECCCCCeeeeeccCCCC
T ss pred
                   eEEEEECCCCCEEEEeccCCceEEEecc
Q ss pred
Q Fri_Mar_04_23: 306 EVWSVSWNLTGTILSSAGDDGKVRLWKAT 334 (349)
                306 ~i~~v~~spdg~~las~s~D~~v~iW~~~ 334 (349)
                .|++++|+|+|+++|+++.|+.|+|++.
381 -v----s-d--1-----dg-i-iw--- 409 (428)
381 AITYGGFSEDASKLTVCCVGGDVNMYSLG 409 (428)
T Consensus
T 4o9d B
T ss dssp
                   CEEEEECTTSSEEEEEETTSCEEEEECC
T ss_pred
                   cceEEEEcCCCEEEEEecCC
                            SCOPe POB®
No 64
                                               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 2ce9 A
Probab=100.00 E-value=4.7e-32 Score=239.08 Aligned_cols=285 Identities=16% Similarity=0.218 Sum_probs=0.0
Probab=100.00
                   CCCCEEEEEECCCCCEEEEEeCCCCCCeeEeeec--cccceEEEEECCCCCCEEEEE
0 ss pred
Q Fri_Mar_04_23:
                 7 GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWR--AHDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                                       84 (349)
                 84 (349)
                T Consensus
                                                                                      124 (337)
                49 NHGEVVCAVTISNPTRHVYTGG-KGCVKVWDISHP-GNKSPVSQLDCLNRDNYIRSCKLLP--DGCTLIVGGEASTLSIW
T 1gxr A
                                                                                      124 (337)
T ss dssp
                   {\tt CCSSCCCEEEECSSSEEEEC-BSEEEEETTST-TCCSCSEEEECSCTTSBEEEEEECT--TSSEEEEEESSSEEEEE}
T ss pred
                   CCCCeEEEEecCCCceEEEec-CCCeEEEEEccCC-cccCcccccCCCCCeEEEEECC--CCcEEEEE
Q ss pred
                   eccCccccccccceeEEEEcCCCCcEEEEEECcCCCCcEEEEEeCCCCCCCEEEEEECCCCCCcc
Q Fri Mar 04 23:
                85 EEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANH
                                                                                      164 (349)
                Q Consensus
                                                                                      164 (349)
                              .....+..|...+..+++|+|+|+ +...+++++++++|++||+..+....+
T Consensus
                125 d----dg-i---d------
                                                                                      182 (337)
T 1gxr A
                125 DLAAPTP-----RIKAELTSSAPACYALAISPD-SKVCFSCCSDGNIAVWDLHNOTLVROF-----OGH
                                                                                      182 (337)
                   ECCCC-----EEEEEECSSSCEEEEECTT-SSEEEEEETTSCEEEEETTTTEEEEEE.-----CCC
T ss dssp
                   eCCCCcc-----ceeeeecccccEEEEECCC--CCEEEEEcCCCceeEEE------cCc
T ss_pred
Q ss_pred
                   ccceeEEEEcccCCCCceEEecCCc-eEEEEecCCccEEEEEEccCCCcceeEEEECCCCCcceEEEE
Q Fri_Mar_04_23: 165 LQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIF
                                                                                      243 (349)
Q Consensus
                165 ~~~~~
                           -----h---v--v--sp-----las-s-d--v-vw
                                                                                      243 (349)
                T Consensus
                                                                                      251 (337)
                183 TDGASCIDISN---DGTKLWTGGLDNTVRSWDLREGRQLQQH----DFTSQIFSLGYCPTG---EWLAVGMESSNVEVL
T 1gxr A
                                                                                      251 (337)
T ss_dssp
                   SSCEEEEECT---TSSEEEEEETTSEEEEEETTTTEEEEEE---ECSSCEEEEEECTTS----SEEEEEETTSCEEEE
T ss_pred
                   CCCeEEEECC---CCCEEEEECCCCCEEEEECCCCcccc----CEEEEEECCCC----CEEEEE
Q ss pred
                   Q Fri_Mar_04_23: 244 KITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSA
                                                                                      322 (349)
O Consensus
                322 (349)
               T Consensus
                                                                                      324 (337)
                252 HVNKPDKYQLHLHESCVLSLKFAYCGKWFVSTGKDNL-----LNAWRTPYGASIFQ-SKESSSVLSCDISVDDKYIVTG
                                                                                      324 (337)
T 1gxr A
                   ETTSSCEEEECCCSSCEEEEECTTSSEEEEEETTSE-----EEEEETTTCCEEEE-EECSSCEEEEECTTSCEEEEE
eCCCCcceEEecCCCCEEEEECCCCCEEEEECCCC-----EEEEECCCCcceee-cCCCCceeEEEECCCCCeEEE
T ss_dssp
T ss_pred
                   cCCCeEEEeccc
Q ss pred
Q Fri_Mar_04_23: 323 GDDGKVRLWKATY 335 (349)
               323 s~D~~v~iW~~~~
 Q Consensus
                               335 (349)
                  +.|+.|++|++.+
               325 ~~dg~i~~w~l~~ 337 (337)
T Consensus
               325 SGDKKATVYEVIY 337 (337)
T 1gxr A
T ss_dssp
                   ETTSCEEEEEEC
T ss pred
                   cCCCeEEEEecC
No 65
                                      NCBI Pub Med
        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=8.8e-35 Score=297.19 Aligned_cols=291 Identities=12% Similarity=0.087 Sum_probs=0.0
                   Q ss pred
Q Fri_Mar_04_23:
                 1\ \texttt{MQPFDSGHDDLVHDVVYDFYGR-HVATCSSDQHIKVFKLDKDTSNWELSDS-WRAHDSSIVAIDWASPEYGRIIASASYD}
                                                                                       78 (349)
                 1 ------h---v----s-d----l-t-s-D--v-iwd-------h---v--v--v------las-s-D ++.+..||.+.|+++|+|||+ +|+|||+.+|+||+.+|
 Q Consensus
                                                                                       78 (349)
T Consensus
               1062 \ v \sim l \sim gH \sim V \sim va \sim spdg \sim -laSgS \sim DgtVrlWd \sim -va \sim -va \sim -W \sim V \sim svafsp - dg \sim -laSgS \sim D \ 1139 \ (1460)
```

```
T 5dfz B
             1062 IATLMENEPNSITSSAVSPGETPYLITGSDQGVIKIWNLKEIIVGEVYSSSLTYDCSSTVTQITMIP--NFDAFAVSSKD 1139 (1460)
T ss dssp
                 ERRECSCSSSCCSCRERECSSSCRERECCTTSRERERHHHHHTTCCCSCSRERECSSCRERERECT--TSSCRERERTT
T ss_pred
                 EEEecCCCCCCEEEEEEcCCCCCEEEEEeCCCcceEEEECCccccceeeccccCCCcceEEEEEC--CCCEEEEEeCC
                 CeeeeeccCccccccccee-----EEEEcCCCceeeeEEEECcCcceeeEEEECCCCc
Q ss pred
 Q Fri_Mar_04_23:
              79 KTVKLWEEDPDQEECSGRRWNK-----LCTLNDSKGSLYSVKFAPAHLGL-KLACLGNDGILRLYDALE 141 (349)
Q Consensus
               79 g~v~lwd~~~~~d~i~iwd~~
                                                                                141 (349)
                 gt-iWd-tg-----ir----l-gH---V--v-fsp--g--L-Sgs-D-tI-iWDl-t 1208 (1460)
             1140 gtl~iWd~~tg-----
T Consensus
             1140 GQIIVLKVNHY-----QQESEVKFLNCECIRKINLKNFGKNEYAVRMRAFVNE-EKSLLVALTNLSRVIIFDIRT 1208 (1460)
 T 5dfz B
                 TEEEEEEEEE.----EETTEEEEEEEEEEEGGGGSSCCCCCEEEEECS--SCEEEEECTTCEEEEEETTT
T ss_dssp
T ss_pred
                 CCEEEEEeeCC-----CCCCCCCCCCeeeEEEeCCCCCCCeeEEEEEECC--CCeEEEEEECCC
Q ss_pred
                 CCcceeeeccccEEEeecCCCc--ccceeEEEEcccCCCCceEEecCCc-eEEEEecCCccEEEEEEcc-CCCCceeE
Q Fri_Mar_04_23: 142 PSDLRSWTLTSEMKVLSIPPAN--HLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLP-GHKSLIRS 217 (349)
O Consensus
              142 -----
                                         ~~~~~~~~~~~h~~~v~~
                                                                                217 (349)
             +..+..+ + |...+..++| + +...++++.| + ++|+|... ++..+.+|...|.+

1209 g-l-tl------g-H---V-svafsp--dg-LaSgs-DgtIrlWDl-tg-----tl--gh---V-- 1269 (1460)
T Consensus
             1209 LERLQIIE----NSPRHGAVSSICIDE--ECCVLILGTTRGIIDIWDIRFN---VLIRSWSFGDHAPITH 1269 (1460)
T 5dfz B
                 TEEEEEEE-----CCGGGCSBCCCEECS--SSSEEEEEBTTSCEEEEETTTT--EEEEEEBCTTCCCCCE
T ss_dssp
                 Cceeheec-----CCcccCCeEEEEEeC---CCCEEEEEECCCC---ceeEEEecCCCCceeE
T ss pred
                 Q ss pred
218 v----sp-----las-s-d--v-vwd--
 Q Consensus
                                                                                267 (349)
             T Consensus
             1270 VEVCQFYGKNS----VIVVGGSSKTFLTIWNFVKGHCQYAFINSDEQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVS 1345 (1460)
T 5dfz B
T ss_dssp
                 EECCSTTCTTE---EEEECSSSSEEEEEETTTTEEEEEEEEBSSCCCHHHHSCBCSCCTTCCCCCCCSTTSCCCEEE
T ss_pred
                 Q ss pred
Q Fri_Mar_04_23: 268 -ADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD------HNGEVWS
                                                                                309 (349)
Q Consensus
              268 -
                                                                                309 (349)
                  +.+.+.++.+.
              1346 ~g~~l~Sgs~Dg~-----IrvWd~~~~~i~g~~~~~i~g~~~~~~l~vv~~~~~l~gH~~~V~~ 1419 (1460)
T Consensus
             1346 NDKILLTDEATSS-----IVMFSLNELSSSKAVISPSRFSDVFIPTQVTANLTMLLRKMKRTSTHSVDDSLYHHDIINS 1419 (1460)
T 5dfz B
                 TTEEEEEETTTTE-----EEEEESSCTTTCEEEECCSSCCCEEEEEEETTEEEEEECC------CCCCCCCEEE
T ss_dssp
                 CCCEEEECCCCCE-----EEEEECCCcccEEEECCCCCCcceeeccCcceEEEEEEcCCCCcccCCCcchhhh
T ss pred
Q ss_pred
                 EEECC--CCCEEEEecCCCeEEEec
Q Fri_Mar_04_23: 310 VSWNL--TGTILSSAGDDGKVRLWKA 333 (349)
              310 v~~sp--dg~~las~s~D~~v~iW~~ 333 (349)
O Consensus
             |+|+| ++..||||.||+|+|+
1420 va-----laSgs-DG-IkvW-- 1445 (1460)
T Consensus
             1420 ISTCEVDETPLLVACDNSGLIGIFQG 1445 (1460)
T 5dfz B
T ss_dssp
                 EEEEECSSSEEEEEEETTSCEEEEC-
T ss_pred
                 hheeecCCccEEEEEcCCCeEEEEeC
                          PDB<sup>IM</sup> SMDB
PROTEIN DATA BANK NCBI
                                            Pub Med
🗌 >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=5.2e-32 Score=260.55 Aligned_cols=320 Identities=13% Similarity=0.144 Sum_probs=0.0
Q ss pred
                 Q Fri_Mar_04_23:
               2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQH------IKVFKLDKDTSNWELSDSWRA--HDSSIVAIDWASPEYG
                                                                                 69 (349)
               2 -----h---v---s-d---l-t-s-D--------v-iwd-------h---v--v--v------
O Consensus
                                                                                 69 (349)
              +..+.+|.+.|.++|+||++|++|++|++|.++|
104 -----h--v--a-spd--lasg-----dg----i-iwd------l---h--v---fs---dg
                                                                                179 (655)
T Consensus
              104 QRHYAGHNDDVKCLAVHPDRITIATGQVAGTSKDGKQLPPHVRIWDSVTL----NTLHVIGIGFFDRAVTCIAFSKSNGG
T 4ci8 A
T ss_dssp
                 EEEECCCSSCEEEEECTTSSEEEEEEBCCCCSSCCCCCCEEEEETTTC----CEEEEECTTTCCSBEEEEEECSSSSS
                 T ss_pred
Q ss_pred
                 CEEEE--EeCCCeEEEeeccCcccccccceeEEEEcCCCCcEEEEEECCCCCcee
 Q Fri Mar 04 23:
               70 RIIAS--ASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRS
                                                                                147 (349)
              O Consensus
                                                                                147 (349)
T Consensus
                                                                                248 (655)
              180 TNLCAVDDSNDHVLSVWDWQKE-----EKLADVKCSNEAVFAADFHPT--DTNIIVTCGKSHLYFWTLEGSSLNKK 248 (655)
T 4ci8 A
                 CCEEEEECSSSCEEEEEEGGGT-----EEEEEEECCSSCEEEEEECSS-CTTEEEEEBTEEEEEETTEEEEE
T ss_dssp
T ss pred
                 CEEEEECCCCEEEEECCCC-----cEEEEeecCCCCEEEEEECCC--CCCEEEEEECCCEEEEE
Q ss pred
                 Q Fri_Mar_04_23:
              148 W-----TLTSEMKVLSIPP------AN-HLQSDFCLSWCPSRFSPEKLAVSALEQ-AI
                                                                                192 (349)
              148 ~_____
              325 (655)
T Consensus
              249 QGLFEKQEKPKFVLCVTFSENGDTITGDSSGNILVWGKGTNRISYAVQGAHEGGIFALCMLR---DGTLVSGGGKDRKLI
T 4ci8 A
                                                                                325 (655)
                 ECBCTTSCCCSBEEEEEECTTSCEEEEETTSCEEEECTTCSBEEEEETTSSSSCEEEEEECT---TSCEEEEETTTCEEE
T ss dssp
                 T ss pred
```

```
Q ss pred
                  Q Fri Mar 04 23: 193 IYQRGKDGKLH-------VAAKLPGHKSLIRSISWAPSIGRWYQLIATG
                                                                                  234 (349)
O Consensus
               193 i-----h---y--y--sp------las-
                                                                                  234 (349)
               326 -wd------h---v-----h---v----
               {\tt 326~SWSGNYQKLRKTEIPEQFGPIRTVAEGKGDVILIGTTRNFVLQGTLSGDFTPITQGHTDELWGLAIH ASK----SQFLTC}
 T 4ci8 A
                                                                                  401 (655)
T ss_dssp
                  EECTTCCEEEEECCTTTCSEEEEECSTTCEEEEETTSCEEEECTTCCCEEEECCCSSCEEEEEECSSS----SEEEEE
T ss_pred
                  EeCCCCcEeeEEEccccCcEEEEEeCCCCEEEEEecCCceEEEEEccCCceEEEEEccCCc----CEEEEE
Q ss_pred
                  Q Fri_Mar_04_23: 235 CKDGRIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWN
O Consensus
               235 s~d~v~vwd~~~~h~~i~v~s
                                                                                 313 (349)
                  +.|++|++||+....|++++...+.+..+..
                                                          ..+++....+.+.+|...|.+++|+
               402 s~d~v~iwd~~~~~v~~~~v~~~~sp~q~~l~~~~dq~~~~i~v~d~~~~~~~
T Consensus
                                                                               ~~S
               402 GHDKHATLWDAVGHRPVWDKIIEDPAQSSGFHPSGSVVAVGTLTGR-----WFVFDTETKDLVTVHTDGNEQLSVMRYS
T 4ci8 A
                                                                                  475 (655)
                  ETTSEEEEEETTTTEEEEEECSSCEEEEECTTSSEEEEESSSE-----EEEEETTTCCEEEEEECSSSCEEEEEC
T ss dssp
T ss pred
                  Q ss pred
                  CCCCEEEEecCCCeEEEEecccCc-EEEEEeeccC
Q Fri_Mar_04_23:
               314 LTGTILSSAGDDGKVRLWKATYSNE-FKCMSVITAQQ 349 (349)
               314 pdg~~las~s~D~~v~iW~~~~~~~
                                                349 (349)
               | | | | + | | + | + | + | | + | + | + + + + + + + | . | 476 pdg~la~~~d~i~iw~~~~~~h~
T Consensus
                                                512 (655)
               476 PDGNFLAIGSHDNCIYIYGVSDNGRKYTRVGKCSGHS
T 4ci8 A
                                                512 (655)
                  TTSSEEEEETTSCEEEEEETTTTEEEEEEECCCS
 T ss_dssp
                  CCCCEEEEeCCCCEEEEEECCCCCcceEEeEECCCC
T ss_pred
                            PDB"
No 67
                                    NCBI
                                                   Pub Med
       WD repeat-containing protein 48; UAF1, USP, deubiquitinase, DUB, protein BI; 3.00A {Homo sapiens} PDB:
Probab=100.00 E-value=4e-32 Score=258.42 Aligned_cols=306 Identities=17% Similarity=0.211 Sum_probs=0.0
Q ss pred
                  Q Fri_Mar_04_23:
                3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
 Q Consensus
                82 (349)
                  ..+.+|.+.|++++|+|+++|++|++|++|++|++|
                                                 ....+.+|...|.+++|++ ++++|++++.|+.|+
               84 ----h---V--l--s-dg--l-sgs-Dg-I-vwd------h---V--l--s---dg--l--s---dg--I--84 ASMEHHTDWVNDIVLCCNGKTLISASSDTTVKVWNAHKG----FCMSTLRTHKDYVKALAYAK--DKELVASAGLDROIF
T Consensus
                                                                                  157 (598)
T 5cvl A
                                                                                  157 (598)
                  EEECCCSSCEEEEEEGGGTEEEEETTTSCEEEEETTTT----EEEEEECCCSSCEEEEEET--TTTEEEEEETTSCEE
 T ss_dssp
 T ss_pred
                  EeeccCCCCeEEEEecCCCEEEEEeCCCeEEEEECCCC----ceeeEecCCCcceEEEEEcC--CCCEEEEEeCCCeEE
Q ss pred
                  EeeccCcccccccceeEEEccCCCcEEEEECcCCCcEEEEEecCCCcceeeeccccEEEeecCCC
O Fri Mar 04 23:
               83 LWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                                  162 (349)
               83 lwd~~~
                        -----p----l----d--i-iwd--
O Consensus
                                                                                  162 (349)
                  +||+.+...+..|+..|++|+|+|+ +..|+++.|+.|++||+++...+..+
               T Consensus
                                                                                  222 (598)
T 5cvl A
                                                                                  222 (598)
                  T ss dssp
                  EEECCCCcccccCCccceecccCCCCCEEEEEECCC--CCEEEEEcCCCCEEEEecCCCCceeEEE------
T ss pred
Q ss_pred
                  Q Fri_Mar_04_23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR
                                                                                  241 (349)
Q Consensus
               163 ~
                                       ---i----sp---
                                                                      ~~~las~s~d~~v~
                                                                                  241 (349)
                  -h---v--l--sp---dg--l-sgs-dg-V-lwd-----h---v--h---v--l--s-dg-
                                                                      -~~1~sg~~dg~v~
T 5cvl A
               223 GHTDNVKALLLNR---DGTOCLSGSSDGTIRLWSLGOO---RCIATYRVHDEGVWALOVNDAF----THVYSGGRDRKIY
                                                                                  292 (598)
T ss dssp
                  CCSSCEEEEECT---TSSEEEEEETTSEEEEEETTTT---EEEEEEECCSSCEEEEEECTTS----CEEEEEETTCEEE
T ss_pred
                  CCCCCEEEEEeC---CCCEEEEEECCCC---ceEEEEecCCCCEEEEEECCCC----CEEEEECCCCeEE
297 (349)
Q Consensus
               297 (349)
                  +||+... ...+..+...|++++. ..+..+.. ...+++..
               293 vwd------v--l--sp-g----l-s-s-dg----I-iwd-----
                                                                                  369 (598)
T Consensus
               293 CTDLRNPDIRVLICEEKAPVLKMELDRSADPPPAIWVATTKST---VNKWTLKGIHNFRASGDYDNDCTNPITPLCTQPD
                                                                                  369 (598)
T 5cvl_A
                  EEESSSTTCEEEEECSSCEEEEEECCSSSSCCEEEEEESSSC--EEEEECTTHHHHHHTC-----CCCCSCSSCS
 T ss dssp
                  T ss pred
                  eeccCCceEEEEEcccCcEEEEeccCCceEEEE
Q ss pred
               298 SEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMS
Q Fri Mar 04 23:
 O Consensus
               298 ----h---i--v--spdg--las-s-D--v-iW------
               ..+.+|..|.+++|+|||+++++.|+.|++|++.....+.
370 ~~~g~~-i~~~s~dg~~l~t~~dg~V~lWdi~s~~~~~414 (598)
370 QVIKGGA-SIIQCHILNDKRHILTKDTNNNVAYWDVLKACKVEDLG 414 (598)
T Consensus
T 5cvl A
 T ss_dssp
                  EEECBCC-CEEEEECTTSSEEEEEETTCCEEEEETTTTEEEEEEE
                  eEecCCC-CeEEEEEcCCccEEEEecCCCCEEEEeccCC
T ss pred
No 68
                            PDB"
                                    NCBI
                                             Pub Med
>4aez_A CDC20, WD repeat-containing protein SLP1; cell cycle, KEN-BOX, D-BOX, APC/C; 2.30A {Schizosaccharomyces
 nombel
Probab=100.00 E-value=6.5e-32 Score=244.89 Aligned_cols=254 Identities=17% Similarity=0.366 Sum probs=0.0
```

