

```
☐ 29 1nr0_A Actin interacting prote 28.1 3E+02 0.0095

                                                                                                         7-87 (611)
                                                                      25.0
                                                                              9.2
                                                                                     81
                                                                                          20-143
| 29 inr0_A Actin interacting prote | 28.1 | 3E+02 | 0.0095 | 30 | 3odt_A Protein DOA1; ubiquitin | 27.7 | 2.3E+02 | 0.0072 | 31 | 3148_A Outer membrane usher protein | 26.5 | 28 | 0.00088 | 32 | 4aez_A CDC20, WD repeat-contai | 26.1 | 3.1E+02 | 0.0097 | 33 | 4gga_A P55CDC, cell division | 26.0 | 1.7E+02 | 0.0055 | 34 | 4kt3_B Putative lipoprotein; growth | 25.5 | 70 | 0.0022 | 35 | 3ow8_A WD repeat-containing protein; growth | 24.8 | 2.5E+02 | 0.0078 | 36 | 1nwz_A PYP, photoactive yellow | 24.7 | 50 | 0.0016 | 37 | 4gn4_B | 0body AMZEP06; beta bar | 24.7 | 56 | 0.0018 | 38 | 3frx_A Gianine pucletide-bid | 24.2 | 2.8E+02 | 0.0087 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 24.2 | 
                                                                      22.1 13.7 126
                                                                                            41-213
                                                                                                       184-309 (313)
                                                                       25.5
                                                                               1.5
                                                                                      18 188-205
                                                                                                        4-21 (94)
                                                                       23.0
                                                                                            51-202
                                                                                                       102-207 (401)
                                                                             11.3
                                                                                     106
                                                                       24.9
                                                                                            51-143
                                                                                                       114-175 (420)
                                                                       25.3
                                                                               3.6
                                                                                      39
                                                                                            72-143
                                                                                                        56-94
                                                                                                                (137)
                                                                       21.5
                                                                               9.6
                                                                                      74
                                                                                            36-143
                                                                                                       243-318 (321)
                                                                       25.4
                                                                               2.7
                                                                                      14 128-142
                                                                                                        29-42 (125)
                                                                       24.0
                                                                               2.9
                                                                                      21 189-209
                                                                                                        33-53
                                                                                                                (108)
   38 3frx_A Guanine nucleotide-bind 24.2 2.8E+02
                                                                       22.6
                                                                                                       241-314 (319)
                                                            0.0087
                                                                                            45-143
   39 3odt_A Protein DOA1; ubiquitin 24.0 2.7E+02
                                                            0.0085
                                                                       21.6
                                                                                     100
                                                                                            55-202
                                                                                                       117-216 (313)
   40 3vl1_A 26S proteasome regulato
                                            23.7 3.3E+02
                                                                                                       294-420 (420)
                                                               0.01
                                                                       22.5
                                                                             15.1
                                                                                     122
                                                                                            45-201
   41 1mzu_A PPR; photoactive yellow 23.2
                                                       56
                                                            0.0018
                                                                       25.4
                                                                              2.7
                                                                                      14 128-142
                                                                                                        34-47 (129)
   42 3fm0 A Protein CIAO1: WDR39.SG 23.0 2.6E+02
                                                                                                       267-332 (345)
                                                            0.0084
                                                                       23.0
                                                                               7.2
                                                                                      66
                                                                                            55-143
   43 1pgu A Actin interacting prote 22.3 4.1E+02
                                                                                                         8-94 (615)
                                                            0.013
                                                                       23.1 10.3
                                                                                            21-143
                                                                                      85
   44 2pm9 A Protein WEB1, protein t 22.2 1.9E+02
                                                            0.0061
                                                                       23.8
                                                                                                       129-194 (416)
   45 2xet_A CAF1A usher, F1 capsule 21.8 47
                                                            0.0015
                                                                       23.6
                                                                               1.9
                                                                                      15 191-205
                                                                                                       1-15 (89)
   46 2k50_A Replication factor A re 21.6
                                                       76 0.0024
                                                                       23.1
                                                                               3.1
                                                                                      43 166-210
                                                                                                        12-59 (115)
                                                                                                       564-647 (716)
   47 1zvu_A Topoisomerase IV subuni 21.4 1.5E+02 0.0048
                                                                       29.5
                                                                               6.0
                                                                                      79 126-215
   48 4ggc_A P55CDC, cell division c 20.0 3.3E+02
                                                             0.011
                                                                       21.2
                                                                                      70
                                                                                                       240-312 (318)
                                                                               7.9
                                                                                            41-143
                                          SCOP
                                                  PDB<sup>™</sup>
PROTEIN DATA BANK
  No 1
                               NCBI
                                                                               Pub Med
 🗌 >1xks_A Nuclear pore complex protein NUP133; beta-propeller, helical insertions, protein transport; 2.35A {Homo
  sapiens | SCOP: b.69.14.1
  Probab=100.00 E-value=2.9e-40 Score=311.13 Aligned cols=172 Identities=11% Similarity=0.112 Sum probs=0.0
                            EEEecCCCEEEEEcC-CCchhhhhhhhhcccccCCCcEEEEEeCCCCEEEEEecCCc
  Q Fri Sep 06 02:
                        10 KILTETEKYSVTKLS-TDLSFLPGSNGNNNTIDTHHFEGLVDTALOKALVNDLDHIYIWNYNSIO--KDTPICKISLHDD
                                                                                                                              86 (220)
                         10 ~vLt~n~~y~Vs~l~~~p~l~~~~q~iDs~sGyALv~s~~~~VW~Y~s~~--~p~~~fplp~~
  O Consensus
                                                                                                                              86 (220)
                            T Consensus
                          7 ~~~e~~~y~V~~~
                                                                                                                              83 (450)
  T 1xks A
                         7 HSITESVNYDVKTFGSSLPVKVM-EALTLAEVD-DQLTINID-EGGWACLVCKEKLIIWKIALSPITKLSVCKELQLPPS
                                                                                                                              83 (450)
  T ss_dssp
                            ----CCSSEEEEECSSCCCHHHH-HHHHHCCTT-SCEEEEC-TTSEEEEEETTEEEEECCSSCCGGGCCEEEEECCCC
  T ss_pred
                            eEeeccCceEEeeCCCcCCHHHH-HHhhccCCC-cceEEEEC-CCcEEEEEecCcEEEEEeecCCCCCcccceeccCCcc
  Q ss_pred
                            Q Fri Sep 06 02:
                        87 YSVLSSPPICLFTSSISSTNNDTANYNNNASG-----NINSGKFNNGICIINKKNSQFLYFEDISTINNLYTKLSKSKA
                                                                                                                            160 (220)
  Q Consensus
                         T Consensus
                                                                                                                            132 (450)
                        84 DFHWSADLVALSYSS-----PSGEAHSTQ----AVAVMVATR-EGSIRYWPSLAGE-----DTY
  T 1xks A
                                                                                                                            132 (450)
                            SSCCCGGGEEEECC-----TCC
  T ss_dssp
  T ss pred
                            cccCCcEEEEcCC------CcccccCC------CceEEEEcC-CccEEEcccCCC------Cce
  Q ss pred
                            eEEecCCCCCeEEEeccCCceEEEEeccCccEEEEeecCCCCE
  Q Fri_sep_06_02: 161 HVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDSTGKPKLELKQQLIKPQNSF 220 (220)
                        161 ~~~~l~L~~gE~vt~l~n~ePaG~IlaTS~gRl~~itirD~~Gkp~l~~~~~lik~~~~
                           +++.+.|..+|+|+||+|||||||+||+||++||+||++|
                                                                                        |++|+++||
                       133 ~ei~~L~~~E~vt~l~n~epaGfIlaTStgrl~~lsir~--Gkp~l~~~~~l~~~~G~
                                                                                                     187 (450)
  T Consensus
                        133 TEAFVDSGGDKTYSFLTAVQGGSFILSSSGSQLIRLIPE---SSGKIHQ--HILPQGQGM
  T 1xks A
                                                                                                    187 (450)
                            EEEECC----CCEEEEEETTTEEEEEETTCCEEEEEEC---TTSCEEE--EECTTCCCC
  T ss dssp
                            EEEEecCCCceEEEEeecCCceEEEEeccceEEEEec---CCceEEE--EEecCCCcc
  T ss pred
                                         PDB NCBI Pub Med
  No 2
 >4g3n_A DNA gyrase subunit A; DNA gyrase C-terminal domain, beta-propeller, topoisomerase isomerase; HET: DNA;
  1.40A {Mycobacterium tuberculosis} PDB: 3uc1 _A*
  Probab=89.33 E-value=3.8 Score=36.50 Aligned_cols=135 Identities=9% Similarity=0.174 Sum_probs=0.0
                            eCCCCEEEEEcCCeEEEeeCCCCCCCCeEEEE---CCCccccCCCCceEEEeCCcccccccCCCCcccccCCCC
  0 ss pred
  Q Fri_Sep_06_02:
                        50 DTALQKALVNDLDHIYIWNYNSIQKDTPICKIS---LHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN 126 (220)
                         |--...+.+++++++ -+..-.+|.++ ||+......|+..|+..|+.-....