```
Q ss_pred
                 Q Fri Mar 04 23:
               2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                               81 (349)
               2 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v----las-s-Dq-v
O Consensus
                                                                               81 (349)
                 +.+..+|...|.+++|+|+|++|++|+.||+|++||+...
              127 -----v--v--s-dg--l--g--dg-v-iwd-----h---v--l-----l--sg--dg-i
T Consensus
                                                                              198 (401)
              127 ALAETDESTYVASVKWSHDGSFLSVGLGNGLVDIYDVESQ----TKLRTMAGHQARVGCLSWN----RHVLSSGSRSGAI
                                                                              198 (401)
T 4aez A
                 EEEECCTTCCEEEEEECTTSSEEEEEETTSCEEEEETTTC---CEEEEECCCSSCEEEEEE---TTEEEEEETTSEE
T ss_dssp
                 EEEecCCCCcEEEEEcCCCCEEEEEcCCCC=---eEeeEecCCCCEEEEEC----CCEEEEEcCCCCE
T ss pred
Q ss_pred
                 EEeeccCccccccccceeEEEccCCCcEEEEEEccCCCccEEEEEecCCCcceeeecccEEEeecCC
Q Fri Mar 04 23:
              82 KLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGTLRLYDALEPSDLRSWTLTSEMKVLSTPP
                                                                              161 (349)
                                          ---p----l----d--i-iwd-----
O Consensus
              82 ~lwd~~~~~~~~~~
                                                                              161 (349)
                 ++||+.....
              T Consensus
                                                                              255 (401)
              199 HHHDVRIANHQ-----IGTLQGHSSEVCGLAWRSD-GLQLASGGNDNVVQIWDARSSIPKFTK-----
T 4aez A
T ss_dssp
                 EEEETTSSSCE-----EEEEECCSSCEEEEECTT-SSEEEEEETTSCEEEEETTCSSEEEEE
                 EEEEcccCCcc-----EEEEccCCCCEEEEEEcCC--CCEEEEEECCCCeEEEEECCCCceeEEe------
T ss_pred
                 CcccceeEEEEcccCCCCceEE--ecCc-eEEEEecCCCcEEEEEEccCCCcceeEEEECCCCCceEEEE--EcC
Q ss_pred
 Q Fri Mar 04 23:
              162 ANHLQSDFCLSWCPSRFSPEKLAV--SALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIAT--GCK
                                                                              236 (349)
              162 -----h--v--v-sp-----las---s-
 Q Consensus
                                                                              236 (349)
              T Consensus
                                                                              325 (401)
              256 TNHNAAVKAVAWCPW-QSNLLATGGGTMDKQIHFWNAATGARVNTVD---AGSQVTSLIWSPHS----KEIMSTHGFP
                                                                              325 (401)
T 4aez A
                 CCCSSCCCEEECTT-STTEEEEECCTTTCEEEEEETTTCCEEEEEE----CSSCEEEEEECSS----SEEEEEECTT
T ss dssp
                 T ss pred
Q ss pred
                 Q Fri_Mar_04_23: 237 DGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG
              237 d~~v~vwd~~~
                 |+.|++||+...
                                                           .....+.+|...|.+++|+|||
                                                        ----spdq
              326 d~~i~vw~~~~~
T Consensus
                                                                              361 (401)
              326 DNNLSIWSYSSS------GLTKQVDIPAHDTRVLYSALSPDG
T 4aez A
                                                                              361 (401)
T ss dssp
                 TCEEEEEEEETT-----EEEEEEEECCSSCCCEEECTTS
 T ss_pred
                 CEEEEecCCCeEEEEeccCCCcEE
Q ss_pred
Q Fri_Mar_04_23: 317 TILSSAGDDGKVRLWKATYSNEFK 340 (349)
             317 ~~las~s~D~~v~iW~~~~~~
O Consensus
                 ++|++|+.|++|++|++..+...
T Consensus
              362 ~~l~s~s~d~~i~iw~~~~~~
                                    385 (401)
T 4aez A
              362 RILSTAASDENLKFWRVYDGDHVK 385 (401)
                 SEEEEECTTSEEEEEECCC----
T ss dssp
T ss pred
                 CEEEEeCCCceee
                          PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
No 69
                                                Pub Med
>3mkq A Coatomer beta'-subunit; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
 cerevisiae} PDB: 2ynp _A
 Probab=100.00 E-value=1.6e-32 Score=270.56 Aligned_cols=257 Identities=15% Similarity=0.249 Sum probs=0.0
                 Q ss_pred
               1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
Q Fri Mar 04 23:
                                                                               80 (349)
               1 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v----las-s-Dg-
                                                                               80 (349)
                 .++.+.+|.+.|++++|+|+|++|++|+.||+|+||+.+.
T Consensus
               78 (814)
               5 IKKTFSNRSDRVKGIDFHPTEPWVLTTLYSGRVEIWNYETO----VEVRSIOVTETPVRAGKFIA--RKNWIIVGSDDFR
T 3mkq A
                                                                               78 (814)
                 CEEEEEECSCEEEEECSSSEEEEETTSEEEEETTTT----EEEEEEECCSSCEEEEEEG--GGTEEEEEETTSE
T ss dssp
                 cceeecccceeeeecccceeeeecccc----ceeeeeecccceeeeecccce
T ss_pred
Q ss_pred
                 EEEeeccCccccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCeEEEEECCCC-CcceeeeccccEEEeec
Q Fri_Mar_04_23:
              81 VKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP-SDLRSWTLTSEMKVLSI
                                                                              159 (349)
               81 v-lwd-----d--i-iwd-----
Q Consensus
                                                                              159 (349)
                 |++||+.++
                         +.+..+.+|...|.+++|+|+ +...|++++.|+.|++||+.++ .....+.
                                     ----v---spd--g--l-s---d--i-iwd-----
T Consensus
               79 i~vwd~~~~----
               79 IRVFNYNTG-----EKVVDFEAHPDYIRSIAVHPT--KPYVLSGSDDLTVKLWNWENNWALEQTFE-----
T 3mkg A
                                                                              137 (814)
T ss dssp
                 ERRETTTC-----CEERRECCSSCREEERCSS--SSEREEETTSEEEREGGGTSEREEEE-----
                 EEEEECCCC------ceeeeeecccceeeeeecc--cceeeeeeccccceeeeec-----
T ss_pred
                 Q ss_pred
Q Fri_Mar_04_23: 160 PPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHK-SLIRSISWAP--SIGRWYQLIATGC
                                                                              235 (349)
O Consensus
                 -----h-_-v-v-sp-_---las-s
                                                                              235 (349)
              160
                  T Consensus
              138 ---GHEHFVMCVAFNPK--DPSTFASGCLDRTVKVWSLGQST---PNFTLTTGQERGVNYVDYYPLPDK----PYMITAS
T 3mkq_A
                                                                              205 (814)
                 ---CCSSCEEEEEETT--EEEEEEEETTSEEEEEETTCSS---CSEEEECCCTTCCCEEEECCSTTC----CEEEEC
T ss_dssp
T ss_pred
                 ---CCCCcEEEEEeCC--CCCEEEEEECCCCEEEEEECCCC---cceEEeCCCCCEEEEEEECCCC----CEEEEE
Q ss pred
                 Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLT
                                                                              315 (349)
 Q Consensus
              236 ~d~~v~vwd~~~~
                                                             -----h---i--v--spd
                                                                              315 (349)
                                                             +.+..+.+|...|.+++|+|+
                 .|+.|++||+..+
```

```
T Consensus
               206 ~d~~i~lwd~~~~
                                                                                       239 (814)
                206 DDLTTKTWDYOTK-----SCVATLEGHMSNVSFAVFHPT 239 (814)
T 3mkq_A
T ss dssp
                   TTSEEEEETTTT-----EEEEEECCSSCEEEEECSS
T ss pred
                   CCCEEEEECCCC-----eEEEEEeCCCCeEEEEEeCC
Q ss_pred
                   CCEEEEcCCCceeeee
Q Fri_Mar_04_23: 316 GTILSSAGDDGKVRLWKATYSNEFKCM 342 (349)
Q Consensus
                316 q~~las~s~D~~v~iW~~~~~~~~
                                           342 (349)
                |++|++|+.|++|++.....+
240 g~~l~s~~dg~i~iwd~~~~~~
T Consensus
T 3mkq_A
                240 LPIIISGSEDGTLKIWNSSTYKVEKTL 266 (814)
T ss dssp
                   SSEEEEETTSCEEEEETTTCSEEEEE
                   CCEEEEeCCCEEEEEE
T ss_pred
No 70
->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}
            E-value=1.5e-32 Score=268.32 Aligned_cols=299 Identities=24% Similarity=0.418 Sum_probs=0.0
                   Q ss pred
Q Fri_Mar_04_23:
                 1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                        80 (349)
Q Consensus
                      ~~~h~~~v~~~s~d~~l~t~s~D~~v~iwd~~~~~~~h~~~v~~v~~v~~~~~las~s~Dg~
                                                                                        80 (349)
                   |..++.||.+.|+++|+||+|++|++|+.|++||+...+. .....+.+|...|+++.|+|+..+|++|+.||.
 T Consensus
                    ---l~gH---V--l--s-dg--latg--dg-I-vwd------l--h---V--l-fs-----l-s-s-Dg-
                                                                                        78 (753)
                 1 MVVIANAHNELIHDAVLDYYGKRLATCSSDKTIKIFEVEGETH--KLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGK
T 3jro A
                                                                                        78 (753)
T ss dssp
                   -----CCCCERRECCCSSSCCERRETTTERREFERETTER--ERREFECCCSSCERREFECCTTSCSERREFETTSC
                   CceccccCceEEEEcCCCCEEEEecCCCccEEEEeecCCcc--ceeeeeccCccEEEEEecCCCCCEEEEEeCCCc
T ss pred
Q ss_pred
                   EEEeeccCcccccccceeEEEEccCCCcEEEEEEccCCCcEEEEEeccCccceeeecccEEEeecC
Q Fri_Mar_04_23:
                81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                       160 (349)
 O Consensus
                160 (349)
                                 |++||+.++..
T Consensus
                 79 T~vWd~~~~~
                               ---------h---v--l--s---g--l-s---dg-i-iwd----
                                                                                       142 (753)
                 79 VLIWKEENGRW-----SQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVVEFKENGTTSPIIID------
T 3jro_A
                                                                                       142 (753)
T ss_dssp
                   EEEEEEETTEE-----EEEEEECCCSSCEEEEEECCGGGCSEEEEEETTSEEEEEECCSSSCCCCEEEE-----
T ss pred
                   EEEEecCCCcc-----cccccCCCCCceeEEEECCCCCCEEEEEeCCCCCccccccc-----
                   CCcccceeEEEEccCCCC-------CceEEecCCc-eEEEEecCCCcE-EEEEEccCCCCceeEEEECCCCC
Q ss pred
                161 PANHLQSDFCLSWCPSRFSP------EKLAVSALEQ-AIIYQRGKDGKL-HVAAKLPGHKSLIRSISWAPSIG
 Q Fri Mar 04 23:
 Q Consensus
                161 -----h-v-v-v-sp---
                                                                                       225 (349)
                     .+...+.++|+| ++
                                              T Consensus
                                                                                       215 (753)
T 3jro_A
                143 --AHAIGVNSASWAP---ATIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPT--
                                                                                       215 (753)
                   --CCSSCEEEEECC---CC--------CGGGCCEEEEETTSCEEEEEEETTTTEEEEEEEECCCSSCEEEEEECCC-
T ss dssp
T ss_pred
                   --CCCCceEEEEcC---CCCcccccCCCCccEEEEEcCCCcEEEEecCCccceEeEecCCccceEEEEecCC--
                   Q ss pred
Q Fri Mar 04 23:
                226 RWY---QLIATGCKDGRIRIFKITE----KLSPLAS--EESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNL---
                                                                                       292 (349)
                   ~~~-las~s~d~~v~vwd~~~----
                                                                                       292 (349)
 Q Consensus
                                            ....+.. +......|++++...+.+..+..
                        .+|++++.|+.|++||+..
T Consensus
                216 --g----i-s-s-dg-i-iwd------v-v-spdg--l-s-s-dg-----i-iwd----g 287 (753)
216 --VLLRSYLASVSODRTCIIWTODNEOGPWKKTLLKEEKFPDVLWRASWSLSGNVLALSGDNK------VTLWKENLEG 287 (753)
T 3jro_A
                   --CSSSEEEEEEESSSCEEEEEESSSSCCBCCBSSSSCCSCCCEEECTTTCCEEEECSSSC-----EECCBCCSSS
T ss dssp
T ss_pred
                   --CCCCCeEEEecCCCeEEEecCCCCccchhcccccCcCeEEEEEcCCCCEEEEEecCCCe-----EEEeccCCCc
Q ss_pred
                   CCEEEECCCCCEEEEECCCCCEEEEECCCCCEEEEECC
Q Fri Mar 04 23: 293 QVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKA 333 (349)
                293 -----h---i--v--spdg--las-s-D--v-iW--
O Consensus
                                                      333 (349)
                   288 ~~~~~~
T Consensus
                                                       327 (753)
T 3jro_A
                288 KWEPAGEVHQGGGG-SGGGGATSKEFDGPCQNEIDLLFSEC
                                                       327 (753)
T ss_dssp
                   CCBCCCCBC-----
                   chhhceeeccCCC-ceeEecCccceeccCCccceehhhh
T ss pred
                             PDB<sup>IM</sup>
PROTEIN DATA BANK
                                      NCBI
                                                       Pub Med
>4xvh A Kinetochore protein MIS16: centromere, CENP-A, MIS18 complex, histone: 2.30A {Schizosaccharomyces
 japonicus}
 Probab=100.00 E-value=1.2e-32 Score=252.12 Aligned_cols=251 Identities=19% Similarity=0.336 Sum_probs=0.0
                   CCCCEEEEEECC-CCCEEEEEeCCCCEEEEEECCCCCC----ceeEeeeeccccceEEEEEECCCCCC-EEEEEeCCCC
Q ss_pred
Q Fri Mar 04 23:
                 7 GHDDLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTS----NWELSDSWRAHDSSIVAIDWASPEYGR-IIASASYDKT
                                                                                        80 (349)
                      ~v~~~~s~-d~~l~t~s~D~~v~iwd~~~~~____nas~s~Dq~
O Consensus
                                                                                        80 (349)
                206 (430)
T Consensus
T 4xyh A
                129 HHEGDVNKARFMPONPDIIATLGLNGNGYIFDLNLYREOPIVOTGHOACLRHHTSEGFGLGWNF--IQEGTLATGTEDTS
                                                                                       206 (430)
T ss_dssp
                   EESSCCCEEEETTEEEEEEECGGGCEEEEEGGGCSSCSEETTCCSEEECCCSSCCCEEEECS--SSTTEEEEECTTSC
T ss pred
                   CCCCceEEEEcCCCCCEEEEECCCCccccccCCCCCEEEecCC--CCCCEEEEcCCCCC
 Q ss pred
                   EEEeeccCccc-----cccccceeEEEEcCCCcEEEEEECcCCCcEEEEEECCCC---Ccceeee
 Q Fri Mar 04 23:
                81 VKLWEEDPDQE-----ECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP---SDLRSWT 149 (349)
O Consensus
                81 v-lwd-----d--i-iwd-----
                                                                                       149 (349)
```

```
T Consensus
                                                                                                                     278 (430)
                     207 ICVWDIKGKSLSLEKSIDVAP------VSVYHRHTAVVNDLQFHLQH-EALLTSVSDDCTLQIHDTRLPSSSSASQCVK
 T 4xyh_A
                                                                                                                     278 (430)
                         EEEEECTTCCCBTTBCEEECC-----SEEECCCSSCEEEEEECTTC-TTEEEEEEETTSCEEEEE
 T ss dssp
 T ss_pred
                          EEEEECCCCccccCCCcccc-----ceeecCCCccEeeEEECCCC-CCEEEEECcCCCcCCCcceEec
                         GGGGEEEeecCCCccccceeeeeeeccCCCCCc-eeeecCCc-eeeeecCCcceeeeeeeccCCcceeeeeee
 Q ss pred
 Q Fri Mar 04 23: 150 LTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEK-LAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRW
                                                                                                                     227 (349)
                                                                                                                     227 (349)
                                                     -----h----y--sp-----
 Q Consensus
                                        .+...+..+|+| ++... ++++..++ +.+|+..... .+..+.+|...|.+++|+|+|+.
                     279 -----heopyngvafnp---fndyllatasadhtvalwdlrrino-rihtleghedevynvowsphde-
 T Consensus
 T 4xyh_A
                                                                                                                     338 (430)
                         -----CCSSCEEEEECS---SCTTEEEEEETTSCEEEEETTCTTS--CSEEECCCSSCEEEEECSSCT--
 T ss dssp
                          -----cccceeeeecc--ccceeeeeccc--ccceeeeeccccc--
 T ss pred
 Q ss pred
                         Q Fri Mar 04 23: 228 YQLIATGCKDGRIRIFKITE-----KLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQ
                                                                                                                     293 (349)
                     228 ~~~las~s~d~~v~vwd~~~-----
 Q Consensus
                                                                                                                     293 (349)
                          .+|++++.|+.|++||+..
                     339 ---1-s-s-Dg-i-iwd------
 T Consensus
                     339 -PILVTSSTDRRVCVWDLSKIGEEQTVEDSEDGAP-----
 T 4xyh A
                                                                                                                     372 (430)
                         -TEEEEEETTSCEEEEEGGGTTCCCCHHHHTSCCT-----
 T ss_dssp
                          -CEEEEeCCCcEEEEECCcCcccccccccCCc-----
 T ss_pred
                         ceeeeccCCceEEEEECCCCC-EEEEecCCCeEEEEecc
 Q ss pred
 Q Fri_Mar_04_23: 294 VELLSEHDDHNGEVWSVSWNLTGT-ILSSAGDDGKVRLWKAT 334 (349)
 O Consensus
                    294 -----h---i--v--spdg---las-s-D--v-iW---
                                                                          334 (349)
                     .+..+|...|+++|+|+|++++|+.|+|++
373 -----dg-v-iw---
 T Consensus
                                                                         413 (430)
 T 4xyh_A
                     373 -ELMFMHGGHTNRVSDLSWNPNNKWVLASLADDNILOIWSPS 413 (430)
                       -TEEEEECCCSSCEEEEEECSSSTTCEEEEETTSEEEEEEEC
 T ss_dssp
 T ss pred
                          -eeEEEeCCcCCceEEEEECcccccEEEEeccccc
                                      POTEN DATA BANK
PROTEIN DATA BANK
PROTEIN DATA BANK
PUBLICATION
PU
 No 72
->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=7.7e-32 Score=259.39 Aligned_cols=295 Identities=15% Similarity=0.217 Sum probs=0.0
                         Q ss pred
 Q Fri_Mar_04_23:
                       6 SGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRA-HDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                                                                      84 (349)
 O Consensus
                       6 ~~h~~~v~~~s~d~~l~t~s~D~~v~iwd~~~~~~~h~~~v~~v~~v~~~~~las~s~Dq~v~lw
                                                                                                                      84 (349)
                         T Consensus
                                                                                                                     327 (655)
                     255 QEKPKFVLCVTFSENGDTI-TGDSSGNILVWGKGTN----RISYAVQGAHEGGIFALCMLR--DGTLVSGGGKDRKLISW
                                                                                                                     327 (655)
 T 4ci8 A
                          {\tt SCCCSBEEEEECTTSCEE-EEETTSCEEEECTTCS----BEEEEETTSSSSCEEEEEECT--TSCEEEEETTTCEEEEE}
 T ss_dssp
                         CCCCceEEEEEcCCCCEE-EEcCCCceEEEEcCCCc----EEEeeecccCCcEEEEEEec--CCeEEEEeCCCCCEEEE
 T ss pred
                         eccCccccccceeEEE-------EcCCCcEEEEEECcCCCC
 Q ss pred
 Q Fri_Mar_04_23:
                      85 EEDPDQEECSGRRWNKLCT-----
                                                                                                                     122 (349)
 Q Consensus
                      85 d~~~
                                                                                                                     122 (349)
                                                                                             +.+|...|.+++|+|+ +
 T Consensus
                     328 d-----v----v------
                                                                                             ----h---v------
                                                                                                                     395 (655)
                     328 SGNY-----QKLRKTEIPEQFGPIRTVAEGKGDVILIGTTRNFVLQGTLSGDFTPITQGHTDELWGLAIHAS--K
 T 4ci8 A
                                                                                                                     395 (655)
 T ss dssp
                         CTTC-----CEEEEECCTTTCSEEEEECSTTCEEEEETTSCEEEECTTCCCEEECCCSSCEEEEECSS-S
                          CCCC-----cEeeEEEcccCCcEEEEEecCCCcEEEEEecCCCceEEEEEccCCcc
 T ss_pred
                         Q ss pred
 Q Fri_Mar_04_23: 123 LKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGK
                                                                                                                     201 (349)
                     123 --1----d--i-iwd-----
 O Consensus
                                                                                                                     201 (349)
                         ..|++++.|+.|++||+.+.....
                                                                     .+...+.++|+| ++..+++..++ +.+|+....
 T Consensus
                     457 (655)
                     396 SOFLTCGHDKHATLWDAVGHRPVWDK-----IIEDPAQSSGFHP--SGSVVAVGTLTGRWFVFDTETKD-
 T 4ci8 A
                                                                                                                     457 (655)
                         SEEEEEETTSEEEEEETTTTEEEEEE.-----ECSSCEEEEEECT--TSSEEEEEEESSSEEEEETTTCC-
 T ss dssp
                         CEEEEECCCCeEEEEECCCCeEEEEE.-----ecCCCcEEEEEECC---CCCEEEEEECCCCE
 T ss_pred
 Q ss_pred
                         Q Fri_Mar_04_23: 202 LHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK-----LSPLASEESLTNSNMFDNSADVDMDAQ
                                                                                                                     275 (349)
                                                      ~~~~las~s~d~~v~vwd~~~~
 Q Consensus
                     202 ----h---v--v--sp----
                                                                                                                     275 (349)
                                                       .+|+++.|+.|++||+...
                                     ~~~v~~~~spdg----~la~~~d~~i~iw~~~~~~h~~~v~~l~
 T 4ci8 A
                     458 --LVTVHTDGNEOLSVMRYSPDG----NFLAIGSHDNCIYIYGVSDNGRKYTRVGKCSGHSSFITHLDWSVNSOFLVSNS
                                                                                                                     531 (655)
 T ss dssp
                         --EEEEECSSSCEEEEECTTS----SEEEEEETTSCEEEEEEETTTTEEEEEEECCCSSCEEEEEBTTSSCEEEE
                         T ss_pred
                         ccccccccccccccccceeeeeccC-------CCceEEEEECCCCCEEEEecCCCCeEEE
 Q ss_pred
 Q Fri_Mar_04_23: 276 GRSDSNTEEKAELQSNLQVELLSEHDD-------HNGEVWSVSWNLTGTILSSAGDDGKVRL
                                                                                                                     330 (349)
                     276 ~~~~~h~~i~v~spdq~las~s~D~vvi
 Q Consensus
                                                                                                                     330 (349)
                                                                                   |...|++++|+|+|++||+|+.|+.|+|
----v---s----la----dg-v-l
                     532 ~d~~---i~iwd~~~~~
                                                                                                                     605 (655)
 T Consensus
                     532 GDYE-----ILYWVPSACKQVVSVETTRDIEWATYTCTLGFHVFGVWPEGSDGTDINAVCRAHEKKLLSTGDDFGKVHL
                                                                                                                     605 (655)
 T 4ci8 A
 T ss_dssp
                         TTCC-----CEEEEGGGTEECCCHHHHTTCCBSCCCCSSSTTTTTSSCTTCCTTSEEEEEECSSSSEEEEEETTSCEEE
 T ss pred
                         CCCe-----EEEEECCCCeecChhhccceeEccccCCCcceeECcCCCCcceEEEECCCCCEEEE
```

```
Q ss pred
                   EecccCceEEEEEeeccC
Q Fri Mar 04 23: 331 WKATYSNEFKCMSVITAQQ 349 (349)
T Consensus
                606 w-----h-
                                    624 (655)
                606 FSYPCSQFRAPSHIYGGHS 624 (655)
T 4ci8 A
                   EESCCCSSSCCCEEECCCS
T ss dssp
                   EccccccccceEeccch
T ss pred
                            PDB<sup>IM</sup>
PROTEIN DATA BANK
No 73
                                                Pub Med
>1r5m_A SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A
 {Saccharomyces cerevisiae}
Probab=100.00 E-value=2.1e-32 Score=249.02 Aligned_cols=301 Identities=14% Similarity=0.205 Sum_probs=0.0
                   CCgcgCCCc--CeEEEEEECC-CCCEEEEEeCCCeEEEEECCCCC-----ceeEeeee--------ccgcgceEEEE
Q ss_pred
O Fri Mar 04 23:
                 1 MQPFDSGHD--DLVHDVVYDF-YGRHVATCSSDQHIKVFKLDKDTS-----NWELSDSW------RAHDSSIVAI
                                                                                        61 (349)
                 1 ~~~~~h~_~~v~~~~s~-d~~~l~t~s~D~~v~iwd~~~~~~~
                                                                                        61 (349)
Q Consensus
                   ....+.+|. +.|.+++|+| ++++|++|+.|+.|++|++.....
T Consensus
                114 (425)
                35 FVKILKEIVKLDNIVSSTWNPLDESILAYGEKNSVARLARIVETDQEGKKYWKLTIIAELRHPFALSASSGKTTNQVTCL
T 1r5m A
                                                                                       114 (425)
                   CCEECEEEECSCCSEEEECSSCTTEEEEEETBTEEEEEEEC-----CEEEEEEEECCCCCC------CBCEEEE
T ss dssp
                   T ss_pred
Q ss_pred
                   Q Fri Mar 04 23:
                62 DWASPEYGRIIASASYDKTVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE
                                                                                       141 (349)
                62 -----las-s-Dg-v-lwd-----v--
                                                                ~~p~~~~l~~~~d~~i~iwd~~~
O Consensus
                                                                                       141 (349)
                   +|+| ++++|++|+.||.|++||.+.
                                             +.+..+..|...|.+++|+|+ +...|++++.|+.|++||+.+
                       --~~~l~~~~dg~v~vw~~~~--
T 1r5m A
                115 AWSH--DGNSIVTGVENGELRLWNKTG------ALLNVLNFHRAPIVSVKWNKD--GTHIISMDVENVTILWNVIS
                                                                                       180 (425)
T ss dssp
                   EECT--TSSEEEEETTSCEEEEETTS-----CEEEEECCCCSCEEEEECCTT--SSEEEEEETTCCEEEEETTT
                   EECC--CCCEEEEECCCCEEEEECCC------CeEEEEcCCCCCEEEEEECCC--CCEEEEECCCC
T ss pred
Q ss pred
                   \texttt{CCcceeeeccc--EEEeecCCCccceeEEEEcccCCCCceeEeecCc--eEEEEeccCCcceeEE}
 Q Fri_Mar_04_23: 142 PSDLRSWTLTSE--MKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSI
                                                                                       218 (349)
Q Consensus
                142 ~~~~~~~~h~~~v~v
                                                                                       218 (349)
                   ._~~~~~~~g~i~~<sup>'</sup>d~~~~~__
T Consensus
                181 GTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVD----DDKFVIPGPKGAIFVYQITEKT---PTGKLIGHHGPISVL
T 1r5m A
T ss_dssp
                   TEEEEEECCC-----CCCBSCCEEEE---TTEEEEECGGGCEEEETTCSS--CSEEECCCSSCEEEE
T ss_pred
                   CceeeeeecccCccceeecccCCccEEEEEcC----CCEEEEEcCCCcEEEEEcCCCc---EEeeeccCCCceeEE
                   Q ss pred
Q Fri_Mar_04_23: 219 SWAPSIGRWYQLIATGCKDGRIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVEL
                                                                                       296 (349)
                219 --sp-----las-s-d--v-vwd-----
O Consensus
                                                                                       296 (349)
               T Consensus
                                                                                       322 (425)
                254 EFNDTN----KLLLSASDDGTLRIWHGGNGNSQNCFYGHSQSIVSASWVGDDKVISCSMDGS------VRLWSLKQNTL
T 1r5m A
                                                                                       322 (425)
                   EEETTT----TEEEEEETTSCEEEECSSSBSCSEEECCCSSCEEEEEETTTEEEEEETTSE-----EEEEETTTEE
 T ss_dssp
                   EECCCC----CEEEEEeCCCEEEEEECCCcccchhcccceEEEEECCCCeEEEEeCCCc------EEEEECCCCCe
T ss_pred
                   eeeccCCceEEEEEccCccEEEEec
Q ss pred
Q Fri_Mar_04_23: 297 LSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKA 333 (349)
               297 ~~~~h~~~i~~v~~spdg~~las~s~D~~v~iW~~
               +..+..|...|.++|+|+|++++.|+.|+||++
323 ------i----s----l-----dg-v-iwd- 359 (425)
T Consensus
               323 LALSIVDGVPIFAGRISQDGQKYAVAFMDGQVNVYDL 359 (425)
T 1r5m A
T ss_dssp
                   EEEEECTTCCEEEEEECTTSSEEEEEETTSCEEEEEC
T ss_pred
                   eEEEecCCCceEEEECC
                            PDB
                                                     Pub Med
3826 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* 3iiy A* 3ij0 A* 3ij1 A* 2qxv A
Probab=100.00 E-value=4.9e-32 Score=241.42 Aligned_cols=289 Identities=11% Similarity=0.152 Sum_probs=0.0
Q ss pred
                   CCccCCCcceEEEEEECCCCC----EEEEEECCCeEEEEECCCCCceeEeeeecccc-----eEEEEEEcCCCCC-
                 Q Fri_Mar_04_23:
                                                                                        69 (349)
                T Consensus
                                                                                        83 (366)
T 3k26_A
                10 VNSLKEDHNQPLFGVQFNWHSKEGDPLVFATVGSNRVTLYECHSQ----GEIRLLQSYVDADADENFYTCAWTY--DSNT
                                                                                        83 (366)
T ss dssp
                   EEEEECTTCSCEEEEEECTTCCTTSCEEEEEEEETTEEEEEECGG----GCEEEEEEECSCTTCCEEEEEEEE--CTTT
T ss_pred
                   EEeecCCCccceeEEEEccCCCCccEEEEEEccCC----cceEEeeccCCccCCcEEEEEeec--CCCC
Q ss pred
                   --CEEEEEeCCCeEEEeeccCcccccccccceeEEEEcCCCCcEEEEEECc-CCCCcEEEEEEECCCCcce
Q Fri_Mar_04_23:
                70 --RIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP-AHLGLKLACLGNDGILRLYDALEPSDLR
                                                                                       146 (349)
                Q Consensus
                                                                                       146 (349)
                    ++|++|+.||.|++||+.+.
                                            +.+..+.|...|.+++|+| + +..|++++.|+.|++||+.+....
                84 ----dg-v-iwd-----
T Consensus
                                                              -----l~s~~~da~v~vwd~~~~~
                                                                                       152 (366)
                84 SHPLLAVAGSRGIIRIINPITM-----QCIKHYVGHGNAINELKFHPRD--PNLLLSVSKDHALRLWNIQTDTLVA 152 (366)
T 3k26 A
```

```
T ss_dssp
                 CCEEEEEETTCEEEEECTTTC-----CEEEEEESCCSCEEEEEECSSC-TTEEEEEETTSCEEEEETTTTEEEE
T ss_pred
                 ee---ecccEEEeecCCCccceeEEEEcccCCCCceEEecCCc-eEEEEecC-----
Q ss_pred
 Q Fri_Mar_04_23: 147 SW---TLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGK----------------------
                                                                              198 (349)
              147 -----i-----i
 O Consensus
                                                                              198 (349)
                              .+...+.++|+| ++...++++.++ +..+|+...
                                       ----l----d--i-iwd----
                     ~_____v~~v~~~v
T Consensus
              153
                                                                              216 (366)
              153 IFGGVE-----GHRDEVLSADYDL--LGEKIMSCGMDHSLKLWRINSKRMMNAIKESYDYNPNKTNRPFIS
T 3k26 A
                                                                              216 (366)
 T ss_dssp
                 EECSTT----SCSSCEEEEECT--TSSEEEEEETTSCEEEEESCSHHHHHHHHHHHTCCGGGCSSCCCC
                 T ss pred
                 -CCCEEEEEccCCCCceeEEEECCCCCCceEEEEEcCCcc
Q ss pred
Q Fri Mar_04_23: 199 -DGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLS-------PLASEESLTNS
                                                                              261 (349)
                    -----h---v--v-sp-----las-s-d--v-vwd-------------
                                                                              261 (349)
              T Consensus
                                                                              290 (366)
              217 QKIHFPDFSTRDIHRNYVDCVRWLGD-----LILSKSCENAIVCWKPGKMEDDIDKIKPSESNVTILGRFDYSQCDIWY
T 3k26 A
                                                                              290 (366)
T ss dssp
                 EEECCCSEEECSSCSSCCCEEEEETT-----EEEEECSSSEEEEEEESSTTCCGGGCCTTCCCEEEEEEECSSCCSSC
 T ss_pred
                 eeeccCcccccccceEEEEecCC-----EEEEEcCCCCEEEEEccccccccCCCccceeeeccCCCcCcceEE
                 Q ss pred
Q Fri Mar 04 23: 262 NMFDNS--ADVDMDAQGRSDSNTEEKAELQSNLQVELL----SEHDDH--NGEVWSVSWNLTGTILSSAGDDGKVRLWKA
                                                                              333 (349)
                     -_----h----i--v--spdg--las-s-D--v-iW--
              262 ~~
                                                                              333 (349)
Q Consensus
                                    ..+++...+.+
                                               ..+.+| ...|++++|+|+|++|++|+.|+.|+|++
-----v----v---s----l~s---dg-i-iw--
                   -s-----l-vwd------
T Consensus
              291 ~~
                                                                              364 (366)
              291 MRESMDEWOKMI.ALGNOVGK-----I.YVWDI.EVEDPHKAKCTTI.THHKCGAATROTSESRDSSII.TAVCDDASTWRWDR
T 3k26 A
                                                                              364 (366)
                 CCCECTTSSEEEECTTSC----EEEEECCSSGGGCEEEECCTTCCSCEEEEECTTSSEEEEEETTSEEEEEC
T ss dssp
T ss pred
                 EEEccCCCCCEEEEecCCCe-----EEEEecCCCCccceeEEeecccCCcEEEEEECCCCEEEEecc
Q ss_pred
Q Fri_Mar_04_23: 334 T 334 (349)
              334 ~ 334 (349)
Q Consensus
T Consensus
              365 ~ 365 (366)
T 3k26 A
              365 L
                   365 (366)
T ss_dssp
                 C
T ss_pred
                          PDB"
PROTEIN DATA BANK
                                 NCBI
                                                Pub Med
🔝 >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=7.7e-32 Score=258.66 Aligned_cols=306 Identities=17% Similarity=0.211 Sum_probs=0.0
                 Q Fri_Mar_04_23:
               3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
3 ~~~~h~~v~~~s~d~~l-t~s~D~v~iwd~~~~~~h~~v~v~~~~~las~s~Dg~v~
                                                                              82 (349)
Q Consensus
                                                                              82 (349)
               T Consensus
                                                                              142 (677)
               69 ASMEHHTDWVNDIVLCCNGKTLISASSDTTVKVWNAHKG----FCMSTLRTHKDYVKALAYAK--DKELVASAGLDRQIF
T 5cvo A
                                                                              142 (677)
T ss_dssp
                 EEECCCSSCEEEEECSTTCCEEEEETTSCEEEEETTTT----EEEEEECCCSSCCCEEEEET--TTTEEEEECTTSCEE
T ss_pred
                 EEecCCCCCeEEEEecCCCEEEEEECCC----eEeEEECCCCcEEEEEEeC--CCCEEEEEeCCCEEE
                 EeeccCccccccccceeEEEEccCCCcEEEEEEccCCCcEEEEEecCCCcceeeeccccEEEeecCCC
Q ss pred
 Q Fri_Mar_04_23:
               83 LWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                              162 (349)
O Consensus
               162 (349)
                 T Consensus
              207 (677)
              143 LWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQL-GTIIVSGSTEKVLRVWDPRTCAKLMKL-----K
                                                                              207 (677)
T 5cvo A
                 T ss_dssp
T ss_pred
                 EEECCCCcccccCCccceeeeeCCCCCEEEEEEcCC--CCEEEEEeCCCEEEEEe
                 Q ss pred
Q Fri_Mar_04_23:
              163\ \ \text{NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR}
                                                                              241 (349)
 Q Consensus
                              ~~~~~~~~i~~~~~i~~~~~h~~~v~~v~sp~~~~las-s~d~~v~
                                                                              241 (349)
              T Consensus
                                                                              277 (677)
              208 GHTDNVKALLLNR---DGTQCLSGSSDGTIRLWSLGQQ---RCIATYRVHDEGVWALQVNDAF----THVYSGGRDRKIY
T 5cvo A
                                                                              277 (677)
 T ss_dssp
                 CCSSCEEEEECT---TSSEEEEEETTSEEEEEETTTT---EEEEEEECCSSCEEEEEECTTS----CEEEEEETTCEEE
                 CCCCCEEEEEcC---CCCEEEEEecCCEEEEEECCCC---cEEEEEecCCCCEEEEEECCCC---CEEEEE
T ss_pred
Q ss pred
                 242 IFKITEK--LSPLASEESLTNSNMFDNSAD---VDMDAQGRSDSNTEEKAELQS-----NLQVELL
Q Fri Mar 04 23:
                                                                              297 (349)
 Q Consensus
                                                                              297 (349)
              T Consensus
                                                                              354 (677)
              278 CTDLRNPDIRVLICEEKAPVLKMELDRSADPPPAIWVATTKST---VNKWTLKGIHNFRASGDYDNDCTNPITPLCTQPD
T 5cvo A
                                                                              354 (677)
                 EEESSCTTCEEEEEECSSCEEEEEECCSSSSCSEEEEEESSSC--EEEEECTTHHHHHHHCC------CCCSCSSCS
T ss dssp
                 EEECCCCceeeeccCCCceEEEEECCCCCceEEEEEECCCe---EEEEECCCCcceeeccCCCcccccccccCCCCC
T ss pred
Q ss pred
                 eeccCCCceEEEEECCCCCEEEEecCCCCeEEEE
```

```
Q Fri_Mar_04_23: 298 SEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMS 343 (349)
                      298 ----h---i--v--spdg--las-s-D--v-iW------ 343 (349)
..+.+|..|.+++|+||+++++.|+.|++|++....-+.
 O Consensus
                      355 ~~i~g~~~I~~v~~spdg~~Latgs~DG~V~lWdv~sg~~~
 T Consensus
                                                                                   399 (677)
                      355 QVIKGGA-SIIQCHILNDKRHILTKDTNNNVAYWDVLKACKVEDLG 399 (677)
 T 5cvo A
                           EEECBCC-CEEEEECSSTTEEEEEETTCCEEEEETTTTEEEEEEE
 T ss_dssp
                           eEEcCCC-CeEEEEEcCCCCEEEEEcCCCcEEEEECccCcEehhcC
 T ss pred
                                         SCOPe PROTEIN DATA BANK
 No 76
                                                                                           Pub Med
>2ymu_A WD-40 repeat protein; unknown function, two domains; 1.79A {Nostoc punctiforme} SCOP: b.69.4.0 b.69.4.0
 Probab=100.00 E-value=9e-32 Score=254.81 Aligned cols=280 Identities=25% Similarity=0.406 Sum probs=0.0
                           CccCCCcCeEEEEECCCCCEEEEECCCCCEEEEECCCCCceeEeeeccccceEEEEECCCCCCEEEEEECCCCE
 Q ss_pred
 Q Fri_Mar_04_23:
                        2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV
                                                                                                                             81 (349)
                        2 -----h---v---s-d---l-t-s-D--v-iwd------h---v--v--v--v-----las-s-Dg-v
 O Consensus
                                                                                                                             81 (349)
                        ...+.+|...|.+++|+| +|++||+++.|+.|
 T Consensus
                                                                                                                             81 (577)
                        9 RNRLEAHSSSVRGVAFSPDGQTIASASDDKTVKLWNRNGQ----LLQTLTGHSSSVWGVAFSP--DGQTIASASDDKTV
 T 2vmu A
                                                                                                                             81 (577)
 T ss dssp
                           EEEECCCSSCEEEEECTTSSCEEEEETTSEEEEECTTSC----EEEEEECCSSCEEEEEECT-TSSEEEEEETTSCE
                           eeEEecCCCceEEEECCCCCEEEEECCCc-----EEEEEEcCCCCEEEEECC--CCCEEEEEECCCCeE
 T ss_pred
                           EEeeccCccccccccceeEEEEcCCCCcEEEEEEcCCCCcEEEEEecCCCcceeeeccccEEEeecCC
 Q ss pred
 Q Fri_Mar_04_23:
                       82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPP
                                                                                                                           161 (349)
                       82 ~1wd~~~~
                                                          ---v----p-----l----d--i-iwd-----
                                                                                                                           161 (349)
 Q Consensus
                                              +.+..+.|...|.+++|+|+ +..|++++.|+.+++||.......
                           ++||...
                                                          ----v----s-d--g--1----d--v-iw-------
 T Consensus
                       82 ~iw
                                                                                                                           135 (577)
                       82 KLWNRNG-----QLLQTLTGHSSSVRGVAFSPD-GQTIASASDDKTVKLWNRNGQLLQTL-----
 T 2vmu A
                                                                                                                           135 (577)
 T ss dssp
                           EEEETTS-----CEEEEECCCSSCEEEEEECTT-SSEEEEEETTSCEEEEETTCCEEEEE
 T ss_pred
                           EEEECCC-----ceeeeeccccceeeeeeccc--cceeeeeecccceeeee
 Q ss_pred
                           CCCCCeeEEEEccCCCCCceEEecCCc-eEEEEccCCCcEEEEEEccCCCCeeEEEEECCCCCCeEEEEE
 Q Fri_Mar_04_23: 162 ANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRI
                                                                                                                           240 (349)
 Q Consensus
                      162 ~~
                                           {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} {}^{-} 
                                                                                                                           240 (349)
                           .++...+.|+| ++..+++..++ +..+|+.... ....+.+|...|.+++|+|+|
 T Consensus
                      ----v---s-dg----i
                                                                                                                           204 (577)
                      136 TGHSSSVWGVAFSP---DGQTIASASDDKTVKLWNRNGQ----LLQTLTGHSSSVWGVAFSPDG----QTIASASDDKTV
 T 2ymu A
                                                                                                                           204 (577)
                           CCCSSCEEEEECT---TSSCEEEEETTSEEEEECTTSC---EEEEEECCSSCEEEEEECTTS----SCEEEEETTSEE
 T ss_dssp
 T ss pred
                           Q ss_pred
                           Q Fri Mar 04 23: 241 RIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTIL 319 (349)
 O Consensus
                      241 ~vwd~~~~i~~v~spdg~~l 319 (349)
                           ++||....|++++...+.+..
                                                                                ..+++ .....+..+|...|++++|+|+|++|
                      T Consensus
                      205 KLWNRNGQLLQTLTGHSSSVRGVAFSPDGQTIASASDDKT-----VKLWN-RNGQLLQTLTGHSSSVNGVAFRPDGQTI
 T 2ymu A
                           EEECTTSCEEEEECCSSCEEEEECTTSSCEEEEETTSC-----EEEEC-TTSCEEEEECCCSSCEEEEECTTSSEE
 T ss dssp
 T ss_pred
                           EEEcCCCceEEEEcCCcccEEEEECCCCCEEEEEeCCCc-----EEEEc-CCCcEEEEEECCCCCEE
 Q ss_pred
                           EEecCCCeEEEe
 Q Fri_Mar_04_23: 320 SSAGDDGKVRLWK 332 (349)
                      320 as~s~D~~v~iW~ 332 (349)
 Q Consensus
                      ++++.|+.|++|+
278 ~~~~d~~i~~w~ 290 (577)
 T Consensus
                      278 ASASDDKTVKLWN 290 (577)
 T 2ymu_A
                           EEEETTSCEEEEE
 T ss dssp
 T ss pred
                           EEecCCCcEEEe
                                          PDB
 No 77
                                                                            Pub Med
           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=1.3e-31 Score=250.67 Aligned cols=285 Identities=17% Similarity=0.196 Sum probs=0.0
                           CCCCeEEEEEC-----CCCCEEEEEECCCCEEEEEECCCCCceeEeeec----cccceEEEE
 Q ss pred
 Q Fri Mar 04 23:
                        7 GHDDLVHDVVYD-----AHDSSIVAI
                                                                                                                             61 (349)
                        Q Consensus
                                                                                                                             61 (349)
                                                              |++++|++|+.|++|+||+...
                                                                                                              +|...|+++
                          +|.+.|.+++|+
 T Consensus
                      128 ~H~~~V~~v~~s~~
                                                                                                               ~h~~~V~~v
                                                                                                                           202 (514)
                      128 EHDDWVSAVDVLSATSPAGRWSSAANSSAAVQPGQERVLSASYDGLLRIWNASGS----VIATSPSGSHGGHTASIKAA
 T 5cxb_A
                                                                                                                           202 (514)
 T ss dssp
                           ECSSCEEEEEECTTSHHHHHHHTCSSSCCCCTTCCEEEEEETTSC======EEEECCCGGGTSCSSCEEEE
 T ss pred
                           cccCceeeeEeeccccccccccccccccCCCCEEEEEeCCCC=----EEEeecCCcCCCCCCCCCCEEEE
                           EECCCCCCEEEEEeCCCeEEEeeccCcccccccccceeEEEEcCCCCcEEEEEECCCCcEEEEEECCC
 0 ss pred
 Q Fri_Mar_04_23:
                        62 DWASPEYGRIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE
                                                                                                                           141 (349)
                        62 ~~~~~las~s~Dg~v~lwd~~~~~~~v~~~~v~~~~p~~~~l~~~~d~i~iwd~~~
                          T Consensus
                      203 ----l-s-s-d-v-iwd-------h---v--l-s-s-dq-i-iwd---
                                                                                                                           275 (514)
                      203 KFLT---SDRLASAGMDRTVRVWKYTESDHF--TGELKPTLELYGHTGSVDWLDVDGH--SKHILTASADGAIGFWSASK
 T 5cxb A
                                                                                                                           275 (514)
                           T ss dssp
 T ss pred
                           EEEC---CCeEEEEeCCCeEEEEecCCCcc--ccceeEEEEecCcCCCeEEEEEcCC--CCEEEEECCCC
 Q ss_pred
                           CCC-----ceeeecccEEEeecCCCcccceeEEEEcccCCCCCceE-EecCCc
```