                         42 D-i----t-d-ll-----fT--G--y-l-v--iP-------G--i--ll-l----E-I-------------------
  T Consensus
                                                                                                                            109 (327)
                        42 DIVAHFFVCSTHDLILF----FTTQGRVYRAKAYDLPEASRTARGQHVANLLAF-QPEERIAQVIQIRGYTD-----A
  T 4q3n A
                                                                                                                            109 (327)
                            GCEEEEEETTSEEEE----EETTSEEEEEEGGGSCBCCTTCCCEEHHHHTTC-CTTCCEEEEEEESSTTS----S
  T ss dssp
  T ss_pred
                            CEEEEEEEcCCCEEEE----EeCCCeEEEEEcccCcccccCCCcccccc-CCCCeeeeccccccc------c
                            Q ss_pred
  Q Fri Sep 06 02: 127 NGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCEPSG-IIIATSLGRVLFITIKDSTGK
                                                                                                                            204 (220)
  O Consensus
                        204 (220)
                            T Consensus
                        180 (327)
  T 4g3n A
                        110 PYLVI.ATR-NGLVKKSKI.TD------FDSNRSGGTVAVNI.RDNDELVGAVI.CSAGDDI.I.I.VSANGOSTRESATDEALR
                                                                                                                            180 (327)
                            SEEEEET-TSEEEEEEGGG-----GCCCCSSEESCCCCTTCCEEEEEECTTCEEEEEETTSEEEEEECCTTTSC
  T ss dssp
  T ss_pred
                            eEEEEEec-Cceeeeeccce-----eeccCccceEEEeccCCccceeEEeccCCccceeEEeeccCccccc
  Q ss pred
  Q Fri_Sep_06_02: 205 P 205 (220)
  Q Consensus
                       205 p 205 (220)
  T Consensus
                               181 (327)
                        181 P
  T 4q3n A
                              181 (327)
  T ss dssp
                            В
  T ss_pred
                            С
```

```
PDB"
 No 3
                                                            NCBI
                                                                                    Pub Med
             Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 1.70A
  {Escherichia coli}
 Probab=84.38 E-value=3.7 Score=35.18 Aligned cols=69 Identities=14% Similarity=0.276 Sum probs=0.0
                              EEEEECCCceEEEEecccccccccccccccceeEEe--cCCCCCeEEEeEccCcce-EEEEeccCcEEEEEE
 Q ss pred
 Q Fri_sep_06_02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINCEPSG-IIIATSLGRVLFITIKDSTGK
                         129\ lliV-p-tG-v-yWesIs-a--l---L---k------l-L--gE-vt-l-n-ePaG--IlaTS-gRl---itirD--Gk \\ 204\ (220)
                          T Consensus
                                                                                                                                      118 (256)
 T 1zvt_A
                          47 VVFVDS-TGRS-YAIDPITLPS----ARGQGEPLTGKLTLPPGATVDHMLMESDDQKLLMASDAGYGFVCTFNDLVAR 118 (256)
 T ss_dssp
                              EEEEET-TSEE-EEECGGGSCC-----SSSCCEEGGGTCCCCTTCCEEEEEECCCTTCEEEEEBTTSEEEEEEGGGGCCC
 T ss_pred
                              EEEEeC-CCeE-EEEEHHHCCC-----CCCCCeEeeeeecCCCCCEEEEEEECCCCEEEEEEHHHhccc
 No 4
                                                         PDB
                                                                       NCBI
                                                                                      Pub Med
                                             SCOP
🗌 >1suu_A DNA gyrase subunit A; topoisomerase,DNA gyrase, beta-propeller, beta-pinwheel, ISO; HET: DNA; 1.75A
  {Borrelia burgdorferi} SCOP: b.68.10.1
 Probab=84.05 E-value=2 Score=37.69 Aligned cols=76 Identities=16% Similarity=0.241 Sum probs=0.0
                              EEEEECCCceEEEEeccccccccccceeEE----ecCCCCCCeEEEeEcc----CCceEEEEeecCcEEEEEEC
 Q ss pred
 Q Fri_Sep_06_02:
                        129 \ \text{ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVL----DLKLKDNENITSTINC----EPSGIIIATSLGRVLFITIKD} \\
                                                                                                                                        200 (220)
                         129 \ lliV-p-tG-v-yWesIs-a-cl---ck---cl-L--gE-vt-l-n-----ePaG-IlaTS-gRl--itirD
                          T Consensus
                                                                                                                                        133 (312)
                          61 LFMISN-EGKLYLINAYEIK-----DSSRASKGQNISELINLGDQEEILTIKNSKDLTDDAYLLLTTASGKIARFESTD
 T 1suu_A
                                                                                                                                       133 (312)
                              EEEEET-TSEEEEEEGGGSC-----C-CBGGGTSCCCTTCCEEEEEEESCCCTTCEEEEEEETTSEEEEEEGGG
 T ss dssp
 T ss_pred
                              EEEEEC-CCeEEEEEHHHCC-----CCCccCCCcChhhccCCCCCEEEEEEEeccCCCCCEEEEEEHHH
 Q ss pred
                              C----CCCEeEEEee
 O Fri Sep 06 02:
                        201 S----TGKPKLELKO 211 (220)
                         201 ~----Gkp~1~~~
                                                     211 (220)
 Q Consensus
                                    . . . . + . +++
 T Consensus
                        134 ~~~~r~~Ġ~~~i~L~~
                                                    149 (312)
                         134 FKAVKSRGVIVIKLND
 T 1suu A
                                                    149 (312)
                              GCC----CEECBCCCT
 T ss dssp
                              hhccCCCcEEEecCC
 T ss_pred
 No 5
                                                                                     Pub Med
3ucl A DNA gyrase subunit A; DNA binding protein, topoisomerase, isomerase; HET: DNA; 1.65A {Mycobacterium
 Probab=82.15
                  E-value=2.8 Score=37.27 Aligned_cols=78 Identities=18% Similarity=0.282 Sum_probs=0.0
 Q ss pred
                              EEEEECCCceEEEEecccccccccccccccccceeEe--cCCCCCCeEEEeEccC----CceEEEEeccCcEEEEEec--
 O Fri Sep 06 02:
                        129 ICIINKKNSOFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINCE----PSGIIIATSLGRVLFITIKD--
                                                                                                                                       200 (220)
 Q Consensus
                         129 lliV-p-tG-v-yWEsIs-a--l---k----k-----l-L--gE-vt-l-n-e----PaG-IlaTS-gRl--itirD--
                          T Consensus
                                                                                                                                        130 (327)
 T 3uc1 A
                          56 TIFFTT-OGR-VYRAKAYDI.PEAS---RTARGOHVANI.J.AFOPEERTAOVIOIRGYTDAPYI.VI.ATRNGI.VKKSKI.TDFD
                                                                                                                                       130 (327)
 T ss dssp
                              EEEEET-TSE-EEEEEGGGSCBCC---SSSCCEEHHHHTTCCTTCCEEEEEEESSTTSSSEEEEEETTSEEEEEEGGGGC
                              EEEEeC-CCe-EEEEEHHHCCCCC---cCCCEEHHHccCCCCCCEEEEEEECCCCCEEEEEEEHHHhh
 T ss_pred
 Q ss_pred
                              ---CCCCEEEEee
 Q Fri Sep 06 02: 201 ---STGKPKLELKQ 211 (220)
 O Consensus
                        201 ---~Gkp~l~~~
                                                  211 (220)
                                  ..|+-.+.++
                         131 ~~~r~G~~~i~lke
 T Consensus
                                                 144 (327)
 T 3uc1_A
                         131 SNRSGGIVAVNLRD
                                                  144 (327)
 T ss_dssp
                              CCCSSCEESCBCCT
 T ss pred
                              cccCceEEEEECC
                                              PDB"
                                                            NCBI
>3uc1 A DNA gyrase subunit A; DNA binding protein, topoisomerase, isomerase; HET: DNA; 1.65A {Mycobacterium
 tuberculosis}
 Probab=81.74 E-value=19 Score=31.85 Aligned cols=134 Identities=8% Similarity=0.167 Sum probs=0.0
                              Q ss_pred
                         50 DTALOKALVNDLDHIYIWNYNSIOKDTPICKIS---LHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN
                                                                                                                                       126 (220)
 Q Fri Sep 06 02:
                          O Consensus
                                                                                                                                  ~~e
                                                                                                                                       126 (220)
                              |.-...+.+++.+.-=
                                                           .-.++.++
                                                                            | | + . . . . - . | + . . + + . - . . + + . . . . + + . - . . .
                                -----t-d-ll-fT-----Gr-y-----lp---r---G--i---l-l----e-i-----
 T Consensus
                          42 DIVAHFFVCSTHDLILFFTT----QGRVYRAKAYDLPEASRTARGQHVANLLAF-QPEERIAQVIQIRGYTD-----A
 T 3uc1 A
                                                                                                                                       109 (327)
 T ss_dssp
                              GCEEEEEETTSEEEEEET----TSEEEEEEGGGSCBCCSSSCCEEHHHHTTC-CTTCCEEEEEEESSTTS-----S
                              CEEEEEEeCCCCEEEEEeC----CCeEEEEEHHHCcCCCccCCCEEHHHccCCC-CCCCEEEEEEEeccCCC-----C
 T ss_pred
 Q ss pred
                              Q Fri_Sep_06_02:
                        127 \ \texttt{NGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCE-PSGIIIATSLGRVLFITIK--D--INCOMPACTION CONTROL OF STREET 
                                                                                                                                       200 (220)
                                                                                                                                       200 (220)
 Q Consensus
                         127 pGlliV-p-tG-v-yWEsIs-a--l---k-----l-L--gE-vt-l-n-e-PaG-IlaTS-gRl---itir--D--
                                                                +..++...+. ++|++|+..+..+. ..-+++.|+.||++++.+- +
                              +-+++........................
```

```
T Consensus
                 110 PYLVLATR-NGLVKKSKLTD-----FDSNRSGGLVAVNLRDNDELVGAVLCSAGDDLLLVSANGOSTRFSATDEALR
 T 3ucl A
                                                                                              180 (327)
 T ss dssp
                    SEEEEET-TSEEEEEEGGG-----GCCCCSSCEESCBCCTTCCEEEEEECTTCEEEEEETTSEEEEEECCTTTSC
                    CEEEEECC-CCEEEEeEHHH------hhccccCceEEEEECCCCEEEEEECCCCEEEEEECCcccC
 T ss pred
 Q ss_pred
                    CCCC
 Q Fri_Sep_06_02: 201 STGK 204 (220)
 Q Consensus
                 201 ~~Gk
                         204 (220)
                    .+||
                 181 ~~gr
 T Consensus
                          184 (327)
                 181 PMGR
 T 3uc1 A
                          184 (327)
 T ss dssp
                    CCCT
 T ss_pred
                    cCCc
                                          NCBI
                                                           Pub Med
□ >316v_A GYRA, DNA gyrase subunit A; gyrase A C-terminal domain, GYRA C-terminal domain, DNA wrapping,
 beta-strand-bearing proline, ATP-binding; HET: DNA; 2.19A {Xanthomonas campestris PV}
 Probab=79.89 E-value=4 Score=37.05 Aligned_cols=78 Identities=13% Similarity=0.289 Sum_probs=0.0
                    EEEEECCCceEEEEecccccccccccccceeEEe--cCCCCCceEEEeEcc----CCceEEEEEecc---
 Q Fri_sep_06_02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINC---EPSGIIIATSLGRVLFITIKD--
                                                                                              200 (220)
                 129 lliV~p~tG~v~yWEsIs~a~~l~~~k~~~~~l~L~~qE~vt~l~n~----ePaG~IlaTS~qRl~~itirD--
 Q Consensus
                                                                                              200 (220)
                  T Consensus
                                                                                              134 (370)
                  60 LLTFTS-SGKV-FWLPVHQLPEAG---SNARGRPIINWIPLESGERVQAVLPVREYADNRYVFMATRNGTVKKTPLSEFA
 T 316v A
                                                                                              134 (370)
 T ss dssp
                     EERERT-TSEE-EEEEGGGSCBCC---TTSCCEEGGGSCCCCTTCCEEEEEEESCCCTTCEEEEEETTSEEEEEGGGGC
                    EEEEeC-CCeE-EEEEHHHCcCCC---cccCCcCHhhccCCCCCEEEEEEeccCCCcEEEEEeCCCeEEEeEHHHhh
 T ss pred
 Q ss_pred
                    ---CCCCEeEEEee
 Q Fri_Sep_06_02: 201 ---STGKPKLELKQ 211 (220)
 O Consensus