```
Q Fri_Mar_04_23: 142 PSD------LRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLA-VSALEQ 190 (349)
O Consensus
            142 ~~~
                                                                      190 (349)
                                                .++...+.++|+| ++..++ +++.++
            276 ~-
                                        -----l~s~sd~
T Consensus
                                                                      339 (514)
            276 ASAPEPDASLLPGAHVSKRRKATSSVSTAQRGPLGLW-----SIHTAPATAAIFDP---RDRTVAYSASQDH
T 5cxb A
               TTCCCCCGGGSTTCCCC-----CEEECCSEEE------CCCSSCEEEEEECS--SCTTEEEEEETTS
T ss_dssp
               T ss pred
               Q ss pred
Q Fri_Mar_04_23:
            191 -AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAP----SIGRWYQLIATGCKDGRIRIFKIT-----EKLSPLASEESLTN
                                                                      260 (349)
            T Consensus
T 5cxb_A
            340 TVRTLDLTTGQVVSTLT----LTHPLLSLSALTRAGTTS----PLLAAGTSARHITMVDPRASSATTSVMTLRGHANKVV 411 (514)
T ss_dssp
               EEEEEETTTCCEEEEEE----CSSCEEEEEEECCTTCSS----CEEEEEETTSCEEEECSSSCSSCC-CEEECCCSSCEE
               EEEEEECCCCcEEEEEe----cCcceeEEEEccCCCCC----CEEEEECCCCcEEEEEEcCCCccEE
T ss_pred
Q ss pred
               ----eeeccCCCceEEEE
Q Fri Mar 04 23: 261 SNMFDNSADV-DMDAQGRSDSNTEEKAELQSNLQVEL-----LSEHDDHNGEVWSV
                                                                      310 (349)
                                                                      310 (349)
Q Consensus
             412 ~l~sp~~~ll~s~s~Dg~----v~iwd~~~~~~~~~h~~V~~v
T Consensus
                                                                      485 (514)
             412 SLSPSPENEYSLVSGSHDGT-----CRVWDLRSVRPATKEEGSLGGVSEPVYVIERESWASKGKKKRPVAGDGCKVFSV
                                                                      485 (514)
T 5cxb A
               EEEECSSCSSEEEEETTSC----EEEEETTCCEECCGGGTSCSEEECEEEEECCHHHHTTTCSSCCGGGTTTCEEEE
T ss_dssp
               T ss_pred
Q ss_pred
               EECCCCCEEEEecCCCeEEEEeccc
Q Fri Mar 04 23: 311 SWNLTGTILSSAGDDGKVRLWKATY 335 (349)
            311 ~~spdg~~las~s~D~~v~iW~~~~
Q Consensus
                                 335 (349)
               +|+ +++|++|+.|++|+||+++.
                -s----i~s-s-D--i~iW----
T Consensus
                                 508 (514)
             486 VWD--KLGIFSGGEDKKVQVNRGRN 508 (514)
T 5cxb A
               EEE--TTEEEEEETTSEEEEEEC--
T ss_dssp
               EeC--CCcEEEEecCceEEEEecCc
T ss pred
No 78
                               NCBI
                                            Pub Med
>4nsx A U3 small nucleolar RNA-associated protein 21; ribosome biogenesis, UTPB complex, 90S preribosome, small
SU processome, protein binding; HET: FLC; 2.10A {Saccharomyces cerevisiae}
          E-value=3e-31 Score=256.38 Aligned_cols=299 Identities=12% Similarity=0.144 Sum_probs=0.0
Q ss_pred
               Q Fri Mar 04 23:
             5 DSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGR-IIASASYDKTVKL
                                                                       83 (349)
              O Consensus
                                                                       83 (349)
               +.+|...|.+++|+|+++++|++|++|++|++||+...
             202 SNEFPDOTTTAEPAPVI.DITAIGTVTGEVIMFNMRKG---KRIRTIKIPOSRISSI.SFRT--DGSSHI.SVGTSSGDI.IF
T 4nsx A
                                                                      275 (684)
T ss_dssp
               CCCCSSCEEEEECSSTTEEEEEESSSEEEEETTTT----EEEEEEECTTCCEEEEEECC--SSSCEEEEETTSCEEE
               T ss pred
               Q ss pred
Q Fri_Mar_04_23:
             84 WEEDPDQEECSGRRWNKLCTLND-S--KGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE-----PSDLR 146 (349)
Q Consensus
             84 wd-----v---p----1----d--i-iwd--------
                                                                      146 (349)
                        +.+..+.. | ...|.+++|+|+|+ +...|++++.|+.+++|++...
                                          -----l-s---d--i--w-------
T Consensus
             276 wd-
             {\tt 276~YDLDRR------SRIHVLKNIHRESYGGVTQATFLNG--QPIIVTSGGDNSLKEYVFDPSLSQGSGDVVVQPPRYLR}
T 4nsx A
                                                                      344 (684)
T ss_dssp
               EETTTT----EEEEEETTSSCGGGTSCSEEEECTT-SSEEEEECSSSEEEEECCC------CCCEEEE
T ss_pred
               EECCCC-----cceEEEecccCCCCCeeEEEEECC--CCEEEEecCCCCEEEEEecCCCccccccCCCcceeE
               eeecccEEEeecCCcccceeEEEEcccCCCCceEEecCCc-eEEEEeccCCcEEEE-----
Q ss_pred
Q Fri_Mar_04_23: 147 SWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVA-------
                                                                      205 (349)
Q Consensus
             205 (349)
            T Consensus
                                                                      409 (684)
             345 SRG-----GHSQPPSYIAFADS--QSHFMLSASKDRSLWSFSLRKDAQSQEMSQRLHKKQDGGRVGGSTIKS
T 4nsx A
                                                                      409 (684)
T ss_dssp
               EEE-----CCSSCEEEEEECCT--TSCEEEEEETTSCEEEEECSTTCCEEECBCC-----
               T ss_pred
               -----EECCCCCCceEEEEECCCCCEE
Q ss pred
Q Fri_Mar_04_23: 206 ------AKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR 241 (349)
               -----h---v--sp-----las-s-d--v-
                                                            ++|++++.|+.|+
                                            .....|...|.+++|+|++
T Consensus
                         -q------s--q-----l--q--dq-i-
                                                                      485 (684)
             410 KFPEIVALAIENARIGEWENIITAHKDEKFARTWDMRNKRVGRWTFDTTDDGFVKSVAMSOCG----NFGFIGSSNGSIT
T 4nsx A
                                                                      485 (684)
T ss dssp
               CCCCEEEEECSTTTTTSCCEEEEETTCSEEEEEETTTTEEEEEEECSSSCCEEEEEECTTS----CEEEEEETTSEEE
T ss_pred
               cCCceEeeccCccccceEEEecCCCeEEEEECCCccceeEeecCCCCcEEEEEE
Q ss_pred
               Q Fri_Mar_04_23: 242 IFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTIL 319 (349)
             242 vwd-----h--i--v--spdg--1 319 (349)
Q Consensus
            T Consensus
                                                                      558 (684)
T 4nsx_A
             486 IYNMQSGILRKKYKLHKRAVTGISLDGMNRKMVSCGLDGI-----VGFYDFNKSTLLGKLKLD-APITAMVYHRSSDLF 558 (684)
```

```
T ss_dssp
                             EEETTTCCEEEEEECCSSCEEEEECTTSCEEEEEETTSE-----EEEEESSSCCEEEEEECS-SCEEEEEETTTTEE
T ss_pred
                             EEECCCCccceeeeccccceeeeeeccccceeeecccccee
                             EEecCCCeEEEEeccCCceEEEEEeeccC
Q ss_pred
Q Fri_Mar_04_23: 320 SSAGDDGKVRLWKATYSNEFKCMSVITAQQ
                                                                        349 (349)
                        320 as-s-D--v-iW-----
                                                                        349 (349)
O Consensus
                             |+++.|+.|+||++... .++..+|.
                                ~~~d~~i~vwd~~~~h~
T Consensus
                        559
                                                                        585 (684)
                        559 ALALDDLSIVVIDAVTQ---RVVRQLWGHS
T 4nsx A
                                                                        585 (684)
                             EEEETTSCEEEEETTTT---EEEEEECCCS
T ss_dssp
                             EEEeCCCeEEEEECCCC---eEEEEEeCCC
T ss pred
                                               PDB"
No 79
                                                                                        Pub Med
            Protein WEB1, protein transport protein SEC31; beta propeller; 3.30A {Saccharomyces cerevisiae}
Probab=100.00 E-value=1e-32 Score=251.08 Aligned_cols=268 Identities=14% Similarity=0.236 Sum_probs=0.0
                             CCCCeEEEEECCCCCEEEEEeCCCceEEEEECCCCCceeEeeeeccccceEEEEECCCCC-CCEEEEEeCCCceEEeee
0 ss pred
Q Fri_Mar_04_23:
                          7 \ \ \mathsf{GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEY-GRIIASASYDKTVKLWE}
                                                                                                                                              85 (349)
                           7 ~h~~~v~~~s~d~~~l~t~s~D~~v~iwd~~~
Q Consensus
                                                                              ----h---v--v---
                                                                                                                  -~~~las~s~Dg~v~lwd
                                                                                                                                             85 (349)
                             T Consensus
                                                                                                                                            142 (416)
                         65 OVDSKFNDLDWSHNNKIIAGALDNGSLELYSTNEANNAINSMARFSNHSSSVKTVKFNA--KODNVLASGGNNGEIFIWD
T 2pm9 A
                                                                                                                                            142 (416)
T ss_dssp
                             CCSSCEEEEECSSSSCEEEEESSSCEEECCSSTTSCCCEEEECCCSSSCCCEEECS--SSTTBEEEECSSSCEEBCB
                             T ss pred
                             ccCcccccccceeEEEEcCCCCcEEEEEECcCCCccEEEEEeCCCCcceEEEE
Q ss pred
O Fri Mar 04 23:
                         86 EDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHL
                                                                                                                                            165 (349)
                                                                        -p----l----d--i-iwd---
O Consensus
                                                                                                                                            165 (349)
                               T Consensus
                                                                          -----l-s---dg-v-iwd-------------
                                                                                                                                            214 (416)
T 2pm9_A
                        143 MNKCTESPSNYTPLTPGOSMSSVDEVISLAWNOSL-AHVFASAGSSNFASIWDLKAKKEVIHLSYTSPN-----SGIK
                                                                                                                                            214 (416)
                             TTTTSSCTTTCCCBCCCCSCCSCCCCEEECSSC-TTEEEEESSSSCEEEEETTTTEEEEEECCCCCS-----SCCC
T ss dssp
                             \tt CCCCcccccCCCCCCCCCCCCCEEEEECCCC-CCEEEEECCCCCEEEEECCCCcceEeecCCcc-----cCCC
T ss pred
Q ss_pred
                             GGeerereggCCCCCGereegCCc----erreegcCCCGreereregcCCCCGeereregcCCCCGerereregcCCCC
Q Fri_Mar_04_23: 166 QSDFCLSWCPSRFSPEKLAVSALEQ----AIIYQRGKDGKLHVAAKL-PGHKSLIRSISWAP-SIGRWYQLIATGCKDGR
                                                                                                                                            239 (349)
Q Consensus
                        166 ~~~
                                           ~~~~las~s~d~~
                                                                                                                                            239 (349)
                                                                    +.+|+..... ....+ .+|...|.+++|+| ++
                                                                                                                          .+|++++.|+.
                                        286 (416)
                        215 QQLSVVEWHPK--NSTRVATATGSDNDPSILIWDLRNANT--PLQTLNQGHQKGILSLDWCHQDE----HLLLSSGRDNT
T 2pm9_A
                                                                                                                                            286 (416)
T ss dssp
                             CCEEEEECSS--CTTEEEEECCSSCCCCEETTSTTS--CSBCCCSCCSCEEEEECSSCS----SCEEEEESSSE
T ss pred
                             CceEEEECCC--CCCEEEEEECCCCCceEEEEeccCCC--cceeeccCcCCEEEEEecCCCC----CeEEEEeCCCCC
Q ss_pred
                             Q Fri_Mar_04_23: 240 IRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG-TI
                                                                                                                                            318 (349)
Q Consensus
                        240 v~vwd~~~~~~~~~~
                                                                                                  318 (349)
                                                                                                        +.+..+.+|...|.+++|+|+| ++
                             |++||+...
                        287 v~iwd~~
T Consensus
                                                                                                                                            320 (416)
                                                                                                                               ~sp~
                                                                                                                                            320 (416)
T 2pm9_A
                        287 VLLWNPESA--
                                                                                                  ----EOLSOFPARGNWCFKTKFAPEAPDL
                             EEEECSSSC------CEEEEEECSSSCCCCEEECTTCTTE
T ss_dssp
T ss pred
                             EEEEccccc-----ceeecccccceEEEEEccccccE
                             EEEecCCCeEEEEeccCCCc
Q ss pred
Q Fri_Mar_04_23: 319 LSSAGDDGKVRLWKATYSNE
                                                           338 (349)
                        319 las~s~D~~v~iW~~~~~
O Consensus
                                                           338 (349)
                             |++++.|++|+||++....
T Consensus
                        321 l~s~s~dg~v~iw~~~~~~
                                                           340 (416)
                        321 FACASFDNKIEVQTLQNLTN
T 2pm9 A
                                                           340 (416)
T ss_dssp
                             EEECCSSSEEEEESCCCCC
T ss pred
                             EEEEeCCCcEEEecCCCCc
                                               PDB"
No 80
                                                                                       Pub Med
            Elongator complex protein 2; ELP2, translation; 3.20A {Saccharomyces cerevisiae S288C}
Probab=100.00 E-value=7.7e-32 Score=264.23 Aligned_cols=321 Identities=12% Similarity=0.144 Sum_probs=0.0
                             0 ss pred
Q Fri_Mar_04_23:
                           2 \ \mathtt{QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTV} \\ 
                                                                                                                                              81 (349)
                           2 \  \  \, \sim \sim \sim \sim h - \sim v \sim v \sim -s - d \sim \sim 1 - t - s - D \sim v \sim iwd - \sim \sim \sim \sim \sim -h \sim \sim v \sim v \sim \sim \sim \sim \sim 1 as - s - Dg \sim v \sim 1 - s \sim 1 
                                                                                                                                              81 (349)
                             T Consensus
                         12 -----gh---v----sp-g--la-g--d--i-vwd-----l--h---v---s----l-s-s-dg-v
                                                                                                                                             87 (792)
                         12 EAIFIGANKQTQVSDIHKVKKIVAFGA-GKTIALWDPIEP-NNKGVYATLKGHEAEVTCVRFVP--DSDFMVSASEDHHV
T 4xfv A
                                                                                                                                             87 (792)
T ss_dssp
                             EEEEECCCSSTTCEEECTTTCCEEEE-TTEEEEECSSCS-SCCCEEEEEECCSSCEEEEECT-TSSEEEEEESSSCE
T ss pred
                             Q ss_pred
                             EEEeccCccccccccccceEEEEcCCCCcEEEEEECcCCCCCEEEEEECCCC------
Q Fri_Mar_04_23:
                         82 KLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE------
                                                                                                                                            141 (349)
                                                                                     ~~1~~~~d~~i~iwd~~~-----
Q Consensus
                         82 ~lwd~~~
                                                                                                                                            141 (349)
                                                                            ~~p~~
                             ++||+.+
                                               +...+.+..+|...|.+++|+|+
                                                                                     .|++++.|+.|++||+.+
T Consensus
                                                                                ~----1~s~~~d~~v~~wd~~~~
                         88 KIWKFTD-----YSHLQCIQTIQHYSKTIVALSALPS----LISVGCADGTISIWRQNIQNDEFGLAHEFTIKKGFFYP 157 (792)
T 4xfv A
T ss dssp
                             EEEEESS-----SSCEEEEEEECCCSSCCCEECCTT----EEEEECTTSEEEEEEECSSSSSEEEEEEECC--CCCE
```

```
T ss_pred
                EEEEccC-----CCcceEEEeecCcCccEEEEEecCC----eEEEEeCCCeEEEEEccCCcccceeeEEEecccccc
                -----CCcceeecccc----EEEeecCCcccceeEEEEcc----cCCCCCceEEecCCc-e
0 ss pred
Q Fri_Mar_04_23: 142 -----PSDLRSWTLTSE----MKVLSIPPANHLQSDFCLSWCP---SRFSPEKLAVSALEQ-A 191 (349)
                               142 ------
                                                                         191 (349)
             T Consensus
                                                                         234 (792)
             158 LCLSLSKVEEKKYLLAIGGTNVNVFIASFILSDSGIEKCRVVAELEGHEDWVKSLAFRHQETPG---DYLLCSGSQDRYI
T 4xfv_A
                                                                         234 (792)
                EEEEEECSSSEEEEEEESSSSEEEEEECCTTSCEEEEEEECCCSSCEEEEEEECSSSS---CEEEEEEESSSCE
T ss dssp
T ss_pred
                eeeeeecCCCceEEEEEcCCCeEEEEEecCCCCcccceeeeEecccccEEEEEEecCCCCC---CcEEEEecCCCCEE
               EEEEecCCCce------EEEEEccCCCceeEEEEEcCCCCce
Q ss pred
Q Fri Mar 04 23: 192 IIYQRGKDGKL------HVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR 241 (349)
          192 ~i~~~~~
                        -----h--v--v--sp-----las-s-d--v-
O Consensus
T Consensus
             235 -iwd------l-s---d--i-
                                                                         310 (792)
T 4xfv_A
            235 RLWRIRINDLIDDSEEDSKKLTLLSNKQYKFQIDDELRVGINFEALIMGHDDWISSLQWHESR----LOLLAATADTSLM
                                                                         310 (792)
                EEEEEECSCCC-----CCCCEEEECSSTTCCEEEEEEECSCSSCCEEEEEECSSS---SCEEEEESSSEEE
T ss_dssp
T ss pred
                Q ss_pred
                Q Fri_Mar_04_23: 242 IFKIT-----EKLSPLASEESLTNSNMFD-NSADVDMDAQGRSDSNTEEKAELQSNLQVELLSE--- 299 (349)
             242 vwd~~-----
Q Consensus
                                                     +||+.
             311 ~wd~~~~~
                            ------v-iw----
T Consensus
                                                                         384 (792)
             311 VWEPDETSGIWVCSLRLGEMSSKGASTATGSSGGFWSCLWFTHERMDFFLTNGKTGS-----WRMWATKDNIICDQRLG 384 (792)
T 4xfv_A
T ss dssp
                EEECC--CCSCEEEEEEC------CCCCCCC
                EEeCCCCccceeecccccccccccccccccccceeecccCcEEEEEeCCCCCEEEEEeCCCCcceeeecc
T ss_pred
Q ss_pred
                ccCCceEEEEECCCCCEEEEecCCCeEEEEecccC-----cEEEEEEeeccC
Q Fri_Mar_04_23: 300 HDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSN-----EFKCMSVITAQQ 349 (349)
O Consensus
             300 ~~h~~i~v~~spdg~~las~s~D~~v~iW~~~~~~-----
                                                          349 (349)
               T Consensus
                                                          443 (792)
             385 ISGATKDVTDIAWSPSGEYLLATSLDQTTRLFAPWIYDASGRKREIATWHEFSRPQIHG 443 (792)
T 4xfv A
                BCCBSSCEEEEECTTSSCEEEEETTSCEEEEEECCCTTSSCCSSCEEEEEEECCS
T ss_dssp
T ss_pred
                ccCCCCceEEEECCCCCEEEEecCCCCCEEEEccCccCcccceeEEEeecccccc
No 81
                         PDB"
                                        Pub Med
>3odt_A Protein DOA1; ubiquitin, nuclear protein; HET: MSE MES; 1.35A {Saccharomyces cerevisiae}
Probab=100.00 E-value=1.7e-31 Score=234.17 Aligned cols=282 Identities=17% Similarity=0.182 Sum probs=0.0
                Q ss_pred
Q Fri_Mar_04_23:
             1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                          80 (349)
              1 -----h---v---s-d---l-t-s-D--v-iwd------h---v-v--v--v-----las-s-Dg-
O Consensus
                                                                          80 (349)
             T Consensus
                                                                          82 (313)
T 3odt A
              10 LSATLKGHDQDVRDVVAVDD-SKVASVSRDGTVRLWSKDDQ----WLGTVVYTGQGFLNSVCYDS--EKELLLFGGKDTM
                                                                          82 (313)
                T ss_dssp
                EEEEEECCCCEEEEEECCC-CEEEEEeCCCC----eeeeEEecCCceEEEEECC--CCCEEEEecCCCc
T ss_pred
Q ss pred
               EEEeeccCccccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEEcCCCCcceeeeccccEEEeecC
Q Fri_Mar_04_23:
             81 VKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                         160 (349)
              160 (349)
                +++|++.. ....+.+.+|...|.+++|+.. .|++++.|++|++|++....+.
T Consensus
              83 i-----l-gh---v-----l-gs-s-D--v-iW-------
                                                                         139 (313)
             83 INGVPLFA-----TSGEDPLYTLIGHOGNVCSLSFODG----VVISGSWDKTAKVWK--EGSLVYNLO------
T 3odt A
                                                                         139 (313)
              EEEEETTC-----CTTSCC-CEECCCSSCEEEEEETT----EEEEEEETTSEEEEEE--TTEEEEEEE
T ss dssp
T ss_pred
                ceeEccc-----CCCCceeEEEcccC----EEEEEcCCCCEEEEe---CCCeEEEE
                CCcccceeEEEEccCCCCceEEEcCCc-eEEEEecCCccEEEEEEccC-CCceeEEEEEccCCccceEEEEE
Q ss pred
Q Fri_Mar_04_23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPG-HKSLIRSISWAPSIGRWYQLIATGCKDG 238 (349)
                   238 (349)
Q Consensus
             161 ~~~
                 ---v----1-s---d-
T Consensus
                                                                         205 (313)
T 3odt_A
             140 --AHNASYWDAKYVSF--SENKFLTASADKTIKLWOND----KVIKTFSGIHNDVVRHLAVVDD----GHFISCSNDG
                                                                         205 (313)
               --CCSSCEEEEEET--TTTEEEEEETTSCEEEEETT----EEEEEECSSCSSCEEEEEEET----TEEEEEETTS
T ss dssp
                --CCCCcEEEEEEc--CCCeEEEEeCC-----CccceeccCCCceEEEEcCC-----CeEEEEcCCC
T ss pred
Q ss_pred
                Q Fri_Mar_04_23: 239 RIRIFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG 316 (349)
Q Consensus
             239 ~v~vwd~~~=-~~~h~~i~v~~spdg 316 (349)
               206 ~i~iwd~~~~~~h~~~v~~~~~1~s~s~D~~~~~v~iWd~~~~~~~
T Consensus
T 3odt_A
             206 LIKLVDMHTGDVLRTYEGHESFVYCIKLLPNG-DIVSCGEDRT-----VRIWSKENGSLKQVITLPAISIWSVDCMSNG
T ss_dssp
                EEEEEETTTCCEEEEEECCSSCEEEEECTTS-CEEEEETTSE-----EEEECTTTCCEEEEEEECSSSCEEEEEECTTS
                eEEEEECCCCCEEEEEcCCcceEEEEEccCC-CEEEEecCCE-----EEEEEECCCCeeEEEEEccCCccEEEEEecCCC
T ss_pred
               CEEEEecCCCeEEEEecc
Q ss pred
Q Fri_Mar_04_23: 317 TILSSAGDDGKVRLWKAT 334 (349)
            317 ~~las~s~D~~v~iW~~~ 334 (349)
```