                 201 ---~Gkp~l~~~~
                                   211 (220)
                       .. +-.+.++
                    ~~~~Ġ~~ai~L~~
 T Consensus
                                   148 (370)
                 135 FRLARGKIAINLDE 148 (370)
 T 316v_A
 T ss_dssp
                    SCCTTCEESSCCCT
 T ss_pred
                    cccCcceEEEEeCC
                                PDB
 No 8
🗌 >1zvu_A Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 3.00A
 {Escherichia coli}
 Probab=76.20 E-value=4 Score=40.64 Aligned cols=76 Identities=17% Similarity=0.306 Sum probs=0.0
 Q ss_pred
                    EEEEECCCceEEEEeccccccccccccccceeEe--cCCCCCCeEEEeEccCCc-EEEEeccCcEEEEEEeCCC---
 Q Fri_Sep_06_02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINCEPSG-IIIATSLGRVLFITIKDST---
                                                                                              202 (220)
                 O Consensus
 T Consensus
                    VVFVDS-TGRS-YAIDPITLPS----ARGQGEPLTGKLTLPPGATVDHMLMESDDQKLLMASDAGYGFVCTFNDLVARN
 T 1zvu_A
                                                                                              589 (716)
                     EEEEET-TSEE-EEECTTTSCC----CC--CBSTTTSCCCTTCCEEEEEEBTTSEEEEEEGGGGCCCS
 T ss_dssp
 T ss_pred
                     EEEEec-CCce-EEEEeeeccc----ccccCeeHHhccCCCCCCeEEEEEecCCceEEEEecHHHhcccC
                    --CCEeEEEee
 Q ss pred
 Q Fri_Sep_06_02: 203 --GKPKLELKQ 211 (220)
 O Consensus
                 203 --Gkp~1~~~~
                                211 (220)
                      |+-.+.++
                 590 ~~g~~ai~L~~
                                600 (716)
 T Consensus
 T 1zvu_A
                 590 RAGKALITLPE
                                600 (716)
                    TTCEECBCCCT
 T ss dssp
 T ss_pred
 No 9
                                       PDB"
PROTEIN DATA BANK
                                                                  Pub Med
                                                  S NCBI
                               SCOP
> > 1wp5_A Topoisomerase IV; broken beta-propeller, hairpin-invaded beta-propeller, six- bladed beta-propeller;
 1.79A (Geobacillus stearothermophilus) SCOP: b.68.10.1
Probab=75.85 E-value=9.3 Score=33.77 Aligned_cols=67 Identities=12% Similarity=0.252 Sum_probs=0.0
                    EEEEECCCceEEEEecccccccccccccceeEEe--cCCCCCCeEEEeEccC----CceEEEEEecC
 Q ss pred
                 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINCE----PSGIIIATSLGRVLFITIKD
 Q Fri_Sep_06_02:
                 129 lliV-p-tG-v-yWEsIs-a--l---L---k-----l-L--gE-vt-l-n-e----PaG-IlaTS-gRl--itirD 200 (220)
 O Consensus
                  T Consensus
                                                                                            125 (323)
                  53 LLLFTN-KGNY-LYCPVHELPDIR---WKDLGQHIANIIPIDRDEEIIKAIPINDFELNGYFLFVTRNGMVKKTELKH
 T 1wp5 A
                                                                                            125 (323)
                    EEEEET-TSEE-EEEEGGGSCBCC---TTSCCEEGGGTSCCCTTCCEEEEEECSCTTSSCEEEEEETTSEEEEEEGGG
 T ss dssp
                     EEEEEC-CCEE-EEEEHHHCCCCC---CCCCCCChhhccCCCCCEEEEEEecccCCCceEEEEeEEHHH
 T ss_pred
                                PDB"
 No 10
                                         NCBI
                                                    Pub Med
🗌 >1zio_A DNA gyrase subunit A; beta pinwheel, topoisomerase, spiralling beta pinwheel, DNA wrapping, isomerase,
 DNA bindng protein; HET: DNA; 2.60A {Escherichia coli}
 Probab=74.55 E-value=11 Score=32.94 Aligned_cols=67 Identities=18% Similarity=0.276 Sum_probs=0.0
```

```
Q ss pred
                 EEEEECCCceEEEEeccccccccccccccccccceEEe--cCCCCCceEEEeEcc----CCceEEEEEecc
Q Fri_Sep_06_02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTINC----EPSGIIIATSLGRVLFITIKD
                                                                             200 (220)
              129 lliV~p~tG~v~yWEsIs~a~~l~~~k~~~~~-l~L~~gE~vt~l~n~----ePaG~IlaTS~gRl~~itirD
O Consensus
                                                                             200 (220)
               56 \quad \text{ILCFSS-} \\ \text{RGRV-YSMKVYQLPEAT---RGARGRPIVNLLPLEQDERITAILPVTEFEEGVKVFMATANGTVKKTVLTE} \\
T 1zi0 A
                                                                             128 (307)
T ss_dssp
                 EEEEET-TSEE-EEEEGGGSCCCC---SSCCEEGGGTSCCCTTCCEEEEEEESCCCTTCEEEEEETTSEEEEEGGG
                 EEEEEG-CCEE-EEEEhhHCcCCC---CCCCCEEhhhccCCCCCEEEEEEegcCCCCCEEEEEeeCCCeEEEEEHHH
T ss_pred
                                           Pub Med
                          PDB<sup>™</sup>
PROTEIN DATA BANK
                                  NCBI
>3mmy A MRNA export factor; mRNA export, nuclear protein; HET: MES; 1.65A {Homo sapiens}
Probab=73.12 E-value=18 Score=29.37 Aligned cols=123 Identities=11% Similarity=0.002 Sum probs=0.0
Q ss_pred
                 Q Fri_Sep_06_02:
               {\tt 53~LQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDY-----SVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN}
                                                                              126 (220)
O Consensus
               126 (220)
                 ---dg-i-i----
                                                -----v---sp-
T Consensus
                                                                              284 (368)
T 3mmy A
              284 (368)
                 T ss_dssp
                 T ss pred
                 Q ss pred
Q Fri_Sep_06_02:
              127 \ \texttt{NGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDSTGKPK}
              T Consensus
                                                                              352 (368)
T 3mmy_A
              285 HGTLATVGSDGRFSFWD-----KDARTKLKTSEQLDQPISACCFNHNGNIFAYASSYDWSKGHEFYNPQKKNY
                                                                              352 (368)
 T ss dssp
                 TCCEEEEETTSCEEEEE.....TTTTEEEEECCCSSCEEEEECTTSSCEEEEECCCSTTCGGGCCTTSCCE
T ss_pred
                 CCEEEEEccCCeEEEEe.-----CCCCcEEEEecCCCCceEEEEeccccccccccCCCccc
                 EEEee
Q ss pred
Q Fri Sep 06 02: 207 LELKQ
                      211 (220)
 Q Consensus
              207 1~~~
                      211 (220)
T Consensus
              353 i~~~~
                      357 (368)
T 3mmy A
              353 TFLRN
                      357 (368)
T ss dssp
                 EEEEC
T ss pred
                 eeehh
                               PDB<sup>N</sup>
PROTEIN DATA BANK
No 12
                                                       Pub Med
                          SCOP
>1suu A DNA gyrase subunit A; topoisomerase, DNA gyrase, beta-propeller, beta-pinwheel, ISO; HET: DNA; 1.75A
 {Borrelia burgdorferi} SCOP: b.68.10.1
 Probab=71.29 E-value=14 Score=32.30 Aligned_cols=80 Identities=16% Similarity=0.216 Sum_probs=0.0
                 EEEEECCCceEEEEecccccccccccccceeEee-cCCCCCceEEEeEccCCce-EEEEeccCceEEEEEeC--CCCC
Q ss pred
Q Fri Sep 06 02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCEPSG-IIIATSLGRVLFITIKD--STGK
                                                                              204 (220)
              129\ lliV-p-tG-v-yWEsIs-a--l---k-----l-L--gE-vt-l-n-ePaG--IlaTS-gRl---itirD----Gk
                                                                              204 (220)
              T Consensus
                                                                              187 (312)
              117 LLLTTA-SGKIARFESTD-----FKAVKSRGVIVIKLNDKDFVTSAEIVFKDEKVICLSKKGSAFIFNSRDVRLTNR
T 1suu A
                                                                              187 (312)
                 EEEEET-TSEEEEEEGGG------CEECBCCCTTCCEEEEEECTTCEEEEEETTSEEEEEEGGGSCBCCT
T ss dssp
                 EEEEeC-CCeEEEEEHHH------hhccCCceEEEEecCCCCEEEEEeCCCCEEEEEHHHcccCCC
T ss_pred
Q ss_pred
                 EEEEEeEEEccCCCC
Q Fri Sep 06 02: 205 PKLELKQQLIKPQNS 219 (220)
              205 p~l~~~~lik~~~
                             219 (220)
O Consensus
                 ..--+ +++|-..|
              188 ~~~Gv--~~i~L~~
T Consensus
                             200 (312)
              188 GTQGV--CGMKLKEG 200 (312)
T 1suu A
T ss_dssp
                 TBCCE--ECCCCCTT
T ss pred
                 CCCCe--EeEEeCCC
                                           Pub Med
                                  NCBI
🗌 >1zio_A DNA gyrase subunit A; beta pinwheel, topoisomerase, spiralling beta pinwheel, DNA wrapping, isomerase,
DNA bindng protein; HET: DNA; 2.60A {Escherichia coli}
          E-value=60 Score=28.07 Aligned_cols=130 Identities=12% Similarity=0.097 Sum_probs=0.0
                 Q ss_pred
Q Fri Sep 06 02:
               50 DTALOKALVNDLDHIYIWNYNSIOKDTPICKIS---LHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN 126 (220)
               O Consensus
                 42 D-1----a-G----a-G----a-G----a-G--i---l-l----e-i-------
               42 DFIDRLLVANTHDHILCFSS-----RGRVYSMKVYQLPEATRGARGRPIVNLLPL-EQDERITAILPVTEFEE------G
T 1zi0 A
                                                                              109 (307)
T ss_dssp
                 CCEEEEEEETTCEEEEET----TSEEEEEEGGGSCCCCSSSCCEEGGGTSCC-CTTCCEEEEEEESCCCT-----T
                 CEEEEEEECCCCEEEEEC----CCEEEEEEhhHCcCCCCCCCeEhhhccCC-CCCCEEEEEEeccCCC-----C
T ss pred
Q ss pred
                 Q Fri_Sep_06_02: 127 NGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCEPSG-IIIATSLGRVLFITIKD 200 (220)
                                                                           200 (220)
              127 \ pGlliV-p-tG-v-yWEsIs-a--l----k------l-L--gE-vt-l-n-ePaG--IlaTS-gRl---itirD
 Q Consensus
                 +-++++....
                                      +...+...+. ++|.+++..+..+... +++.|+.||++++.+.|
```

```
T Consensus
               110 VKVFMATA-NGTVKKTVLTE-----FNRLRTAGKVAIKLVDGDELIGVDLTSGEDEVMLFSAEGKVVRFKESS 176 (307)
T 1zi0 A
T ss dssp
                  CEEEEET-TSEEEEEGGG-----GTTCCTTCEESSCCCTTCCEEEEEECTTCEEEEEETTSEEEEEEGGG
                  CEEEEEC-CCeEEEEEHHH-----hhccccCCeEEEEECCCCEEEEEECCCCEEEEEHHH
T ss pred
                            PDB<sup>™</sup>
PROTEIN DATA BANK

NCBI
No 14
                                                    Pub Med
>4g3n A DNA gyrase subunit A; DNA gyrase C-terminal domain, beta-propeller, topoisomerase isomerase; HET: DNA;
 1.40A {Mycobacterium tuberculosis} PDB: 3ucl _A*
 Probab=66.47 E-value=18 Score=32.06 Aligned cols=67 Identities=16% Similarity=0.264 Sum probs=0.0
                  EEEEECCCceEEEEeccccccccccccceeEEe--cCCCCCCeEEEeE----ccCCceEEEEEecCcc
0 ss pred
Q Fri Sep 06 02: 129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD--LKLKDNENITSTI----NCEPSGIIIATSLGRVLFITIKD
                                                                                 200 (220)
               129\ lliV-p-tG-v-yWEsIs-a--l----k------l-L--gE-vt-l-----n-ePaG-IlaTS-gRl--itirD
                                                                                 200 (220)
               T Consensus
               56 ILFFTT-QGR-VYRAKAYDLPEAS---RTARGQHVANLLAFQPEERIAQVIQIRGYTDAPYLVLATRNGLVKKSKLTD 128 (327)
T 4g3n_A
                  EEEEET-TSE-EEEEEGGGSCBCC---TTCCCEEHHHHTTCCTTCCEEEEEEESSTTSSSEEEEEETTSEEEEEEGGG
T ss dssp
                  T ss pred
No 15
                            PDB"
                                                    Pub Med
>316v A GYRA, DNA gyrase subunit A; gyrase A C-terminal domain, GYRA C-terminal domain, DNA wrapping,
 beta-strand-bearing proline, ATP-binding; HET: DNA; 2.19A {Xanthomonas campestris PV}
 Probab=65.16 E-value=56 Score=29.40 Aligned cols=143 Identities=15% Similarity=0.118 Sum probs=0.0
Q ss_pred
                  eCCCCEEEEcCCeEEEeeCCCCCCCCCEEEEE---CCCccccCCCCceEEEeCCccccccccCCCccccccCCCCccccccCCCC
Q Fri Sep 06 02:
               50 DTALOKALVNDLDHIYIWNYNSIOKDTPICKIS---LHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN 126 (220)
               O Consensus
                                                                      ----s----e
                                                                                  126 (220)
               T Consensus
                                                                                   113 (370)
                46 DFIDQLWLVNTHDTLLTFTS----SGKVFWLPVHQLPEAGSNARGRPIINWIPL-ESGERVQAVLPVREYAD-----N 113 (370)
T 316v A
T ss dssp
                  CCEEEEEECTTCEEEEET----TSEEEEEEGGGSCBCCTTSCCEEGGGSCCC-CTTCCEEEEEEESCCCT-----T
                  CEEEEEEecCCCEEEEEeC-----CCeEEEEEHHHCcCCCcccCCCCHhhccCC-CCCEEEEEEEeccCCC------C
T ss_pred
Q ss_pred
                  Q Fri_Sep_06_02: 127 NGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCE-PSGIIIATSLGRVLFITIKD-ST
                                                                                   202 (220)
               127 pGlliV~p~tG~v~yWEsIs~a~~l~~~k~~~~-l~L~~qE~vt~l~n~e-PaG~IlaTS~qRl~~itirD--~