```
+ +++|+.|++||||+.+
 T Consensus
                      279 ~-~~~s~D~~i~iw~~~ 295 (313)
                      279 D-IIVGSSDNLVRIFSQE 295 (313)
 T 3odt A
                           C-EEEETTSCEEEESC
 T ss dssp
 T ss_pred
 No 82
                                        SCOPe
                                                       PDB
                                                                   NCBI
                                                                                          Pub Med
                                                                                 >2ymu_A WD-40 repeat protein; unknown function, two domains; 1.79A {Nostoc punctiforme} SCOP: b.69.4.0 b.69.4.0
 Probab=100.00 E-value=2.7e-31 Score=251.54 Aligned cols=279 Identities=25% Similarity=0.432 Sum probs=0.0
                           Q ss_pred
 Q Fri Mar 04 23:
                        3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                                                                           82 (349)
 O Consensus
                        3 ----h---v--v---s-d---l-t-s-D--v-iwd-------h---v--v-v-v-----las-s-Dq-v-
                                                                                                                            82 (349)
                           T Consensus
                                                                                                                          369 (577)
                      297 OTLTGHSSSVWGVAFSPDGOTIASASDDKTVKLWNRNGO-----HLOTLTGHSSSVWGVAFSP--DGOTIASASDDKTVK
 T 2ymu_A
                                                                                                                          369 (577)
                           EEECCCSSCEEEEECTTSSEEEEEETTSCEEEEETTSC-----EEEEECCCSSCEEEEEECT--TSSEEEEEETTSEEE
 T ss dssp
                           EEecCCCCcEEEEEcCCCCEEEEEcCCCc----EeEEEcCCCCcEEEEECC--CCCEEEEECCCCCEE
 T ss pred
 Q ss_pred
                           Q Fri_Mar_04_23:
                       83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                                                                          162 (349)
 Q Consensus
                       83 lwd~~~
                                                         ~~v~~~
                                                                 --p----l----d--i-iwd------
                                                                                                                          162 (349)
                                             +||...
 T Consensus
                      370
                                                         ---v---s-d--g--l----d--i--wd------
                                                                                                                          423 (577)
                      370 LWNRNG-----QLLQTLTGHSSSVRGVAFSPD--GQTIASASDDKTVKLWNRNGQLLQTLT------
                                                                                                                          423 (577)
 T 2ymu A
 T ss dssp
                           EEETTC-----CEEEEECCSSCEEEEECTT-SSCEEEEETTSEEEEECTTCCEEEEEE.-----
                           EECCCC-----ceeeeccccceeeeccc-cceeeeccccceeehh------
 T ss pred
 Q ss_pred
                           \verb|ccccee| EEE | cccccccccee| EEEE | ccccccee| EEEE | ccccccccee| EEEE | ccccccee| EEEE | ccccccccee| EEEE | cccccccee| EEEE | ccccccccee| EEEE | ccccccccee| EEEE | cccccccee| EEEEE | cccccccee| EEEEE | cccccccee| EEEEE| Ccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Ccccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Ccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Ccccccccccee| EEEEE| Cccccccee| EEEEE| Ccccccccee| EEEEE| Ccccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Cccccccee| EEEEE| Ccccccee| EEEEE| Ccccccee| EEEEE| Cccccccee| EEEEE| Ccccc
 Q Fri Mar_04_23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIR
                                                                                                                          241 (349)
                      163 -----h---y--y--sp------las-s-d--y-
                                                                                                                          241 (349)
 O Consensus
                           .+...+..+|+| ++..+++..++ +.+|+.... ....+.+|...|.+++|+|+|
                                      --s---d---l----d--i--wd-----
                                                                                       ~~v~~~s~dg----~l~~~~d~~v~
 T Consensus
                                                                                                                          492 (577)
                      424 GHSSSVWGVAFSP---DDQTIASASDDKTVKLWNRNGQ----LLQTLTGHSSSVRGVAFSPDG----QTIASASDDKTVK
 T 2ymu_A
                                                                                                                          492 (577)
 T ss_dssp
                           CCSSCEEEEECT---TSSEEEEEETTSEEEEEETTSC----EEEEEECCSSCEEEEEECTTS----CEEEEEETTSEEE
                           CCCCCEEEEECC---CCCEEEEECCCCCEEEEeCCCC----EEEEECCCCCEEEEEECCCC----CEEEEEECCCCEE
 T ss pred
 Q ss pred
                           242 IFKITEK-LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILS
 Q Fri Mar 04 23:
 O Consensus
                      242 vwd-----h---i--v--spdg--la
                                                                                                                          320 (349)
                           +||....|++++++++++++
                                                                               ..+|+. ..+.+..+|...|++++|+|||++|+
 T Consensus
                      493 iw-----s-dg--1-s---d----i--w------v-----v----s-dg--1-
                                                                                                                          565 (577)
                      493 LWNRNGQLLQTLTGHSSSVRGVAFSPDGQTIASASDDKT-----VKLWNR-NGQLLQTLTGHSSSVWGVAFSPDGQTIA
 T 2ymu A
                                                                                                                          565 (577)
                           EEETTSCEEEEEECCSSCEEEEEECTTSSCEEEEETTSE-----EEEECT-TSCEEEEEECCSSCEEEEEECTTSSCEE
 T ss dssp
 T ss_pred
                           EECCCcceeeecCCcccEEEEECCCCCEEEEEeCCCc-----EEEEcC-CCCEEEEEECCCCCEEE
 Q ss pred
                           EecCCCeEEEEe
 Q Fri Mar 04 23: 321 SAGDDGKVRLWK 332 (349)
                      321 s~s~D~~v~iW~
                                          332 (349)
 Q Consensus
                           +++.|++|+
                      566 s~~~d~~v~~w~
                                           577 (577)
 T Consensus
                      566 SASSDKTVKLWN
 T 2ymu A
                                           577 (577)
 T ss dssp
                           EEETTSCEEEEC
 T ss_pred
                                          PDB<sup>N</sup>
 No 83
                                                                           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
  3cfv
 Probab=100.00 E-value=3.3e-32 Score=249.14 Aligned cols=272 Identities=20% Similarity=0.332 Sum probs=0.0
                           CCCCeEEEEECC-CCCEEEEEECCC------CCCceeEeeeeccccceEEEEECCCCCCEEEEEECCC
 Q ss pred
 Q Fri_Mar_04_23:
                        7 \ \ \mathsf{GHDDLVHDVVYDF} - \mathsf{YGRHVATCSSDQHIKVFKLDK} ---- - \mathsf{DTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDK}
                                                                                                                           79 (349)
                        7 ~h~~~v~~~s~-d~~l~t~s~D~~v~iwd~~~-----h~~~v~v~~v~~v~~v~~~las~s~Dg
 Q Consensus
                                                                                                                           79 (349)
                      T Consensus
                                                                                                                          204 (430)
 T 2xvi A
                      126 NHEGEVNRARYMPQNACVIATKTPSSDVLVFDYTKHPSKPEPSGECQPDLRLRGHQKEGYGLSWNPN-LNGYLLSASDDH
                                                                                                                          204 (430)
 T ss_dssp
                           EESSCCSEEEEETTEEEEEEECSSSCEEEEEGGGSCSSCCTTCCCCCSEEEECCSSCCCCEEECTT-STTEEEEECTTS
 T ss_pred
                           eEEEeeccCcccccccceeEEEEcCCCCcEEEEEEcCCCCcEEEEEECCC---CCcceeeecccEEE
 Q ss_pred
 O Fri Mar 04 23:
                       80 TVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALE---PSDLRSWTLTSEMKV
                                                                                                                          156 (349)
                           O Consensus
                       80 ~v~lwd~~~~~~~
                                                                                                                          156 (349)
 T Consensus
                      205 -i-lwd-------h---v--v--v----i-s---dg-i-iwd--------
                                                                                                                          274 (430)
 T 2xyi_A
                      205 TICLWDINATPKE--HRVIDAKNIFTGHTAVVEDVAWHLLH-ESLFGSVADDOKLMIWDTRNNNTSKPSHTVD-----
                                                                                                                          274 (430)
 T ss dssp
                           CEEEEETTSCCBG--GGEEECSEECCCSSCEEEEECSSC-TTEEEEEEETTSEEEEEETTCSCSSSCSEEEE-----
                           T ss pred
 Q ss pred
                           eecCCCccceeEEEEcccCCCCceEEecCCc-eEEEEEccCCccEEEEEEccCCCcceeEEEEEc
 Q Fri Mar 04 23: 157 LSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGC 235 (349)
```

```
O Consensus
               157 ~~~~
                     .+...+.+|+|. ....++++++++++++|+..... .+..+.+|...|.+++|+|+|++.
               275 -----h---v--latg--dg-i-iwd------h---v--l--sp------h---v
T Consensus
                                                                                    341 (430)
               275 -----AHTAEVNCLSFNPY-SEFILATGSADKTVALWDLRNLKL--KLHSFESHKDEIFQVQWSPHNE---TILASSG
T 2xvi A
                                                                                    341 (430)
                  ----CCSSCEEEEECSS--CTTEEEEEETTSEEEEETTCTTS--CSEEEECCSSCEEEEECSSCT---TEEEEEE
T ss_dssp
                  ----ccccceeeeeccc--cceeeeecccc--cceeeeccccc--cceeeeccccc--ceeeecccc---ceeeee
T ss pred
Q ss pred
                  Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLT
                                                                                    315 (349)
Q Consensus
                                                                       -h---i--v--spd
                                                                                    315 (349)
T Consensus
               342 ~Dg~v~iwd~~~~-
                                _____h~~v~~~
                                                                                    389 (430)
               342 TDRRLHVWDLSKI------GEEQSTEDAEDGPPELLFIHGGHTAKISDFSWNPN
T 2xyi A
                                                                                    389 (430)
T ss_dssp
                  TTSCCEEEEGGGT-----TCCCCHHHHHHCCTTEEEECCCCSSCEEEEEECSS
T ss_pred
Q ss_pred
                  CC-EEEEecCCCeEEEEecc
Q Fri_Mar_04_23: 316 GT-ILSSAGDDGKVRLWKAT 334 (349)
Q Consensus
               316 g~-~las~s~D~~v~iW~~~
                                    334 (349)
                  ++ . | ++++. | +. | + | | | ++.
               390 ~~~~l~s~s~dg~v~iw~~~
T Consensus
                                    409 (430)
T 2xyi_A
               390 EPWIICSVSEDNIMQVWQMA 409 (430)
T ss_dssp
                  STTEREFFETTSFFFFFFC
                  CCCEEEEeCCCCEEEEeCc
T ss pred
No 84
                            SCOPe
>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=5.5e-32 Score=246.11 Aligned_cols=255 Identities=18% Similarity=0.283 Sum_probs=0.0
                  Q ss_pred
Q Fri_Mar_04_23:
                                                                                    129 (349)
                50 SWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLG
Q Consensus
                50 ----h---v--v--v-----las-s-Dg-v-lwd------
                                                                 ----v----p-----1--
                                                                                    129 (349)
                  .+.+|..+|++++|+| ++.+|+||+.|++||+.++.
T Consensus
               103 ~l~gH~~~V~~v~~p-~~~~l~s~s~bg~i~vwd~~~~~~l~s~s~blacks
                                                                                    169 (410)
               103 ALSGHRSPVTRVIFHP--VFSVMVSASEDATIKVWDYETGDF-----ERTLKGHTDSVQDISFDHS--GKLLASCS
T lvyh_C
T ss_dssp
                  EEECCSSCEEEEECS--SSSEEEEEESSSCEEEEETTTCCC-----CEEECCCSSCEEEEEECTT--SSEEEEEE
T ss pred
                  EccCCCCEEEEECC--CCCEEEEECCCCEEEEECCCCE-----EEEEecccCcEEEEEEccC--CCEEEEEc
Q ss_pred
                  CCCeEEEECCCCCcceeeeccccEEEeecCCCcccceeEEEEcccCCCCcceEEecCCc-eEEEEecCCCcEEEEEEc
Q Fri Mar 04 23: 130 NDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKL
                                                                                    208 (349)
O Consensus
               130 -d--i-iwd------i----i-----i------i-------
                                                                                    208 (349)
                  . | ++ | ++ | | + . + . . . + . . +
                                       .+|...+.++|+| ++..++++.++ +++|+..... ++..+
               230 (410)
T Consensus
               170 ADMTIKLWDFQGFECIRTM------HGHDHNVSSVSIMP---NGDHIVSASRDKTIKMWEVQTGY---CVKTF
T lvyh_C
                  TTSCCCEEETTSSCEEECC-----CCCSSCEEEEEECS--SSSEEEEEETTSEEEEEETTTCC--EEEEE
T ss dssp
                  T ss_pred
Q ss_pred
                  Q Fri Mar_04 23: 209 PGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK-LSPLASEESLTNSNMFDNS------
                                                                                    267 (349)
               209 ~h~~~v~vsp~~~~las-s-d~v~vwd~~~~
.+|..|+++|+|++ .+|++|+.|++|+|+.....|+++
231 ~-h~~v~v~~g----1-s-s-D~v~vwd~~~~~l~h~~v~~~p~~~~~p~~~~~~
Q Consensus
T Consensus
                                                                                    306 (410)
               231 TGHREWVRMVRPNQDG----TLIASCSNDQTVRVWVVATKECKAELREHRHVVECISWAPESSYSSISEATGSETKKSGK 306 (410)
T lvyh_C
                  ECCSSCEEEEECTTS----SEEEEEETTSCEEEEETTTCCEEEEEECCCSSCEEEEEECCCSGGGGGGCCSCC----
T ss_dssp
T ss pred
                  0 ss pred
Q Fri_Mar_04_23: 268 -ADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYSNEFKCMSVIT
                                                                                    346 (349)
               T Consensus
                                                                                    377 (410)
               307 PGPFLLSGRDKT-----IKMWDVSTGMCLMTLVGHDNWVRGVLFHSGGKFLLSCADDKTLRVWDYKNK---RCMKTLN
T 1vyh C
                                                                                    377 (410)
                  -CCEEEEETTSE----EEEEETTTEEEEEEECCSSCEEEEEECSSSCEEEEETTTEEEEECCTTS---CCCEEEE
T ss dssp
                  CCCEEEEECCCCe====--EEEEECCCCEEEEEECCCCCEEEEEECCCCCeEEEEECCCC---eEEEEEC
 T ss pred
Q ss pred
                  CCC
Q Fri Mar 04 23: 347 AQQ 349 (349)
               347 ~~
O Consensus
                      349 (349)
T Consensus
               378 ~h~
                      380 (410)
T 1vyh_C
               378 AHE
                     380 (410)
T ss dssp
                  CCS
T ss pred
                  CCC
No 85
                                                    Pub Med
>4ggb 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=3e-31 Score=235.09 Aligned_cols=250 Identities=15% Similarity=0.167 Sum_probs=0.0
Q ss_pred
                  CCCCeEEEEECCCCCEEEEEECCCCCceeEeeeccccceEEEEECCCCCCEEEEEecCCCcCeEEEeec
```

```
Q Fri_Mar_04_23:
              7 GHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLWEE
                                                                            86 (349)
O Consensus
               7 ~h~~~v~~~~s~d~~~l~t~s~D~~v~iwd~~~~~~~h~~~v~~v~~v~~~~~las~s~Dq~v~lwd~
                                                                            86 (349)
                --v----dg-i-vwd-
T Consensus
                                                                            156 (344)
              80 QTEAGVADLTWVGERGILV-ASDSGAVELWELDENETLIVSKFCKYEHDDIVSTVSVLS--SGTQAVSGSKDICIKVWDL
T 4gqb_B
                                                                            156 (344)
                EESSCEEEEEETTTEEEE-EETTSEEEEEEECTTSSCEEEEEEECCSSCEEEEECT-TSSEEEEEETTSCEEEEET
T ss_dssp
                CCCCCEEEEEeCCCCCEEE-eCCCCEEEEEECCCCCceeeeeeecccCCCccEEEEEeC--CCCeEEEEECCCCEEEEEC
T ss pred
                \verb|ccccccccceeEEEEccCCCceEEEEECcCCCc-EEEEEECcCCCcceeeecccEEEeecCCCccc| \\
Q ss pred
Q Fri_Mar_04_23:
              87 \quad DPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGL-KLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHL
                                                                            165 (349)
                    87 ~~~
              214 (344)
T Consensus
T 4gqb B
              157 AQQ------SAPG 214 (344)
T ss_dssp
                CCC-----eeeeEecCCCCCEEEEEecC--CCCEEEEEECCCCCCceeEEe-----eccC
T ss_pred
                cceeEEEEcccCCCcceEEecCCc-eEEEEecCCCcEEEEEEccCCCcceeEEEE
Q ss_pred
Q Fri Mar 04 23: 166 QSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFK
                                                                            244 (349)
                   -----h---v--sp-----las-s-d--v-vwd
                                                                            244 (349)
Q Consensus
                T Consensus
              215 ~i~~~~s~~~l~~~d~~i~i~d~~_~~v~d~~i~i~d~~~
                                                                            286 (344)
              215 YLPTSLAWHPQ--QSEVFVFGDENGTVSLVDT---KSTSCVLSSAVHSQCVTGLVFSPHSV---PFLASLSEDCSLAVLD
T 4gqb B
                                                                            286 (344)
                CCEEEEECSS--CTTEEEEEETTSEEEEES---CC--CCEEEECCSSCEEEEEECSSSS---CCEEEEETTSCEEEEC
T ss_dssp
                CCeeeEECCCC--CCEEEEEECCCEEEEEeC---CCCcceeEecccCCCEEEEEECCCC---CEEEEEeCCCEEEEE
T ss_pred
Q ss_pred
                Q Fri Mar 04 23: 245 ITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILS-SAG
                                                                            323 (349)
                                                       ----h---i--v--spdg--la-s-s
Q Consensus
              245
                                                                            323 (349)
                                                     .+..+.+|...|.+++|+|+|+++++
              287 ~-
T Consensus
T 4gqb_B
              287 SSLS-----ELFRSQAHRDFVRDATWSPLNHSLLTTVG
                                                                            319 (344)
                TTCC-----EEEEECCCSSCEEEEECSSSTTEEEEE
T ss_dssp
                CCCc-----cceEecCCccEEEEEe
T ss pred
                CCCeEEEEecccC
Q ss pred
 Q Fri_Mar_04_23: 324 DDGKVRLWKATYS 336 (349)
Q Consensus
             324 ~D~~v~iW~~~~~
                           336 (349)
                . | + . | ++ | ++ . . .
T Consensus
              320 ~dg~i~iw~~~~ 332 (344)
             320 WDHQVVHHVVPTE 332 (344)
T 4gqb B
T ss_dssp
                TTSCEEEEECCC-
T ss_pred
                CCCEEEEECCCC
                         PDB"
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=3.5e-31 Score=240.93 Aligned cols=277 Identities=15% Similarity=0.190 Sum probs=0.0
                Q Fri_Mar_04_23:
              1 MQPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                            80 (349)
               1 -----h---v---s-d---l-t-s-D--v-iwd------h---vh---v-v-v--v----las-s-Dg-
Q Consensus
                                                                            80 (349)
              ....+.+|...|++++|+| ++++|++++.|+.
T Consensus
              100 LSASSGKTTNQVTCLAWSHDGNSIVTGVENGELRLWNKTGA----LLNVLNFHRAPIVSVKWNK--DGTHIISMDVENV
T 1r5m A
                                                                            172 (425)
T ss_dssp
                CC-----CBCEEEEECTTSSEEEEEETTSC----EEEEECCCCSCEEEEEECT-TSSEEEEEETTCC
T ss_pred
                hhhhhhacCCCeeeeeecCCCCeeeeecCCCceeeeecCCCC-----eeeeecCCCCCeeeeeecC--CCCeeeeecCCCC
Q ss_pred
                EEEeeccCcccccc------cceeEEEEcCCCcEEE
 Q Fri_Mar_04_23:
              81 VKLWEEDPDQEECSGR------RWNKLCTLNDSKGSLYS
                                                                            113 (349)
              81 v-lwd-----v----v--
Q Consensus
                                                                            113 (349)
                                                      ..+.+..+..|...|.+
----g-i---d------i---
                |++||+.++.....
             173 i~iwd~~~~
T Consensus
                                                                            252 (425)
             173 TILWNVISGTVMQHFELKETGGSSINAENHSGDGSLGVDVEWVDDDKFVIPGPKGAIFVYQITEKTPTGKLIGHHGPISV
T 1r5m A
 T ss_dssp
                EEEEETTTTEEEEEECCC-----CCCBSCCEEEETTEEEEECGGGCEEEEETTCSSCSEEECCCSSCEEE
                EEEEECCCCceeeeeecccCccceeecccCCccEEEEEcCCCcEEEEEccCCcEEeeeccCCCceeE
T ss_pred
                EEECcCCCccEEEEEcCCccceeeeccccEEEeecCCcccceeEEcccCCCcccceEEecCcc-eE
Q ss pred
Q Fri_Mar_04_23: 114 VKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AI 192 (349)
             114 ----p-----l-----d--i-iwd------
                                                                            192 (349)
                ~~~~l~~~~dg~i~i~d~~~~~d~~i~
T Consensus
             253 ~~
                                                                            313 (425)
             253 LEFNDT--NKLLLSASDDGTLRIWHGGNGNSONCF-----YGHSOSIVSASWVG----DDKVISCSMDGSVR
T 1r5m A
                                                                            313 (425)
 T ss_dssp
                EEEETT--TTEEEEEETTSCEEEECSSSBSCSEEE------CCCSSCEEEEEET---TTEEEEEETTSEEE
T ss_pred
                EEECCC--CCEEEEEeCCCCEEEEEECCCccccch------hcccceEEEEEcC----CCeEEEEeCCCcEE
                Q ss pred
Q Fri Mar_04 23: 193 IYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDM 272 (349)
              Q Consensus
                              +|+....
T Consensus
              314 i-d-----
             314 LWSLKQN---TLLALSIVDGVPIFAGRISQDG----QKYAVAFMDGQVNVYDLKKLNSKSRSLYGNRDGILNPLPIPL-- 384 (425)
T 1r5m A
```

```
T ss_dssp
                EEETTTT--EEEEEEECTTCCEEEEEECTTS---SEEEEEETTSCEEEEECHHHHC------CEECCE-
T ss_pred
                ccccccccccccccccccccccceeeeeccCCCceEEEEECCCCCEEEEecc
Q ss_pred
 Q Fri_Mar_04_23: 273 DAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKAT 334 (349)
             273 -----h--i--v-igdq--las-s-D--v-iW--- 334 (349)
 Q Consensus
                                T Consensus
                                                              424 (425)
                      -----YASYQSSQDNDYIFDLSWNCAGNKISVAYSLQEGSVVAIP 424 (425)
T 1r5m_A
                 -----EEEECCTTCCCCEEEEEECTTSSEEEEEESSSCCEEECC
 T ss_dssp
                      -----ceeeccccCCceeEEEEcCCCceEEEEeccCCEEEEecC
T ss pred
                                 NCBI
                         PDB<sup>™</sup>
PROTEIN DATA BANK
No 87
                                              Pub Med
       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=3.4e-31 Score=233.47 Aligned_cols=272 Identities=16% Similarity=0.196 Sum_probs=0.0
                Q ss pred
 Q Fri Mar 04 23:
               3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVK
                                                                            82 (349)
               O Consensus
                                                                            82 (349)
                36 ~~~~
T Consensus
                                                                           110 (326)
T 4jsn D
              36 RTVQHQDSQVNALEVTPDRSMIAAAGYQ-HIRMYDLNSNNPN--PIISYDGVNKNIASVGFHE--DGRWMYTGGEDCTAR
                                                                           110 (326)
                EEEECTTSCCCEEEECTTSSEEEEECBS-CEEEEESSSCSCC--CSEEECCCCSBEEEEEECT--TSSEEEEEETTSEEE
 T ss_dssp
T ss_pred
                EEecCCCCCEEEEECCCCCceEEECCCC-cEEEEECCCCCc--ceEecccCCceeEEEEcc--CCCEEEEEcCCCEEE
0 ss pred
                \texttt{EeeccCccccccceeEEEEccCCCceeEEEEcccCCcceeEEEEecccccceeeeccceEEEeecccc}
Q Fri_Mar_04_23:
              83 LWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPA
                                                                           162 (349)
              83 lwd-----
                                  ----v----p-----l-----d--i-iwd------
                +||+.+...
                             ...+..|..+|.++|+|+ +..++++.|+.|++||+++......
             T Consensus
                                                                           167 (326)
T 4jsn D
                                                                           167 (326)
T ss dssp
                EEETTSCCSS-----SEEEECSSCEEEEECTT--SSEEEEEETTSCEEEEETTTCCEEEEC------S
 T ss pred
                EEECCCCcee-----EEEeeccCCcEEEEEcCC--CCEEEEECCCCceeEec-----
Q ss_pred
                GCCCGeEEEECCCCCCCGEEECCCG-EEEEECCC-----CGEEEEEECCCCCCGeEEEEECCCCCCCGEEEEEECC
Q Fri Mar 04 23: 163 NHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKD----GKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCK
                                                                           236 (349)
              163 -----h--v--v-sp-----las-s
Q Consensus
                                                                           236 (349)
             T Consensus
                                                                           240 (326)
              168 EPEVSITSAHIDP---DASYMAAVNSTGNCYVWNLTGGIGDEVTQLIPKTKIPAHTRYALOCRFSPDS---TILATCSA
T 4jsn_D
                                                                           240 (326)
T ss dssp
                STTSCEEEEECT---TSSEEEEEETTSCEEEEEECCCGGGSCCCEEEEEECCCSSCEEEEECTTS----SEEEEEET
                T ss pred
Q ss pred
                Q Fri_Mar_04_23: 237 DGRIRIFKITEK-----LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGE
                                                                           306 (349)
Q Consensus
              237 d~~v~vwd~~~~~
                                                                  ~~~~~h~~~
                                                                           306 (349)
                 |++|++||+...
              T Consensus
              241 DQTCKIWRTSNFSLMTELSIKSGNPGESSRGWMWGCAFSGDSQYIVTASSDNL----ARLWCVETGEIKREYGGHQKA
T 4jsn D
                                                                           314 (326)
T ss_dssp
                TTEEEEEETTTCCEEEEEECCCSSTTSCCCCCEEEEEECTTSSEEEEEETTSE-----EEEEETTTCCEEEEEECCSSC
T ss_pred
                CCeEEEECCCCceeeeeeccCCCCccceEEEEECCCCCEEEEccCCCC-----EEEEEccCCceeeeecCccce
Q ss_pred
                EEEEECCC
Q Fri_Mar_04_23: 307 VWSVSWNLT 315 (349)
O Consensus
             307 i~~v~~spd 315 (349)
                |++|+|+|.
             315 V~~v~f~~~
T Consensus
                        323 (326)
             315 VVCLAFNDS 323 (326)
T 4jsn D
                EEEEEEEC
T ss_dssp
T ss_pred
                EEEEEecCc
                          PDB
No 88
                                 NCBI
                                               Pub Med
>5a9q_2 Nucleoporin NUP37; transport protein; 23.00A {Homo sapiens}
Probab=100.00 E-value=7.1e-32 Score=237.09 Aligned_cols=285 Identities=14% Similarity=0.212 Sum_probs=0.0
Q ss_pred
                CCCCeEEEEECC----CCCEEEEEeCCCeE----EEEECCCCCC--ceeEeeeecccceEEEEEEcCCCCCC---
Q Fri_Mar_04_23:
               7 GHDDLVHDVVYDF----YGRHVATCSSDQHI----KVFKLDKDTS--NWELSDSWRAHDSSIVAIDWASPEYGR----
                                                                            70 (349)
O Consensus
               7 ~h~~~v~~~s~~---d~~~l~t~s~D~~v----iwd~~~~~~h~~~v~~v~~v~~~v~~~~~~----
              T Consensus
                                                                            90 (326)
T 5a9q_2
              14 DCEDYVHVVEFNPFENGDSGNLIAYGGNNYVVIGTCTFQEEEADVEGIQYKTLRTFH-HGVRVDGIAWSP--ETRLDSLP
                                                                            90 (326)
                T ss dssp
T ss_pred
                Q ss pred
                ---EEEEEeCCCeEEEeeccCcccccccccceeEEEEcCCCCcEEEEEECc-CCCCcEEEEEECCCCcce
              71 ---IIASASYDKTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAP-AHLGLKLACLGNDGILRLYDALEPSDLR
                                                                           146 (349)
Q Fri_Mar_04_23:
              146 (349)
Q Consensus
              ....+..+..+|...|.+++|+| + +..|++++.|+.|++||+ +.....
T Consensus
                                                      160 (326)
              91 PVIKFCTSAADMKIRLFTSD-----LQDKNEYKVLEGHTDFINGLVFDPKE--GQEIASVSDDHTCRIWNL-EGVQTA 160 (326)
T 5a9q 2
```

```
T ss_dssp
                 EEEEEEEETTSCEEEEEET-----TTEEEEECTTTSCSSCEEEEEEEESS-SEEEEEEETTSEEEEEEE-TTTEEE
T ss_pred
                 CCPEREEPOCCEEERPOC------CCCCCCCCCPPCCCCCPPCCCC--CCEREEPCCCCCREEPOCCCCCP
                 Q ss_pred
 Q Fri_Mar_04_23: 147 SWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIG
                                                                                225 (349)
              147 -----h---v--y--sp---
 Q Consensus
                                                                                225 (349)
                  161
T Consensus
                                                                                220 (326)
              161 HF-----VLHSPGMSVCWHPE-ETFKLMVAEKNGTIRFYDLLAQQ--AILSLESEQVPLMSAHWCLKN-
                                                                                220 (326)
T 5a9q 2
                 EE-----ECSSCEEEEEETT-EEEEEEEETTSCEEEEESSSCS--EEEEECCCSSCCCEEEEETTT-
 T ss_dssp
                 EE-----ecCCCEEEEEeCCC--CCcEEEEEeCCCcEEEEECcCCc---EEEEeeccCCCeEEEEECCCC-
T ss pred
                 Q ss pred
Q Fri_Mar_04_23: 226 RWYQLIATGCKDGRIRIFKITEK---LSPLASEESLTNSNMFDNSAD-VDMDAQGRS---DSNTEEKAELQSNLQVELLS
                                                                                298 (349)
              226 ~~~~las~s~d~~v~vwd~~~~---~
                                                                                298 (349)
              T Consensus
                                                                                292 (326)
              221 ---TFKVGAVAGNDWLIWDITRSSYPQNKRPVHMDRACLFRWSTISENLFATTGYPGKMASQ-----FQIHHLGHPQPIL
T 5a9q 2
                                                                                292 (326)
                 T ss dssp
T ss_pred
                 ---CEEEEEeCCCceEEeecccCcceEEccccCcceEEEECCCCccEEEEecccCCCc
                 eccCCCceEEEEECCCCCEEEEeccCCceEEEEeccc
Q ss pred
Q Fri Mar 04 23: 299 EHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATY 335 (349)
              299 ----h---i--v--spdg--las-s-D--v-iW----
                                               335 (349)
Q Consensus
              T Consensus
                                               326 (326)
              293 M--GSVAVGSGLSWHRTLPLCVTG-GDHKLLFWVTEV
T 5a9g 2
                                               326 (326)
                 E--ECSSCEEEEECTTSSEEEEE-ESSEEEEECCC
T ss dssp
                 c--ccCCccceEEECCCCCEEEEe-CCCeEEEEEcC
T ss pred
No 89
                           PDE NCBI
                                                 Pub Med
>5alu_D Coatomer subunit beta'; transport protein, structural protein, COPI, coate vesicles; 13.00A {Mus
musculus PDB: 5alv D 5alw D 5alx D 5aly D
 Probab=100.00 E-value=6.3e-31 Score=261.82 Aligned_cols=288 Identities=13% Similarity=0.200 Sum probs=0.0
Q ss pred
                 Q Fri Mar 04 23:
                1 MOPFDSGHDDLVHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                80 (349)
                1 ------h---v----s-d---l-t-s-D--v-iwd------h---v--v--v--v---las-s-Dg-
Q Consensus
                                                                                80 (349)
                 ++..+.+|.+.|+|+|+|+|++|+.||.|+|||+... ....+.+|...|+++.|+| ++++|++||+.||
T Consensus
                7 ----l--h---v----spdg--la----dg-v-iwd-----
                                                          ----v---sp--dg--la----dg
                                                                                80 (905)
                7 IKRKLTARSDRVKSVDLHPTEPWMLASLYNGSVCVWNHETO----TLVKTFEVCDLPVRAAKFVA--RKNWVVTGADDMO
T 5alu D
                                                                                80 (905)
T ss dssp
                 CEEEEEECSCEEEEECSSSEEEEEESSSCEEEEETTTT----EEEEEECCCSSCEEEEEET--TTTEEEEEETTSC
                 chhhcccCCCCeEEEEeCCCCEEEEEECCCC----eEEEEEecCCCCEEEEEECC--CCCEEEEEECCCE
T ss_pred
Q ss_pred
                 EEEeeccCccccccceeEEEEcCCCcEEEEEECcCCCCEEEEEECCCCC-CcceeeeccccEEEeec
Q Fri_Mar_04_23:
               81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEP-SDLRSWTLTSEMKVLSI
                                                                                159 (349)
Q Consensus
               81 v-lwd-----d--i-iwd-----
                                                                                159 (349)
                         +.+..+..|...|.+++|+|+ +..|++++.|+.|++||+...
                 |++|++.++
                              -----spd--g--l----dg-i-iwd-------
T Consensus
               81 i~vwd~~~~----
               81 IRVFNYNTL-----ERVHMFEAHSDYIRCIAVHPT-QPFILTSSDDMLIKLWDWDKKWSCSQVF-----
T 5alu D
                                                                                138 (905)
T ss_dssp
                 EERRETTTT-----EERREECCCSSCERREERCSS-SSEERREESSSERREETTTTSERREER------
T ss_pred
                 EEEEECCCC-----eEEEEEeCCCCCEEEEEEECC--CCEEEEEECCCCceEEEEE
                 Q ss pred
Q Fri_Mar_04_23: 160 PPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDG
                                                                                238 (349)
O Consensus
              160 -----h--v--y--sp------las-s-d-
                                                                                238 (349)
              T Consensus
              139 --EGHTHYVMQIVINPK--DNNQFASASLDRTIKVWQLGSSS---PNFTLEGHEKGVNCIDYYSGGDK--PYLISGADDR
T 5alu D
                                                                                209 (905)
                 -- \texttt{ECCSSCEEEEECSS} -- \texttt{CTTEEEEEETTTEEEEEETTCSS} -- \texttt{EEEEECCCSSCCCEEECCCSSSC} -- \texttt{CEEEEECTTS}
T ss_dssp
T ss_pred
                 --cCCCcceeeeeccc--ccceeeeecccc--eeeeeccccc--eeeeccccc--ceeeeecccc
                 Q ss pred
Q Fri_Mar_04_23: 239 RIRIFKITEK--LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTG
                                                                                316 (349)
 Q Consensus
              239 ~v~vwd~~~~-
                                                          -----v--spdq
                                                                                316 (349)
                 .|++||+..+ ...+..+..+..+..+..+..+..
              210 -i-iwd-----v----v----spdg--l-s-s-dg-----i-vwd------v--l--spdg
T Consensus
                                                                                283 (905)
              210 LVKIWDYONKTCVQTLEGHAQNVSCASFHPELPIIITGSEDGT-----VRIWHSSTYRLESTLNYGMERVWCVASLRGS
T 5alu D
                                                                                283 (905)
T ss dssp
                 CEEEEETTTCSEEEEECCCSSCEEEEEECSSSSEEEEEETTSC-----EEEEETTTCCEEEEECCSSCCEEEEEECSSS
                 EEEEEECCCCcEEEEEecCCCCeEEEEEcCCCC
T ss_pred
Q ss pred
                 CEEEEcCCCeEEEE
Q Fri_Mar_04_23: 317 TILSSAGDDGKVRLW
                             331 (349)
 Q Consensus
              317 ~~las~s~D~~v~iW
                              331 (349)
                 ++|++|+.|+.|++|
T Consensus
              284 ~~la~g~~dg~v~i~
                              298 (905)
T 5alu_D
              284 NNVALGYDEGSIIVK 298 (905)
T ss dssp
                 SEEEEESSEEEEE
                 CEEEEECCCCEEee
T ss pred
```

```
PDB<sup>IM</sup>
PROTEIN DATA BANK
No 90
                                                 Pub Med
->3vll_A 26S proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A {Saccharomyces
 cerevisiae} PDB: 3acp _A
 Probab=100.00 E-value=1.4e-31 Score=243.87 Aliqned cols=286 Identities=13% Similarity=0.106 Sum probs=0.0
                 Q ss pred
Q Fri Mar 04 23:
                5 DSGHDDLVH-----DVVYDFYGRHVATCSSDQHIKVFKLDK------DTSNWELSDSWR-AHDSSIVAI
                                                                                 61 (349)
                O Consensus
                                                                                 61 (349)
                 +..|.+.++ +++|+||++ ++++.|++|++|+...
                     T Consensus
                                                                                102 (420)
               24 NDENDDEFYINVDKNLNEIKEHKIVVLGNSRG-VDAGKGNTFEKVGSHLYKARLDGHDFLFNTIIRDGSKMLKRADYTAV
T 3vl1 A
                                                                                102 (420)
                 CCSSCCEEEEEEETTEEEEEEECCSTTTC-CBCCTTCEEEEEETTEEEEEETTEEEEEECCSEETTTTSCSCCEEEE
T ss dssp
T ss pred
                 Q ss_pred
                 EECCCCCC-EEEEEeCCCeEEEeeccCcccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEECCC
Q Fri Mar 04 23:
               62 DWASPEYGR-IIASASYDKTVKLWEEDPDOEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDAL
                                                                                140 (349)
O Consensus
               62 ------p----las-s-Dg-v-lwd------d--i-iwd--
                                                                                140 (349)
                 T Consensus
                                                                                169 (420)
              103 DTAK--LQMRRFILGTTEGDIKVLDSNFN------LQREIDQAHVSEITKLKFFPS--GEALISSSQDMQLKIWSVK
T 3vl1_A
                                                                                169 (420)
T ss_dssp
                 EEEC--SSSCEEEEETTSCEEEECTTSC------EEEEETTSSSSCEEEEEECTT--SSEEEEEETT
                 EECC--CCCceEEEECCCCcEEEEECCCC------ceeeeeccccCceeEEEEeCC--CCEEEEEeCCCcEEEEEeCC
T ss_pred
Q ss_pred
                 \tt CCCcceeeecccEEEeecCCCccceeEEEeccCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEE
 Q Fri Mar 04 23:
              141 EPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSIS
                                                                                219 (349)
O Consensus
              141 ------h---y--y-
                                                                                219 (349)
                               ------h---v------l-s---dg-i-iwd------
T Consensus
T 3vl1 A
              170 DGSNPRTLI-----GHRATVTDIAIID---RGRNVLSASLDGTIRLWECGTGTTIHTFNRKENPHDGVNSIA
                                                                                233 (420)
T ss_dssp
                 TCCCCEEEE-----CCSSCEEEEEET--TTTEEEEEETTSCEEEEETTTTEEEEEECBTTBTTCCEEEEE
T ss pred
                 CCCchhhhh------CCcceeeeeecC---CCCeeeeeecCCCceeeeee
Q ss pred
                 220 WAP----SIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNS---NMFDN-SADVDMD
Q Fri_Mar_04_23:
                                                                                273 (349)
 Q Consensus
              220 ~sp-----las-s-d-v-vwd-------
                                                                                273 (349)
                          |+|
T Consensus
              234
                                                                                308 (420)
              234 LFVGTDROLHEISTSKKNNLEFGTYG----KYVIAGHVSGVITVHNVFSK-EQTIQLPSKFTCSCNSLTVDGNNANYIYA
T 3vl1 A
                                                                                308 (420)
                 EEECCCSSCGGGCCCCCTTCSSCTT---EEEEEEETTSCEEEEETTTC-CEEEEECCTTSSCEEEEECSSCTTEEEE
 T ss_dssp
                  EccCCcceEEecccCceeEEEEcCCC----CEEEEEEcCCCEEEEEECCCC-CcceecCCCCceeeEeEecCCCCCEEEE
 T ss_pred
Q ss pred
                 CCCCCCCCCCCCCCCC-Ceeeeec-CCCCceEEEEECCCCCEEEEec
Q Fri Mar 04 23: 274 AQGRSDSNTEEKAELQSNLQ-VELLSEH-DDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKA 333 (349)
                 333 (349)
O Consensus
              T Consensus
                                                                  362 (420)
              309 GYENGM-----LAQWDLRSPECPVGEFLINEGTPINNVYFA-AGALFVSSGFDTSIK-LDI
T 3vl1 A
                                                                  362 (420)
                 EETTSE----EEEEETTCTTSCSEEEEESTTSCEEEEEEE-TTEEEEEETTTEEEE-EEE
T ss_dssp
                 Ecccc----EEEEecccccchheeccccccceeEEEC-cccEEEEEeccccEE-EEE
T ss pred
No 91
                           PDB"
                                                  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=6.2e-31 Score=234.36 Aligned_cols=300 Identities=16% Similarity=0.220 Sum_probs=0.0
Q ss pred
                 O Fri Mar 04 23:
                5 DSGHDDLVHDVVYDFYGRHVATCSS-----DOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYD
                                                                                 78 (349)
                 \  \, 5 \  \, \sim \sim h \sim \sim v \sim s \sim d \sim \sim 1 \sim t - s \sim --- - D \sim v \sim iwd \sim \sim \sim \sim \sim \sim h \sim \sim v \sim v \sim v \sim \sim \sim \sim 1 as \sim s \sim D \, \, 
O Consensus
                                                                                 78 (349)
                 +..+...|++++|+|+|++++++.
                                         |+.|++||+.....|...|...|.+++|++
               38 -----dg-v-i-
T Consensus
               38 PACMEVQIGAVRYRRDGALLLAASSLSSRTWGGSIWVFKDPEGAPNESLCTAGVQTEAGVTDVAWVS---EKGILVASDS
T 4q56 B
                                                                                114 (357)
T ss dssp
                 --CCCSEEEEEECSSSCEEEEECSSSSCCEEEEEESSCC---CGGGCSEEEECSSCEEEEEET---TTEEEEEETT
                 ceeccCcccEEEEccCCCceEEEEcccccccccccceeeccccCCCeEEEEECCCCCCcceeeccccCCCeEEEEECCC
T ss pred
Q ss_pred
                 Q Fri_Mar_04_23:
               79 KTVKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLS
                                                                                158 (349)
               79 g-v-lwd-----d--i-iwd------
                                                                                158 (349)
O Consensus
                              .....+..|...|.+++|+|+ + +..|++++.|+.|++||+.+.....+
                 +.|++||+.....
                                                ------i----dg-i-iwd-----
T Consensus
T 4q56 B
              115 GAVELWEILEKESL----LVNKFAKYEHDDIVKTLSVFSD--GTOAVSGGKDFSVKVWDLSOKAVLKSY------
                                                                                177 (357)
T ss_dssp
                 SCEEC-----CCCCEECCCSSCEEEEECSS-SSEEEEETTSCEEEEETTTTEEEEEE
                 CEEEEECCCcccc----ccceeeeecCCCceEEEEEcCC--CCEEEEEECCC-EEEEE
T ss_pred
Q ss pred
                 Q Fri_Mar_04_23: 159 IPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLP--GHKSLIRSISWAPSIGRWYQLIATGC
                                                                                235 (349)
 O Consensus
              159 ------h----y--y--sp------las-s
                                                                                235 (349)
              ----i---
                                                                                246 (357)
T Consensus
              178 ---NAHSSEVNCVAACPG--KDTIFLSCGEDGRILLWDTRKPK---PATRIDFCASDTIPTSVTWHPEKD---DTFACGD
 T 4g56_B
                                                                                246 (357)
 T ss dssp
                 ---CCCSSCEEEEECTT--CSSCEEEEETTSCEEECCTTSSS---CBCBCCCTTCCSCEEEEEECTTST---TEEEEEE
 T ss_pred
                 ---ecCcCceeEEEcCC--CCCEEEEEeCCCceEEEEECCCC---ccceeeecCCCCeEEEEECCCCC---cEEEEc
```