Q Consensus
                                                                                   202 (220)
               T Consensus
T 316v A
               114 RYVFMATR-NGTVKKTPLSE-----FAFRLARGKIAINLDEGDALVGVALTDGDRDVLLFASNGKTVRFGESTVRSM
T ss_dssp
                  CEEEEET-TSEEEEEEGGG-----GCSCCTTCEESSCCCTTCCEEEEEECSCCEEEEEETTSEEEEEEGGGSCBC
T ss_pred
                  CEEEEEC-CCeEEEeEHHH-----hhcccCCceEEEEECCCCEEEEEEeCCCceEEEEEcccCcc
Q ss_pred
                  CCEeEEEeeEEec
Q Fri_Sep_06_02: 203 GKPKLELKQQLIK 215 (220)
               203 Gkp~l~~~~lik 215 (220)
O Consensus
                  ||.+--+ ++||
               185 gR~a~GV--~~i~
                              195 (370)
T Consensus
               185 GRTATGV--RGIR 195 (370)
T 316v_A
                  CTTCCCE--ECCC
T ss_dssp
                  CCCCCCe--eeEE
T ss pred
                                   PDB
No 16
                           SCOP
> > Imp5_A Topoisomerase IV; broken beta-propeller, hairpin-invaded beta-propeller, six- bladed beta-propeller;
1.79A (Geobacillus stearothermophilus) SCOP: b.68.10.1
Probab=63.76 E-value=77 Score=27.76 Aligned cols=143 Identities=13% Similarity=0.085 Sum probs=0.0
Q ss_pred
                  Q Fri_Sep_06_02:
               {\tt 50~DTALQKALVNDLDHIYIWNYNSIQKDTPICKIS---LHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN}
                                                                                  126 (220)
               O Consensus
                                                                                  126 (220)
                                                                                   106 (323)
T Consensus
T 1wp5_A
                39 DRLLAMLEMNTKDVLLLFTN-----KGNYLYCPVHELPDIRWKDLGQHIANIIPI-DRDEEIIKAIPINDFEL-----N
                                                                                   106 (323)
T ss dssp
                  CCEEEEEEETTSEEEEEET----TSEEEEEEGGGSCBCCTTSCCEEGGGTSCC-CTTCCEEEEEEESCTTS-----S
                  T ss pred
                  Q ss pred
               127 NGICIINKKNSQFLYFEDISTINNLYTKLSKSK-AHVLD-LKLKDNENITSTINCE-PSGIIIATSLGRVLFITIKD--S
 Q Fri_Sep_06_02:
               127 pGlliV-p-tG-v-yWEsIs-a-~l-~~k-~~-k-----l-L-~gE-vt-l-n-e-PaG-IlaTS-gRl-~itirD---
 O Consensus
               T Consensus
                                                                                   177 (323)
               107 GYFLFVTR-NGMVKKTELKH------YKAQRYSKPLTGINLKNDDQVVDVHLTDGMNELFLVTHNGYALWFDESEVSI
T 1wp5_A
                                                                                  177 (323)
                  CEEEEEET-TSEEEEEEGGG-----GCCSCCSSCEECSCCTTCCEEEEEEECSCSEEEEEETTSEEEEEEGGGSCB
T ss dssp
T ss_pred
                  ceeeeec-cceeeeeeHHH-----hhhcccccceeeeeecccceeeeeeecccceeeeeHHHCcc
                  CCCEeEEEeeEEec
Q ss pred
Q Fri Sep 06 02: 202 TGKPKLELKQQLIK 215 (220)
                              215 (220)
               202 ~Gkp~l~~~~lik
 Q Consensus
                  +||..-+ +++|
T Consensus
               178 ~gR~a~GV--~~i~
                              189 (323)
 T 1wp5_A
               178 VGVRAAGV--KGMN
                              189 (323)
T ss_dssp
                  CCSSCCCE--ECCC
```

```
T ss_pred
                   cCCCccE--EEEE
                              PDB
🗌 >3no0_A DNA gyrase subunit A; DNA topology, topoisomerase, C-terminal DO gyrase, DNA binding protein, isomerase;
 HET: DNA GOL; 1.30A {Aquifex aeolicus}
 Probab=63.42 E-value=27 Score=29.97 Aligned cols=65 Identities=18% Similarity=0.288 Sum probs=0.0
                   Q ss pred
 Q Fri_Sep_06_02: 126 NNGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINCE-PSGIIIATSLGRVLFITIKD
                                                                                      200 (220)
                126 \ \text{epGlliV-p-tG-v-yWesIs-a-l---} \\ \text{L---k-----} \\ \text{L---gE-vt-l-n-e-PaG-IlaTS-gRl---itirD}
                                                                                      200 (220)
 Q Consensus
                   +--+++. -|-|+=.-=. +. .+...+. +|+|++..+..+. .-.++..|++..+.
 T Consensus
 T 3no0 A
                 80 GNRLLLATK-KGYVKKIPLAE-----FE-YKAQGMPIIKLTEGDEVVSIASSVDETHILLFTKKGRVARFSVRE 146 (276)
                   CSEEEEET-TSEEEEEEGGG----TT-TCSTTEECSCCCTTCCEEEEEECCSSCEEEEEETTSEEEEEEGGG
 T ss dssp
 T ss pred
                   CCEEEEEC-CCEEEEEHHH------hh-hhcCceEEEecCCCCEEEEEECCCEEEEEEhhh
 No 18
                              PDB
                                                       Pub Med
->1zvt A
        Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 1.70A
 {Escherichia coli}
 Probab=62.98 E-value=5.8 Score=33.95 Aligned cols=41 Identities=20% Similarity=0.360 Sum probs=0.0
                   cCCCCCceEEeeccC-CceEEEeeccCcEEEEEeCC----CCCE
 Q ss pred
 Q Fri Sep 06 02: 165 LKLKDNENITSTINCE-PSGIIIATSLGRVLFITIKDS----TGKP
                                                            205 (220)
                165 \ l\sim L\sim \neg gE\sim vt\sim l\sim n\sim e-PaG\sim IlaTS\sim gRl\sim \neg itirD\sim ----\sim Gkp
                                                             205 (220)
 Q Consensus
                 +++++|+.+..+...-+++.|+.||++++.+-|- +|+
27 ~~lke-D~l~~~~t~~ll~~T~~Gr~~~~elp~~r~~G~
 T Consensus
                                                              73 (256)
                 27 LNYKAGDSFKAAVKGKSNQPVVFVDSTGRSYAIDPITLPSARGQGEP
 T 1zvt A
 T ss dssp
                   SCCCTTCCEEEEEETTSCEEEEETTSEEEEECGGGSCCSSSCCEE
                   T ss pred
                              PDB"
PROTEIN DATA BANK
 No 19
                                       NCBI
                                                        Pub Med
        Guanine nucleotide-binding protein beta subunit-L protein; ribosome, eukaryotic, kinetoplastids,
->3zey 7
 expansion segments; 5.57A {Trypanosoma brucei brucei}
 Probab=55.02 E-value=75 Score=24.52 Aligned_cols=100 Identities=9% Similarity=-0.012 Sum probs=0.0
                   Q ss pred
 Q Fri Sep 06 02:
                 60 DLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINKKNSQF
                                                                                         139 (220)
                 Q Consensus
                                                                                         139 (220)
                   +.-+|+....+|.|
                                                                             .
----l~s~s~D~~i
 T Consensus
                                                                                          91 (318)
 T 3zey 7
                 36 RDKTLLSWGPNPDRHSSECSYGLPDRRLEGHSAFVSDVALSN-----NGNFAVSASWDHSL
                                                                                          91 (318)
 T ss dssp
                   TTSEEEEEECCCCSSSTTSCSSEEEEEEECCSSCEEEEEECS-----SSSEEEEEETTSCE
                   CCCeEEEEeCCCCccceeccCceeEEEecCCCCEEEEEECC------CCCEEEEEEeCCCCE
 T ss pred
                   EEEecccccccccccceeEEecCCCCCeEEEeEccCCceEEEE
 0 ss pred
 Q Fri_Sep_06_02:
                140 LYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFI
                                                                     196 (220)
                140 ~yWEsIs~a~~l~~~k~~~~l~L~~gE~vt~l~n~ePaG~IlaTS~gRl~~i
                                                                     196 (220)
                                     .....++++++++++
 T Consensus
                 92 ~~
                       135 (318)
                 92 RLWNLQNGQ-----CQYKFLGHTKDVLSVAFSPDNRQIVSGGRDNALRV
 T 3zev 7
                                                                     135 (318)
                   EEEETTTTE----EEEEECCCSSCEEEEECCSSCEEEEEETTTEEEE
 T ss_dssp
 T ss pred
                   EEeecccce-----eeeeecCcccceeeeccccCcceeecCCCCcEE
 No 20
                              PDB
                                                        Pub Med
>3no0_A DNA gyrase subunit A; DNA topology, topoisomerase, C-terminal DO gyrase, DNA binding protein, isomerase;
 HET: DNA GOL; 1.30A {Aquifex aeolicus}
 Probab=54.42 E-value=55 Score=27.96 Aligned_cols=66 Identities=17% Similarity=0.209 Sum_probs=0.0
                   EEEEECCCceEEEEecccccccccccccceeEEecCCCCCeEEEeEccCCc-eEEEEeccCcEEEEEEeC
 Q ss pred
 Q Fri_Sep_06_02:
                129 ICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPS-GIIIATSLGRVLFITIKD 200 (220)
                200 (220)
 T Consensus
                                                                                   196 (276)
                130 ILLFTK-KGRV-ARFSVREVPP----STPGARGVQGIKLEKNDETSGLRIWNGEPYLLVITAKGRVKKISHEE 196 (276)
 T 3no0 A
                   EEEET-TSEE-EEEEGGGSCB----CCTTCCCEECCCCTTCCEEEEEEESSCSEEEEEETTSCEEEEEGGG
 T ss dssp
                   EEEEEC-CCEE-EEEEhhhCCC----CCCCCCEEEECCCCCCEEEEEECCCCCEEEEEHHH
 T ss pred
 No 21
                                                               Pub Med
                              SCOP
>lgxr_A ESG1, transducin-like enhancer protein 1; transcriptional CO-repressor, WD40, transcription repressor, WD
 repeat; 1.65A {Homo sapiens} SCOP: b.69.4.1 PDB: 2ce8 A 2ce9 A
 Probab=49.00 E-value=1e+02 Score=24.40 Aligned_cols=117 Identities=7% Similarity=0.090 Sum_probs=0.0
 Q ss pred
                   EEEEeCCCCEEEEEcCCeEEEeeCCCCCCCCCEEEEECCCccccCCCCceEEEeCCcccccccCCCcccccCCC
 Q Fri Sep 06 02:
                 46 EGLVDTALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKF
                 46 ~g~iDs~sGyALv~s~~~~VW~Y~s~~~~p~~~fplp~~~~~~Pl~~~v~p~s~~d~~~
 Q Consensus
                   ...+.+...+..+..+..||+......+....
 T Consensus
                 56 -----v----v
                 T 1gxr A
                   EEEECSSSSEEEEECBSEEEEETTSTTCCSCSEEEECSC----TTSBEEEEEECT------
 T ss dssp
```

```
T ss_pred
                 EEEEecCCceEEEEcCCCceeeeeccccc----CCCcEEEEEcc------
                 0 ss pred
 Q Fri_sep_06_02: 126 NNGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKD 200 (220)
              +..+++...+|.|+.|+-.

108 ----1----d--i---d----------i-----i-----dq-v---d---
T Consensus
                                                                          172 (337)
              108 DGCTLIVGGEASTLSIWDLAA------PTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNIAVWDLHN 172 (337)
T 1qxr A
                 TSSEEEEESSSEEEEECCC-----C-EEEEEEECSSSCEEEEEECTTSSEEEEEETTT
T ss dssp
                 T ss_pred
                          PDB<sup>™</sup>
PROTEIN DATA BANK
No 22
                                  NCBI Pub Med
       Guanine nucleotide-binding protein subunit beta-2; receptor, WD-repeat, beta-propeller; 2.45A {Homo
 sapiens} PDB: 3j3a _g 2zkq _a 3j38 _g
Probab=46.75 E-value=1.2e+02 Score=25.31 Aligned cols=108 Identities=17% Similarity=0.179 Sum probs=0.0
                 0 ss pred
Q Fri_Sep_06_02:
              \tt 55\  \  {\tt KALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINK}
              55 yALv-s----VW-Y-s----p----fplp------Pl----v-p-s--d---
 Q Consensus
                                                            ~~~s~~~~epGlliV~p
                                                                             134 (220)
                 .+-.-...+.||+....
                                  +....+..-.++-.+
                                                                     +..+++...