```
Q ss_pred
                         CCCCEEEEeoCa--connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connectionance-connect
 Q Fri Mar 04 23: 236 KDGRIRIFKITEK--LSPLASEESLTNSNMFDNSAD-VDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSW
                                                                                                                     312 (349)
 O Consensus
                     236 ~d~~v~vwd~~~~
                                                                                                       ~h~~~i~~v~
                                                                                                                     312 (349)
                     247 ~dg~i~i~d~~~~~v~~~~s~~g~~~1~~~~dg~~~~-i~iwd~~~~~~
 T Consensus
                                                                                                                     319 (357)
                     247 ETGNVSLVNIKNPDSAOTSAVHSONITGLAYSYHSSPFLASISEDCT-----VAVLDADFSE-VFRDLSHRDFVTGVAW
 T 4q56 B
                                                                                                                     319 (357)
                         SSSCEERERSSCGGGCERECCCSSCEERERCSSSSCCERERTTSC-----ERRCTTSCE-RERECCCSSCEERER
 T ss_dssp
                         CCCCEEEECCCCCceEEECCCCcceEEEECCCCcEEEEECCCCc-----EEEECCCCC-EEECEEEE
 T ss pred
                         CCC-CCEEEEecCCCeEEEE
 Q ss_pred
 Q Fri Mar 04 23: 313 NLT-GTILSSAGDDGKVRLWKATYSNEFKCM 342 (349)
                     313 spd-g~~las~s~D~~v~iW~~~~~~~~
 O Consensus
                                                              342 (349)
                     +|+ +++|++++.|+.|++|++.....+
320 s-----1-----dg-v---------------
 T Consensus
                     320 SPLDHSKFTTVGWDHKVLHHHLPSEGRTENL 350 (357)
 T 4q56 B
 T ss_dssp
                         CSSSTTEEEEETTSCEEEEECC-----
 T ss_pred
                         CCCCcCeEEEEecCCeEEEEeCCcccccch
                                      PDB<sup>W</sup> NCBI
 No 92
                                                                        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=8.9e-33 Score=259.20 Aligned cols=255 Identities=13% Similarity=0.123 Sum probs=0.0
                         Q Fri Mar 04 23:
                       2 QPFDSGHDDLVHDVVYDFY----G----RHVATCS------SDQHIKVFKLDKDTSNWELSDSWRA
                                                                                                                      53 (349)
                       2 -----h---v---s-d------l-t-s--------D--v-iwd---------
 O Consensus
                                                                                                                      53 (349)
                         ..+..+|.+.|+++|+|+ | ++|++|+
                                                                                      T Consensus
 T 2j04 B
                     126 RGFIYNVGGLVTDIAWLNIEENTDIGKDIQYLAVAVSQYMDEPLNEHLEMFDKEKHSSCIQIFKMNTSTLHCVKVQTIVH
 T ss dssp
                         T ss_pred
                          Q ss_pred
                         Q Fri Mar 04 23:
                      54 HDSSIVAIDWAS-----PEYGRIIASASYDKTVKLWEEDPD------QEECSGRRWNKLCTLNDSKGSLYSVKF
                                                                                                                     116 (349)
                      O Consensus
                                                                                                                     116 (349)
                     206 h---V--l---p------l-s-s-dg-v-iwd-----
 T Consensus
                                                                                     ~~---h~~~v~~
                                                                                                                     274 (524)
                     206 SFGEVWDLKWHEGCHAPHL--VGCLSFVSQEGTINFLEIIDNATDVHVFKMCEKP----SLTLSLADSLITTFDF
 T 2j04 B
                                                                                                                     274 (524)
                          CCCSEEEEECSSCCCSSS-SCEEEEETTSCEEEEECCCCSSSSSEEECCCSC-----SEEECCTTTCEEEEEE
 T ss_dssp
 T ss pred
                          cCCceeeeEECcCCCCcc--cCEEEEEeCCCEEEEEecCCcCccceeEeccc-----eEEEEECCCCceEEEEe
                         0 ss pred
 Q Fri_Mar_04_23: 117 APAHLGLKLACLGNDGILRLYDALEPSDLR-SWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIY
                                                                                                                     194 (349)
                     117 ~p~~~~l~~~~d~~i~iwd~~~~~~
                         +|+ + .|++++.|+.|++||+.+....
                                                                             . | . . . + . + + + + + + . . . . + . . + + + + + + + + + + + + |
                     338 (524)
 T Consensus
                     275 LSP--T-TVVCGFKNGFVAEFDLTDPEVPSFYDQ-------VHDSYILSVSTAYSDFEDTVVSTVAVDGYFYIF
 T 2j04 B
                                                                                                                     338 (524)
                         SSS-S-EEEEEETTSEEEEEETTBCSSCSEEE
 T ss dssp
                          T ss pred
                         Q ss_pred
 Q Fri_Mar_04_23: 195 QRGKDGKLHVAAKLPGHKS--LIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDM 272 (349)
                          -----h----v--v--sp-----las-s-d--v-vwd--
                                                                                                                     272 (349)
                     387 (524)
 T Consensus
                     339 NPKDI---ATTKTTVSRFRGSNLVPVVYCPQI----YSYIYSDGASSLRAVPSRAA-----
 T 2j04 B
                                                                                                                     387 (524)
                         CGGGH---HHCEEEECSCCSCCCEEEETTT----TEEEEECSSSEEEEEETTCT-------
 T ss dssp
                         eCCcC---CccceeeeecCCCccceEECCCC----ceEEEecCCCCEEEEecccc-----
 T ss_pred
 Q ss_pred
                         Q Fri_Mar_04_23: 273 DAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGKVRLWKATYS 336 (349)
                                       -----h---i--v--spdg--las-s-D--v-iW-----
 Q Consensus
                     273 ~~~
                                                                                                   336 (349)
                                               +.+..+.+|...|++|+|+|+|+|+|+.|++|+|++|-..
------h---v--v--sp----l-sgs-dg-v-iwd----
 T Consensus
                     388 -----FAVHPLVSRETTITAIGVSRLHPMVLAGSADGSLIITNAARR 429 (524)
 T 2j04 B
 T ss dssp
                         -----TCCEEEEECSSCEEEEECSSCEEEEECCSSCEEEEETTTEEECCBSCSS
                          -----cceeEecCCCceEEEEecCCCceEEEEecchh
 T ss_pred
                                     SCOPe PROTEIN DATA BANK NCBI
                                                                             Pub Med
>1nro A Actin interacting protein 1; beta propeller, WD40 repeat, ADF, cofilin, structural genomics, PSI, protein structure initiative; 1.70A {Caenorhabditis elegans} SCOP: b.69.4.1 b.69.4.1 PDB: 1pev A
 Probab=100.00 E-value=3.5e-30 Score=244.55 Aligned_cols=309 Identities=17% Similarity=0.226 Sum_probs=0.0
                         cccCCcceEEEEECCCCCEEEEEECCCCCCeEEEEECCCCCcceEeeecc-----ccceEEEEEEcCCCCCCEEEEE
 Q Fri_Mar_04_23:
                       {\tt 3~PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRA------HDSSIVAIDWASPEYGRIIASA}\\
                                                                                                                      75 (349)
                       3 ----h--v---s-d---l-t-s-D--v-iwd-----------h---v-v-v-------las-
 Q Consensus
                                                                                                                      75 (349)
                          T Consensus
 T 1nr0 A
                     184 STFGEHTKFVHSVRYNPDGSLFASTGGDGTIVLYNGVDG----TKTGVFEDDSLKNVAHSGSVFGLTWSP--DGTKIASA
 T ss dssp
                         ERECCCSSCEEREECTTSSEEREETTSCEEREETTTC----CERECBCTTSSSCSSSCEEREECT--TSSEEREE
 T ss_pred
                          eeecCCCCCEEEEECCCCCEEEEeeCCCc===-ccceEecccceeccCCCcEEEEEcc--CCCEEEEE
```

```
Q ss_pred
                 121 (349)
              76 SYDKTVKLWEEDPDQEECSGR------RWNKLCTLNDSKGSLYSVKFAPAHL
O Fri Mar 04 23:
                                                                             121 (349)
Q Consensus
                +.|+.|++||+.+....
T Consensus
             258 ~-d~-i~iwd~~~~~v~~~v~~~v~~~
                                                                             335 (611)
             258 SADKTIKIWNVATLKVEKTIPVGTRIEDQQLGIIWTKQALVSISANGFINFVNPELGSIDQVRYGHNKAITALSSSAD--
T 1nr0 A
                                                                             335 (611)
                 ETTSEEEEEETTTTEEEEEEECCSSGGCEEEEEECSSCEEEEETTCCEEEEETTTTEEEEEECCCSSCEEEEECTT--
T ss dssp
                 T ss pred
Q ss_pred
                 Q Fri Mar 04 23: 122 GLKLACLGNDGILRLYDALEPSDLRSW------TLTSEMK
                                                                             155 (349)
              122 ~~~l~~~~d~~i~iwd~~~~~~~~~~~~
Q Consensus
                                                                             155 (349)
              T Consensus
                                                                             415 (611)
T 1nr0 A
              {\tt 336~GKTLFSADAEGHINSWDISTGISNRVFPDVHATMITGIKTTSKGDLFTVSWDDHLKVVPAGGSGVDSSKAVANKLSSQPL}
                                                                             415 (611)
T ss_dssp
                 SSEREEETTSCEEEETTTCCEEECSSCSCSCEEEEECTTSCEEEEETTTEEEEECSSSSSSCTTSCCEEECSSCEE
                 T ss pred
                                   -----cceeEEEEcccCCCcceEEecCCc-eEEEEecCCCcEEEEEEccCC
Q ss pred
                 EeecCCCccc-
Q Fri_Mar_04_23: 156 VLSIPPANHL-------QSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGH
                                                                             211 (349)
Q Consensus
              156 ~~~~~~~
                          .______i____i
                                                                             211 (349)
              T Consensus
              416 GLAVSADGDIAVAACYKHIAIYSHGKLTEVPISYNSSCVALSN---DKQFVAVGGQDSKVHVYKLSGA--SVSEVKTIVH
T 1nr0 A
                                                                             490 (611)
T ss_dssp
                 EEEECTTSSCEEEEESSEEEEETTEEEEEECSSCEEEEECT---TSCEEEEEETTSEEEEEEEETT--EEEEEEEEC
T ss_pred
                 eeEEcCCCCEEEEEecCcCeeeeccCCcEeEEEcC---CCCEEEEEeCCcEEEEEcCCC--cceeeeccCC
                 Q ss_pred
Q Fri_Mar_04_23: 212 KSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKITEK----LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKA
                                                                             286 (349)
O Consensus
              212 ---v--sp-----las-s-d--v-vwd------
                                                                             286 (349)
              T Consensus
                                                                             560 (611)
              491 PAEITSVAFSNNG----AFLVATDQSRKVIPYSVANNFELAHTNSWTFHTAKVACVSWSPDNVRLATGSLDNS-----V
T 1nr0 A
                                                                             560 (611)
                 SSCEEEEECTTS----SEEEEEETTSCEEEEEGGGTTEESCCCCCCCSSCEEEEEECTTSSEEEEEETTSC----E
T ss_dssp
                 CccEEEEECCCC----EEEEECCCcEEEEEccChhHhhhhhhhacccccceEEEEECCCCCEEEEeeCCCc-----E
T ss pred
                 cccccc-ceeee-ccCCC-ceEEEEECCCCCEEEEecCCCeEEEEeccc
Q ss pred
Q Fri_Mar_04_23: 287 ELQSNLQ-VELLSE-HDDHN-GEVWSVSWNLTGTILSSAGDDGKVRLWKATY
              287 ~~~~~h~~~i~~v~~spdg~~las~s~D~~v~iW~~~~
 Q Consensus
              T Consensus
                                                        611 (611)
             561 IVWNMNKPSDHPIIIKGAHAMSSVNSVIWL-NETTIVSAGODSNIKFWNVPF 611 (611)
T 1nr0 A
T ss_dssp
                 EEEETTCTTSCCEEETTSSTTSCEEEEEE-ETTEEEEEETTSCEEEEECCC
T ss_pred
                 EEEECCCCcceeeeecccCccceEEEEec-CCCEEEEecCCCcEEEeecCC
                         SCOPe PDB<sup>M</sup> PROTEIN DATA BANK
                                                 No 94
                                                        Pub Med
🗌 >1sq9_A Antiviral protein SKI8; WD repeat, beta-transducin repeat, WD40 repeat, beta propeller, recombination;
1.90A {Saccharomyces cerevisiae} SCOP: b.69.4.1 PDB: 4buj C 1s4u X
Probab=100.00 E-value=2.1e-31 Score=240.55 Aligned_cols=295 Identities=15% Similarity=0.176 Sum_probs=0.0
                CCCCCCCCEEEEEECCCCCEEEEEECCCCC------CCeeEeeeeccccceEEEEEECCCCC---CE
Q ss pred
Q Fri_Mar_04_23:
              2 QPFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDT-----SNWELSDSWRAHDSSIVAIDWASPEYG---RI
                                                                             71 (349)
               Q Consensus
                                                                             71 (349)
               T Consensus
                                                                             83 (397)
               9 ANAGKAHDADIFSVSACN--SFTVSCSGDGYLKVWDNKLLDNENPKDKSYSHFVHKSGLHHVDVLOA-IER--DAFELCL
T 1sq9 A
                                                                             83 (397)
                EEESSCSSSCEEEEEECS--SEEEEEETTSEEEEEESBCCTTCCGGGGEEEEECCTTCEEEEEEEE-EET--TTEEEEE
T ss dssp
                 T ss pred
                 EEEEeCCCeEEEeeccCcccccccccccee-----EEEEc-----CCCCcEEEEEECc-CCCC----CEEEEECCCCEEE
Q ss_pred
              72 IASASYDKTVKLWEEDPDQEECSGRRWNK-----LCTLN----DSKGSLYSVKFAP-AHLG---LKLACLGNDGILR
Q Fri Mar 04 23:
                                                                             135 (349)
              72 las-s-Dg-v-lwd------d--i-
Q Consensus
                                                                             135 (349)
                               .. +..+. .|...|.+++|+| + + ..|++++.|+.|+
                 |++++.|+.|++||+..
T Consensus
                                                                             151 (397)
              84 VATTSESGDIJEVRITR-----EDETKKVI FEKI DIJ DSDMKKHSEWALKWGASN-DRIJ SHRI VATDVKGTTY
T 1sq9_A
                                                                             151 (397)
                 EEEEETTSCEEEEEEE....-CTTTCCEEEEEECCSCTTGGGSCEEEEEECCC...-CEEEEEEETTSCEE
T ss dssp
                 EEEecCCCCEEEEEecC------CcccccccccccceeeccccceeEEEEeccCC--CCCCcEEEEECCCceEE
T ss pred
Q ss_pred
                 EEECCCCCcc----eeeeccccEEEeecCCCccc--cceeEEEEcccCCCcceEeecCc-eEEEEecCCCcEE
Q Fri_Mar_04_23: 136 LYDALEPSDL------RSWTLTSEMKVLSIPPANHL--QSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLH 203 (349)
O Consensus
             203 (349)
                 +||+..... + ...+..++|+| ++ .++++..++ +.+|+.... +
              152 iwd-----v---v------h-p---v-----
                                                      -----d--i-i-d-----
T Consensus
              152 IWKFHPFADESNSLTLNWSPTLELQGTVES-----PMTPSQFATSVDISE---RG-LIATGFNNGTVQISELSTL---R
T 1sq9 A
                 EEEEESSSSHHHHTTTCCCCEEEEEEECC----SSSSCCCCCEEECT--TS-EEEEECTTSEEEEEETTTT--E
T ss_dssp
                 EEecCCccccccccccceeecc-----ccccceeEEEECC---Cc-eEEEEECCCeEEEEECCC---c
T ss_pred
                 Q ss pred
 Q Fri_Mar_04_23: 204 VAAKLPG-----HKSLIRSISWAPSIGRWYQLIATGCKD---GRIRIFKITEK--LSPLA------SEESLT 259 (349)
             204 ------h---y--y--y--sp------las-s-d-----v-vwd-----
                                                                             259 (349)
 O Consensus
```

```
|...|.+++|+|++
                                                                .+|++++.| +.|++||+... ...+.
                                                         ------d---g-i-iwd--------
 T Consensus
                      219 ~~~~~~~~
                                            -~~~<del>V</del>~~~~
                                                                                                                  ~~h~~~v 294 (397)
                      219 PLYNFESOHSMINNSNSIRSVKFSPOG----SLLAIAHDSNSFGCITLYETEFGERIGSLSVPTHSSOASLGEFAHSSWV
 T 1sq9_A
                                                                                                                            294 (397)
                           EEEEEECCC---CCCCCEEEEEECSST----TEEEEEEEEETTEEEEEEEECBC------CCBSBSSCE
 T ss dssp
 T ss_pred
                           Q ss pred
 Q Fri Mar 04 23: 260 NSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHD-------DHNGE-----VWSVSWNLTGTI
                                                                                                                            318 (349)
                       260 ~~~
                                                                                               --h----i--v--spdg--
 Q Consensus
                                                                                                                            318 (349)
                                                          ..+|+...+.+..+.
                           .... ++++.+.+.+.
                                                                                                            |++++|+|+|++
                                                                                                . . . . .
                      295 ~~--
                                 ----l~s---dg-----i~iwd------
 T Consensus
                       295 MSLSENDSGETLCSAGWDGK-----LREWDVKTKERITTLNMHCDDIELEEDILAVDEHGDSLAEPGVFDVKFLKKGWR
 T 1sq9_A
                                                                                                                            368 (397)
                           EEEEECSSSSEEEEETTSE----EEEEETTTTEEEEEEEECCGGGCSSGGCCCBCTTSCBCSSCCEEEEEECTTTS
 T ss dssp
 T ss pred
                           EEEEECCCCCEEEEEeCCCE-----EEEEeccCCccccccCccccccccCcceeeccCceeEEEEECCCCce
                           -----EEEecCCCeEEEEeccC
 Q ss pred
                      319 -----LSSAGDDGKVRLWKATYS 336 (349)
 Q Fri Mar 04 23:
                       319 -----las~s~D~~v~iW~~~~~
 Q Consensus
                                                              336 (349)
                                       |++++.|++|+||++..+
                       369 ----- l-s---d--i-iw----g 396 (397)
 T Consensus
                       369 SGMGADLNESLCCVCLDRSIRWFREAGG
 T 1sq9 A
                                                              396 (397)
 T ss_dssp
                           BSTTCTTSCEEEEEETTTEEEEEEEC-
 T ss_pred
                           EeeccCCceEEEecCCCcEEEEEcccC
                                         PDB"
PROTEIN DATA BANK
                                                       NCBI
                                                                              Pub Med
>3v7d B Cell division control protein 4; WD 40 domain, phospho-peptide complex, E3 ubiquitin ligase, cell cycle,
 phospho binding protein, phosphorylation; HET: SEP; 2.31A {Saccharomyces cerevisiae} PDB: 1nex B* 3mks B*
 Probab=100.00 E-value=1.7e-30 Score=240.12 Aligned_cols=256 Identities=19% Similarity=0.264 Sum_probs=0.0
                           CccCCCcce=EEEEEECCCCCEEEEEeCCCeEEEEECCCCCcceeEeeeeccccceEEEEECCCCCCEEEEEeCCCe
 Q Fri Mar 04 23:
                        2 QPFDSGHDDL-VHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                                                             80 (349)
                        2 -----h----y----s-d---l-t-s-D--v-iwd------h----y---y--
 Q Consensus
                                                                                                      ~~~~~~las~s~Dq~
                                                                                                                             80 (349)
                           T Consensus
                                                                                                                            184 (464)
 T 3v7d B
                       114 \ {\tt RTTLRGHMTSVITCLQFE--DNYVITGADDKMIR} {\tt NTTLRGHMTSVITCLQFE--DNYVITGADDKMIR} {\tt NTTLRGHMTSVITCLQFE--DNYVITGADCHMTSVITCLQFE--DNYVITGADCHMTSVITCLQFE--DNYVITGADCHMTSVITCLQFE--DNYVITCLQFE--DNYVITGADCHMTSVITCLQFT--DNYVITGADCHMTSVITCLQFT--DNYVITGADCHMTSVITCLQFT--DNYVITGADCHMTSVITCLQFT--DNYVITCLQFT--DNYVITGADCHMTSVITCLQFT--DNYVITCLQFT--DNYVITCLQFT--DNYVITGADCHMTSVI
                                                                                                                            184 (464)
 T ss_dssp
                           EEREECCSSSCEEEEEE--TTEEEEEETTSCEEEEETTTT----EEEEEECCCSSCEEEEEECS---TTEEEEEETTSC
 T ss_pred
                           eEEEcCCCCCeEEEEEC--CCEEEEEcCCC----eEEEEECCcCccEEEEEECC---CCeEEEEeCCCc
                           EEEeeccCccccccceeEEEEccCCCcEEEEEEccCCCceEEEEEccCCCcceeeeccccEEEeecC
 Q ss_pred
 Q Fri_Mar_04_23:
                       81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP
                                                                                                                            160 (349)
 O Consensus
                       160 (349)
                                         |++||+.++
 T Consensus
                       185 v~vWd~~~q----
                                                                                                                            255 (464)
 T 3v7d B
                       185 VRVWDIKKG-----CCTHVFEGHNSTVRCLDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHT
                                                                                                                            255 (464)
                           EEEEETTTT-----EEEEEECCCSSCEEEEEEESSSCEEEEEETTSCEEEEECCCCCC-----CCSSEEESC
 T ss_dssp
                           EEEecCCCC-----ceeEEECCCCccEEEEEeccCCCCEEEEEecCCCCcceEEEeecCCCCccccCcCccccCcCcceeEecc
 T ss pred
                              -----CcccceeEEEEcccCCCCCceEEecCCc-eEEEEecCCCcEEEEEEccCCCCceeEEEEECCCCCCce
 Q ss pred
 Q Fri_Mar_04_23:
                       229 (349)
 Q Consensus
                       161
                                                               -----h---v--sp----
                                                                                                                            229 (349)
                                                          T Consensus
                       256 ~~
                                                                                                                            323 (464)
                       256 PEENPYFVGVLRGHMASVRTVSGH----GNIVVSGSYDNTLIVWDVAQM---KCLYILSGHTDRIYSTIYDHER----K
 T 3v7d B
                                                                                                                            323 (464)
 T ss dssp
                           GGGCTTEEEEECCCSSCEEEEEE----TTEEEEEETTSCEEEEETTTT---EEEEEECCCSSCEEEEEETTT----T
                           CCCCcEEEEEeccccceEeecCC----CCEEEEecCCCCeEEEEECCCC---CEEEEECCCCCEEEEEECCCC----C
 T ss_pred
 Q ss pred
                           Q Fri Mar 04 23: 230 LIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWS
                                                                                                                            309 (349)
                       230 ~las~s~d~~v~vwd~~
 O Consensus
                                                                                                                            309 (349)
                           ++++|+.|++|++||+..+
 T Consensus
                       324 ~1~sgs~D~~i~iWd~~~g--
                                                                                                         ----l--h---v--
                                                                                                                            357 (464)
                       324 RCTSASMDTTTRIWDLENG------ELMYTLOGHTALVGL
 T 3v7d B
                                                                                                                            357 (464)
 T ss dssp
                           EEEEEETTSCEEEEETTTT-----EEEEEECCCSSCEEE
                           T ss_pred
 Q ss_pred
                           EEECCCCCEEEEecCCCeEEEEeccc
 Q Fri_Mar_04_23: 310 VSWNLTGTILSSAGDDGKVRLWKATY 335 (349)
 Q Consensus
                      310 v--spdg--las-s-D--v-iW----
                                                            335 (349)
                           ++|+ +++|++|+.|++|++||+..
                              -s--~-l~s~s~D~~i~vWd~~~
                      358 LRLS--DKFLVSAAADGSIRGWDAND 381 (464)
 T 3v7d B
 T ss dssp
                           EEEC--SSEEEEETTSEEEEETTT
 T ss pred
                           EEec--CCEEEEEcCCCcEEEECCC
                                         PDB<sup>®</sup>
PROTEIN DATA BANK
                                                       NCBI
                                                                              Pub Med
>4u7a A Ribosome biogenesis protein ERB1; WD40, rRNA binding, beta-propeller, Pro binding; 1.60A (Saccharomyces
 cerevisiae}
 Probab=100.00 E-value=4.6e-31 Score=259.69 Aligned_cols=289 Identities=18% Similarity=0.224 Sum_probs=0.0
 Q ss pred
                           3 PFDSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAH-----DSSIVAIDWASPEYGR--IIAS
```

Q Fri_Mar_04_23:

74 (349)

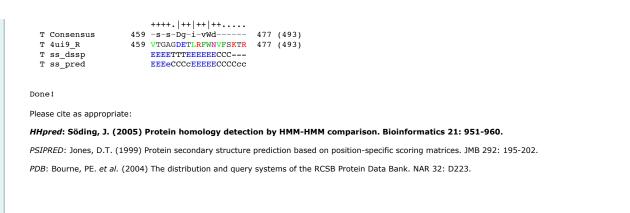
```
Q Consensus
                                                                           74 (349)
T Consensus
                                                                          523 (826)
             450 TIYAGHKGKVRTLSIDPSGLWLATGSDDGTVRVWEILTG----REVYRTTLIDDEENPDYHIECIEWNP--DANNGILAV
T 4u7a A
                                                                          523 (826)
               EEECCCSSCEEEEECTTSCEEEEEETTSEEEEEETTTC----CEEEEEECCSCTTCSSCCEEEEEECS--STTSCCEEE
T ss dssp
               EEEecCCCcEEEEEccCCCceEEEEccCC----cEEEEEEecccccCCCCCeEEEEEcc--CCCceEEEE
T ss pred
Q ss pred
               E-----eCCCeEEEeeccCcccc
Q Fri_Mar_04_23:
             75 A-----SYDKTVKLWEEDPDQEEC
                                                                           93 (349)
Q Consensus
                                                                           93 (349)
                 T Consensus
             524 ~~~
                                                                          603 (826)
             524 AVGENIHLIVPPIFGYDIENNGKTKIEDGFGYDTFGTVKKSNLEVNENGDGDEDGENESAKNAVKKQVAQWNKPSQKQLE
T 4u7a A
                                                                          603 (826)
T ss_dssp
               EETTEEEECCTTSCHHHHHHHHHHHTC------CCEEECCCHHHHT
T ss_pred
               Q ss_pred
               Q Fri_Mar_04_23:
                                                                          170 (349)
             94 SGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDG---ILRLYDALEPSDLRSWTLTSEMKVLSIPPANHLQSDFC
Q Consensus
                  170 (349)
            .+ +..+.|..|.++|+|+ +..|+++.|+ .|+|++....+
604 ------h---V--1--spd--g--1-s-s-Dg----v-iwd------------
T Consensus
                                                                          663 (826)
T 4u7a_A
             604 KD----ICITISCKKTVKKLSWHRK-GDYFVTVQPDSGNTSVLIHQVSKHLTQSPF-----KKSKGIIMD
                                                                          663 (826)
               TT-----EEEEEESSCCCEEECTT--SSEEEEECTTCGGGSEEEEEGGGTEEECCC------SSCCSCEEE
T ss_dssp
               cc----eeEEecCCCcceeeEEcCC--CCEEEEEecCCCCCEEEEEECCCcccccc------cCCCCCEEE
T ss pred
Q ss_pred
               EEEccCCCCCceEEeccCCceEEEEecCCCcEEEEEccCCCCceeEEEECCCCCCceEEEEEccCCCCEEEEEec-Cc-
Q Fri Mar 04 23: 171 LSWCPSRFSPEKLAVSALEQAIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGRIRIFKIT-EK-
                                                                          248 (349)
                                                                          248 (349)
O Consensus
            171 -----las-s-d--v-vwd-----
             ++|+| ++...+++++...+++|+... ..+..++|+|++ ...|.++|+|+ ...|.++|+|+...
664 v--sp--dg-1--sdg-I-vwd1-----1-sgg-Dg-I-vwd------1-sgs-Dg-I-vwd------
T Consensus
             664 AKFHP---FKPQLFVCSQRYVRIYDLSQQ---ILVKKLLPGARWLSKIDIHPRG----DNLIASSFDKRVLWHDLDLAST
T 4u7a A
               EEECS---SSEEEEEESSCEEEETTTT---EEEEEECCCCSCEEEEECTTS----SEEEEEETTSCEEEEETTTCSS
T ss_dssp
               T ss_pred
Q ss_pred
               Q Fri Mar_04 23: 249 -LSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE-----LLSEHDDHNG---EVWSVSWNL
            249 -----h----i-v-sp 314 (349)
Q Consensus
             .+..+.+|.. .|++|+|+|
                                                         ----l~gh----
                                                                  ~V~~v~fsp
T Consensus
                                                                          807 (826)
T 4u7a A
             734 PYKTLRYHEKAVRSVNFHKKLPLFSSAADDGT-----IHVFHATVYDDMMKNPMIVPLKKLTGHKVINSLGVLDAIWHP
                                                                          807 (826)
               CSEEECCCSSCEEEEEECSSSSEEEEEETTSC-----EEEEEEECCSSSSCCCEEEEEEEECCCCCBTTBCEEEEEECS
T ss dssp
               T ss pred
0 ss pred
               CCCEEEEecCCCeEEEec
Q Fri_Mar_04_23: 315 TGTILSSAGDDGKVRLWKA 333 (349)
             315 dg~~las~s~D~~v~iW~~ 333 (349)
               + | ++ | ++++ . | ++ | + | | ++
T Consensus
             808 dg~~L~s~s~Dg~I~lWdl 826 (826)
             808 REAWLFSAGADNTARLWTT
T 4u7a A
                              826 (826)
               SSSCEEEETTSCEEEEC
T ss dssp
T ss_pred
               CCCEEEEeCCCeEEEeeC
                        PDB™
No 97
           NCBI
                                        Pub Med
      Nucleoporin NUP43; structural genomics consortium, SGC, WD40 repeat, cell cycle; 1.75A {Homo sapiens}
Probab=100.00 E-value=1.3e-30 Score=235.85 Aligned_cols=258 Identities=16% Similarity=0.225 Sum_probs=0.0
               CCCeEEEEECC-----EeeeecccceEEEEECCC
0 ss pred
Q Fri Mar 04 23:
              8 HDDLVHDVVYDF-----YGRHVATCSSDQ--HIKVFKLDKDTSNWE-----LSDSWRAHDSSIVAIDWAS
                                                                           65 (349)
              O Consensus
                                                                           65 (349)
               |...|++++|+| ++++|++|++|++|++|+... ....+.+|...|++++|++
T Consensus
                                                                          103 (399)
             28 VSQKISKTRWRPLPPGSLQTAETFATGSWDNEENYISLWSIGDF----GNLDSDGGFEGDHQLLCDIRHHGDVMDLQFFD
T 4i79 A
                                                                          103 (399)
               T ss dssp
               T ss pred
Q ss_pred
               Q Fri_Mar_04_23:
             66 PEYGRIIASASYDKTVKLWEEDPDOEECSGRRWNKLCTLNDSK-----GSLYSVKFAPAHLGLKLACLGNDGILRLYD
                                                                          138 (349)
                 ----las-s-Dq-v-lwd-----v--
                                                        ---p-----l----d--i-iwd
Q Consensus
             66 ~~
                                                                          138 (349)
                  +.+|++++.|+.|+.|++||+.... ..-.....+..|. ..+.+++|+|+|+ +..|++++.|+.|++||
                --~~l~~~~d~~i~iw
                                             -----v----v-----1----dg-i-vwd
                                                                          176 (399)
T 4i79 A
             104 ---OERIVAASSTGCVTVFLHHPNN--OTLSVNOOWTTAHYHTGPGSPSYSSAPCTGVVCN--NPEIVTVGEDGRINLFR
                                                                          176 (399)
T ss dssp
               ---SEEEEEETTSCEEEEEETTT--CCEEEEEETTSSBCC-----CBCCEEEEEE--TTEEEEEETTSEEEEE
T ss_pred
               \verb|CCCCcceeeecccEEEeecCCCccceeEEeccCC-eEEEeecCC-CcEEEEEeccCCCCcee| \\
Q ss_pred
Q Fri_Mar_04_23: 139 ALEPSDLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKD-GKLHVAAKLPGHKSLIR
                                                                          216 (349)
Q Consensus
            216 (349)
                               ..+...+.++|+| ...+++++++++|+....|.
             177
                       -_____v~~~v~~~v
                                          -----d--i-iwd------
T Consensus
                                                                          240 (399)
            177 ADHKEAVRTID-----NADSSTLHAVTFLR----TPEILTVNSIGQLKIWDFRQQGNEPSQILSLTGDRVPLH
                                                                          240 (399)
T 4179 A
T ss_dssp
               TTCSSCSEEEE-----CCCSSCEEEEESS---TTEEEEEETTSEEEEEETTCSSSCCSEEEECSSSSCCEE
T ss pred
               CCCCcceeEe-----CCCCCeEeEEEEeC----CCeEEEEEECCCCCCCcceeeeccCCCCCEE
```

```
Q ss pred
                 Q Fri Mar 04 23: 217 SISWAPSIGRWYQ-LIATGCKDGRIRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVE
                                                                                 295 (349)
               217 ~v~~sp~~~~~las~s~d~~v~vwd~~~~
                                                                                 295 (349)
Q Consensus
              T Consensus
                                                                                 270 (399)
               241 CVDRHPNO---OHVVATGGODGMLSIWDVROG-----T
T 4i79 A
                                                                                 270 (399)
                 EEEECSSC---TTEEEEEETTCCEEEEETTSC----S
T ss dssp
                  EEEEccCC----CCEEEEEccCCCEEEEEECCCC-----
T ss pred
                 e-eeccCCceeeeeecccc-cceeeeccccceeee
Q ss pred
O Fri Mar 04 23: 296 L-LSEHDDHNGEVWSVSWNLT-GTILSSAGDDGKVRLWKATYSNEFKCM 342 (349)
               296 ~-~~~h~~~i~~v~~spd-g~~las~s~D~~v~iW~~~~~~~
                                                         342 (349)
O Consensus
                 T Consensus
               271 MPVSLLKAHEAEMWEVHFHPSNPEHLFTCSEDGSLWHWDASTDVPEKSS 319 (399)
T 4179 A
T ss dssp
                 SCSEECCCSSCEEEEECSSCTTEEEEEETTSCEEEEECC-----
                 CceeEecCCcCEEEEEEcCCCCCEEEEEecCCCcccce
T ss pred
No 98
                                                   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=9.9e-32 Score=262.54 Aligned_cols=292 Identities=17% Similarity=0.238 Sum_probs=0.0
Q ss_pred
                 Q Fri Mar 04 23:
                5 DSGHDDLVHDVVYDFY--GRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEY--GRIIASASYDKT
                                                                                  80 (349)
                5 ---h---v---s-d-----l-t-s-D--v-iwd-------h---v----h---v--v-------las-s-Dq-
O Consensus
                                                                                  80 (349)
                 +.+|...|++++|+| + +++|++|+.||+|++|+.||+. ++......+.+|...|++++|+| + +++|++|+.||-
               T 3jro A
               49 LTGHEGPVWRVDWAHPKFGTILASCSYDGKVLIWKEE--NGRWSOIAVHAVHSASVNSVOWAP--HEYGPLLLVASSDGK
                                                                                 124 (753)
T ss dssp
                 ECCCSSCERERECCTTSCSERERETTSCEREREER-TTREERERECCCSSCERERECC--GGGCSERERETTSE
                  eccCccEEEEEecCCCCCCEEEEEecCC--CCccccccCCCCCCeeEEEECC--CCCCCEEEEEeCCCc
T ss pred
Q ss pred
                 81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLG------LKLACLGNDGILRLYDALEP---S 143 (349)
 Q Fri_Mar_04_23:
               Q Consensus
                                                                                 143 (349)
                                        ..|.+++|+|+ + ..++++.|+.|++|+|+.+.
--v-l-sp------l-sg-dg-I-vwd-----
                  |++||+.++....
                                 125 i~iwd~~~~~-
T Consensus
                                                                                 195 (753)
               125 VSVVEFKENGTTS-----PIIIDAHAIGVNSASWAPA-TIEEDGEHNGTKESRKFVTGGADNLVKIWKYNSDAQTYV
T 3jro A
T ss_dssp
                 EEEEECCSSCCC-----CEEEECCSSCEEEEECCC-C-----CGGGCCEEEEETTSCEEEEEETTTTEEE
T ss_pred
                 ERREPCCCCCCCC-----cccccCCCccREREECCC--CCccccccCCCCCccREREECCCCcccccc
                 Q ss pred
Q Fri_Mar_04_23: 144 DLRSWTLTSEMKVLSIPPANHLQSDFCLSWCPSRFSP--EKLAVSALEQ-AIIYQRGKDGKLHVAAKLPG--HKSLIRS 217 (349)
               O Consensus
                                                                                 217 (349)
                    196 ~~
T Consensus
                                                                                 259 (753)
               196 LESTL-----EGHSDWVRDVAWSP---TVLLRSYLASVSQDRTCIIWTQDNEQGPWKKTLLKEEKFPDVLWR
T 3jro A
                                                                                 259 (753)
 T ss_dssp
                 EEEEE-----CCCSSCEEEEEECC---CCSSSEEEEEEESSSSCEBCBSSSSCCSSCCCC
                  EeEEe------CCCcceEEEEEcC---CCCcCeEEEecCCCccchhcccccCcCcceEE
T ss_pred
                 Q ss pred
Q Fri_Mar_04_23: 218 ISWAPSIGRWYQLIATGCKDGRIRIFKIT----EKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQ--- 289 (349)
              218 v--sp-----las-s-d--v-vwd------
                                                                                 289 (349)
              T Consensus
                                                                                 328 (753)
              260 ASWSLSG----NVLALSGGDNKVTLWKENLEGKWEPAGEVHQGGGG-SGGGGATSKEFDGPCQNEID-----LLFSECN 328 (753)
T 3iro A
                 EEECTTT----CCEEEECSSCEECCBCCSSSCCBCCCCBC-----
T ss dssp
                  EEEcCCC----CEEEEEeCCCeEEEeccCCCcchhhceeecccCCC-ceeEecCccceeccCCccc-----eehhhhh
T ss pred
Q ss pred
                 -cccceeeeccCCcceEEEEECCCCCEEEEecCCCe-EEEEeccCC
Q Fri_Mar_04_23: 290 -SNLQVELLSEHDDHNGEVWSVSWNLTGTILSSAGDDGK-VRLWKATYS 336 (349)
               290 -----h---i--v--spdg--las-s-D---v-iW----- 336 (349)
Q Consensus
                  T Consensus
T 3jro_A
T ss dssp
                 --CCSHHHHHHTTTCCSCCCCCCBCTTSCBCEECSSSTTSEECCCCCCC
                  hhhhhccceeeccCCceeEEEcCCCcEEEeecCCCcceEEEecccc
T ss pred
                           SCOPe PROTEIN DATA RANK
No 99
                                                            Pub Med
>2ovr_B FBW7, F-BOX/WD repeat protein 7, F-box PROT; WD40 domains, double phosphorylation, transcription-C
complex; HET: TPO; 2.50A {Homo sapiens} SCOP: a.158.1.1 b.69.4.1 PDB: 20vg _B* 20vq _B* Probab=100.00 E-value=1.4e-29 Score=232.69 Aligned_cols=290 Identities=16% Similarity=0.285 Sum_probs=0.0
Q ss_pred
                 Q Fri_Mar_04_23:
                2 OPFDSGHDDL-VHDVVYDFYGRHVATCSSDOHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKT
                                                                                  80 (349)
                2 -----h----y----s-d---l-t-s-D--v-iwd------h---y--v-v-v-----las-s-Dg-
Q Consensus
                                                                                  80 (349)
              ...+.||.+. +.+++|+ | ++|+||+.|++||+.+. .+..++.+.|.+.+.+. +++|+||+.|++

111 ---l-gh---vi------g--l-sgs-D--i-iWd---g------l-gh---v-------l-sgs-D--

111 PKVLKGHDDHVITCLQFC-GNRIVSGSDDNTLKVWSAVTG----KCLRTLVGHTGGVWSSQMR----DNIIISGSTDRT
T Consensus
T 2ovr B
                                                                                 180 (445)
T ss dssp
                 CEEECSTTSCEEEEEE-TTEEEEEETTSCEEEEETTTC---CEEECCCCSSCEEEEEE---TTEEEEEETTSC
```

```
T ss_pred
               eeEecCCCCCEEEEEEc--CCEEEEEeCCCcEEEEECCCC----cEEEEEcCCCCCEEEEeec----CCEEEEEeCCCc
                 EEEeeccCccccccceeEEEEcCCCCcEEEEEECcCCCcEEEEEecCCCcceeeeccccEEEeecC
0 ss pred
 Q Fri_Mar_04_23:
              81 VKLWEEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIP 160 (349)
              81 v-lwd-----d-i-iwd-------
 Q Consensus
                                                                             160 (349)
                          +.+..+.+|...|.++.+++. . .+++++.|++||+.++|.....
                 |++||+.++
              T Consensus
                                                                             236 (445)
              181 LKVWNAETG-----ECIHTLYGHTSTVRCMHLHEK---RVVSGSRDATLRVWDIETGQCLHVLM----- 236 (445)
T 2ovr B
                 EEEEETTTT-----EEEEEECCCSSCEEEEEETT----EEEEEETTSEEEEEESSSCCEEEEEE
T ss dssp
T ss_pred
                 EEEEECCCC-----ceeeeeccccceeeeeccc---eeeeecccceeeeec----
                 CCcccceeEEEEccCCCCceEEecCCc-eEEEEEccCCcEEEEEEccCCCcceeEEEECCCCCcceEEEEECCCCC
Q ss pred
Q Fri Mar 04 23: 161 PANHLQSDFCLSWCPSRFSPEKLAVSALEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIATGCKDGR 239 (349)
                                       ---i-----las-s-d--
                                                                              239 (349)
O Consensus
                            +..++++.++ +++|+.... ..+..+|...|.+++|...
T Consensus
             300 (445)
T 2ovr_B
              237 --GHVAAVRCVOYD-----GRRVVSGAYDFMVKVWDPETE---TCLHTLOGHTNRVYSLOFDG------IHVVSGSLDTS
                                                                              300 (445)
                --CCSSCEEEEEC----SSCEEEEETTSCEEEEEGGGT---EEEEEECCCSSCEEEEEECS-----SEEEEEETTSC
T ss_dssp
T ss pred
                 --CCCccEEEEEC-----CEEEEEECCCC---cEEEEECCCCCEEEEEECCC-----CEEEEECCCC
Q ss_pred
                 Q Fri_Mar_04_23: 240 IRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDD---HNGEVWSVSWNLTG 316 (349)
              Q Consensus
                 |++||+..+...+.+...+..+...
              301 i-iwd-----l--h-----h---vwd------h---v--h---v--
T Consensus
                                                                              372 (445)
              301 IRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADST-----VKIWDIKTGQCLQTLQGPNKHQSAVTCLQF--NK 372 (445)
T 2ovr_B
T ss dssp
                 ERREPTTCCEREEECCCCSCEREREPTTEREREPTTSC-----ERREPTTTCCERERECSTTSCSSCREERER--CS
                 EEEEECCCCcEEEEECCCCccEEEEEcCCEEEEEcCCe-----EEEEECCCCCCEEEEEE--CC
T ss_pred
Q ss_pred
                 CEEEEecCCCeEEEEeccCC
 Q Fri_Mar_04_23: 317 TILSSAGDDGKVRLWKATYSNEFKCMSVITAQQ 349 (349)
             317 --las-s-D--v-iW-----
O Consensus
                                           349 (349)
                ++|++|+.|++|+||+..+....+
              373 --1-s-s-Dg-i-iwd---g----1---
T Consensus
                                           405 (445)
             373 NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGG 405 (445)
T 2ovr B
                 SEEEEETTSEEEEEETTTCCEEEEEECTTGG
T ss_dssp
T ss_pred
                 CEEEEECCCCeEEEEECCCCcEeeeeeccccCC
                         PDB™
PROTEIN DATA BANK
No 100
                                                 Pub Med
>4ui9_R Fizzy-related protein homolog; ubiquitination, cell cycle, APC/C; 3.60A {Homo sapiens}
Probab=100.00 E-value=9.3e-30 Score=236.66 Aligned cols=248 Identities=16% Similarity=0.276 Sum probs=0.0
                 CCCCCCEEEEEECCCCCEEEEEeCCCCEEEEEECCCCCCceeEeeeeccccceEEEEECCCCCCEEEEE
Q ss_pred
Q Fri_Mar_04_23:
              5 DSGHDDLVHDVVYDFYGRHVATCSSDQHIKVFKLDKDTSNWELSDSWRAHDSSIVAIDWASPEYGRIIASASYDKTVKLW
                                                                              84 (349)
               O Consensus
                                                                              84 (349)
              T Consensus
                                                                              296 (493)
              225 LSVEGDSVTSVGWSERGNLVAVOTHKGFVQIWDAAAG---KKLSMLEGHTARVGALAWN---AEQLSSGSRDRMILQR
T 4ui9 R
                                                                              296 (493)
                 CSSSTTCEEEEEECTTSSEEEEEETTSCEEEEETTTT----EEEEEECCCSSCEEEEEE----TTEEEEEETTSEEEEE
 T ss_dssp
                 eccccceeeeeecccceeeeeecccc----eeeeeeecccceeeeecccceeeee
T ss_pred
                 \verb|eccCcccccceeEEEEcCCCCceEEEEEcCCCCceEEEEEeCCCceEEEEEECCCCcceeeecccEEEeecCCCcc| \\
Q ss pred
Q Fri_Mar_04_23:
              85 EEDPDQEECSGRRWNKLCTLNDSKGSLYSVKFAPAHLGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKVLSIPPANH 164 (349)
              164 (349)
              T Consensus
                                                                              354 (493)
T 4ui9 R
                                                                              354 (493)
T ss_dssp
                 ESSSSC-----EEEEEECSCCSSCCCEEECTT--SSEEEEECTTSCEEEEETTCSSCSEEE------CCC
                 eCCCCCc-----ceeEecCCCCCEEEEEECCC--CCEEEEEeCCCeeEEEecCCCeeeEEe
T ss pred
                 GCGEEEEECCCCCCCGEEEC--CCC-EEEEECCCCCCEEEEEECCCCCCGEEEEE--ECCCCC
Q ss pred
Q Fri Mar_04 23: 165 LQSDFCLSWCPSRFSPEKLAVSA--LEQ-AIIYQRGKDGKLHVAAKLPGHKSLIRSISWAPSIGRWYQLIAT--GCKDGR
                                                                             239 (349)
                       239 (349)
Q Consensus
                355 ---v-i--sp-----l-sg-gs-d--I-iwd-------v---v---s--g-----l----g--dg-
T Consensus
T 4ui9_R
              355 LAAVKAIAWSPH--OHGLLASGGGTADRCIRFWNTLTGOPLOCI----DTGSOVCNLAWSKHA----NELVSTHGYSONO
                                                                              424 (493)
                 SSCCCEEECSS--STTEEEECCTTTCEEEEEETTTCCEEEEE----ECSSCEEEEECSSS----SEEEEEECTTTCC
T ss dssp
                 ccceeeeecccc--ccceeeeeccccceeeee----cccceeeeeccccc
T ss pred
Q ss_pred
                 Q Fri_Mar_04_23: 240 IRIFKITEKLSPLASEESLTNSNMFDNSADVDMDAQGRSDSNTEEKAELQSNLQVELLSEHDDHNGEVWSVSWNLTGTIL 319 (349)
O Consensus
              240 v~vwd~~~~~
                                                  -----h---i--v--spdg--l 319 (349)
                 |++||+...
                                                          +.+..+.+|...|.+++|+|||++|
                                                        --~~~l~~h~~~V~~l~~spdg~~l
T Consensus
              425 I~vwd~~
                                                                              458 (493)
              425 ILVWKYPSL-----TQVAKLTGHSYRVLYLAMSPDGEAI
T 4ui9 R
T ss_dssp
                 EEEEETTTC-----CCCCCBCCCSSCCCEEECTTSSEE
T ss_pred
                 EEEEecCCC-----ceeeeeeccccee
Q ss_pred
                 EEecCCCeEEEEecccCCc
 Q Fri_Mar_04_23: 320 SSAGDDGKVRLWKATYSNE 338 (349)
             320 as~s~D~~v~iW~~~~~ 338 (349)
 O Consensus
```



© 2008-2016, Dept. of Protein Evolution at the Max Planck Institute for Developmental Biology, Tübingen

Release-2.18.5