              188 l~s~~d~~v~iwd~~~~~h~~~v~~~sp-
T Consensus
                                                                   ---dq~~1~s~~
                                                                             234 (340)
              188 IVSCGWDKLVKVWNLANCK------LKTNHIGHTGYLNTVTVSP------DGSLCASGG
T 4aow A
                                                                             234 (340)
T ss dssp
                 EEEEETTSCEEEEETTTTE-----TSSEEEEEE
T ss_pred
                 EEEeCCCCeEEEEECCCc-----eeEEecCCCcEEEEEEcC----
                 CCceEEEecccccccccccccceeEeecCCCCCeEEEeEccCCceEEEeeccCceEEEeeeE
Q ss pred
Q Fri Sep 06 02: 135 KNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDSTGKPKLELKQQ 212 (220)
              212 (220)
              T Consensus
                                                                            295 (340)
              235 KDGQAMLWDLNE-----GKHLYTLDGGDIINALCFSPNRYWLCAATGP-SIKIWDLEGKIIVDELKQ
T 4aow A
                                                                           295 (340)
                 TTCEEEEEETTT----TEEEEEEECSSCEEEEEECTT-EEEEEETTTTEEEEEECC
T ss_dssp
T ss pred
                 CCCeEEEECCC----CCEEEEECCCCeeeEEEECCCC-cEEEEECCCCceeehhhhhc
                          PDB"
No 23
                                                 Pub Med
>3zey 7 Guanine nucleotide-binding protein beta subunit-L protein; ribosome, eukaryotic, kinetoplastids,
 expansion segments; 5.57A {Trypanosoma brucei brucei}
 Probab=33.52 E-value=1.7e+02 Score=22.40 Aligned cols=73 Identities=8% Similarity=-0.027 Sum probs=0.0
                 Q ss pred
O Fri Sep 06 02:
              45 FEGLVDTALOKALVNDLDHIYIWNYNSIOKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGK 124 (220)
              45 ~~g~iDs~sGyALv~s~~~~VW~Y~s~~~~fplp~~~~~Pl~~~v~p~s~~d~~~
O Consensus
                .....+-+--+
              T Consensus
                                                                             295 (318)
              241 NOICFSPNRYWMCAATEKGIRIFDL--ENKDIIVELAPEHOGSKKIVPECVSIAWSA-----
T 3zey_7
                                                                             295 (318)
                 EEEEECSSSSEEEEETTEEEEET-TTTEEEEEECCCCCSSSCCCEEEEEECT------
T ss dssp
                 eeeeeecccceeccCCeEEEEEC--CCCCEEEEEcCcccCccccCCEEEEEECC-----
T ss_pred
Q ss_pred
                 CCCEEEEECCCCCEEEEE
Q Fri_Sep_06_02: 125 FNNGICIINKKNSQFLYFE 143 (220)
              125 ~epGlliV~p~tG~v~yWE 143 (220)
Q Consensus
                  +.-+|+...+|.|+.|+
T Consensus
              296 -dg~~l~sg~~Dg~v~iWd 313 (318)
T 3zey_7
              296 -DGSTLYSGYTDNVIRVWG 313 (318)
T ss_dssp
                -TSCEEEEEESSCCEEEEE
T ss_pred
                 -CCCEEEEecCCCEEEec
                                          Pub Med
                                  S NCBI
>4aow A Guanine nucleotide-binding protein subunit beta-2; receptor, WD-repeat, beta-propeller; 2.45A {Homo
robab=32.70 E-value=1.2e+02 Score=25.35 Aligned_cols=74 Identities=7% Similarity=-0.044 Sum_probs=0.0
                 Q ss pred
Q Fri_Sep_06_02:
              46 EGLVDTALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKF 125 (220)
              O Consensus
                                                                             125 (220)
              261 ALCFSPNRYWLCAATGPSIKIWDLEGKIIVDELKQEVISTSSKAEPPQCTSLAWSA----- 316 (340)
T 4aow A
T ss dssp
                 EEEECSSSSEEEEETTEEEEEETTTTEEEEEECCC------CCCCCEEEEEECT-------
T ss pred
                 EEEECCCCeEEEEeCCCceeehhhhccccccccCCCcceeEEECC------
                 CceEEEECCCceEEEEe
Q ss_pred
 Q Fri_Sep_06_02: 126 NNGICIINKKNSQFLYFE
                               143 (220)
 Q Consensus
              126 epGlliV~p~tG~v~yWE 143 (220)
                 +.-.|+...+|.|+.|+
              317 dg~~l~sg~~Dg~v~vW~
T Consensus
                               334 (340)
              317 DGQTLFAGYTDNLVRVWQ 334 (340)
T 4aow_A
 T ss dssp
                 TSSEEEEETTSCEEEE
                 CCCEEEEccCCCCEEEEe
T ss pred
```

```
PDB"
No 25
                                                     Pub Med
>4bh6 A APC/C activator protein CDH1; anaphase promoting complex, ACM1, cell cycle, ubiquitination; HET: SEP;
 2.90A {Saccharomyces cerevisiae}
 Probab=32.59 E-value=1.9e+02 Score=22.56 Aligned cols=102 Identities=7% Similarity=-0.042 Sum probs=0.0
                  Q ss pred
Q Fri Sep 06 02:
                53 LOKALVNDLDHIYIWNYNSIOKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICII
                                                                                      132 (220)
                53 sGyALv-s----VW-Y-s----p----fplp------Pl---v-p-s--d----
                                                                              ~epGlliV
O Consensus
                                                                                     132 (220)
                  ..+..+....+++|+.....
                T Consensus
                                             -----v~~~v~~~~
                                                                              _~~~1~~
                                                                                      79 (308)
                34 TDVLAVALGKSIFLTDNNTGDVVHLCD-----TENEYTSLSWIG------AGSHLAV
T 4bh6 A
                                                                                      79 (308)
                  TSEEEEETTEEEEEETTTCCEEEEEE.....TSSEEEE
T ss dssp
T ss pred
                  CCEEEEecCCeEEEECC-----CCCceEEEEcC------CCCEEEE
Q ss_pred
                  ECCCceEEEEeccccccccccccceeEEecCCCCCeEEEeeccCcceEEEEeccCc
Q Fri_Sep_06_02: 133 NKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDST 202 (220)
O Consensus
               133 ~p~tG~v~yWEsIs~a~~l~~~k~~~~l~L~~gE~vt~l~n~ePaG~IlaTS~gRl~~itirD~~
                                                                             202 (220)
                  T Consensus
                                        ----v---v----l----d--i-i-d-----
                80 GQANGLVEIYDVMKRK-----CIRTLSGHIDRVACLSW-NNHVLTSGSRDHRILHRDVRMPD 135 (308)
T 4bh6 A
T ss_dssp
                  EETTSCEEEEETTTTE-----EEEEECCCSSCEEEEEE-ETTEEEEEESSSCEEEEETTSSS
                   ECCCCEEEEECCCCe-----EeEEeccccCceEEEEe-cCCEEEEecCcceEEEECCCCc
T ss_pred
                            PDB<sup>N</sup>
PROTEIN DATA BANK
                                      NCBI
                                                     Pub Med
3v11_A 26S proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A {Saccharomyces
cerevisiae PDB: 3acp A
Probab=32.25 E-value=2.3e+02 Score=23.51 Aligned_cols=81 Identities=11% Similarity=0.025 Sum_probs=0.0
                  Q Fri_Sep_06_02:
                42 THHFEGLVDTALQKALVNDLDH-IYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNI
                                                                                     120 (220)
                42 \  \  \, \hbox{$\sim\sim\sim\sim g$-$iDs$-$sGyALv$-$s$-$\sim\sim-$VW-Y-$s$-$\sim\sim-$plp-$\sim\sim\sim-$Pl-$\sim-$v$-$p-$s$-$d-$\sim\sim-$s$-$\sim-$s
O Consensus
                                                                                     120 (220)
               T Consensus
T 3vl1_A
               335 GTPINNVYFAAGALFVSSGFDTSIKLDIISDPESERPAIEFETPTFLVSNDDAVSQFCYVS------DDE-
                                                                                      398 (420)
T ss_dssp
                  TSCEEEEEETTEEEEEETTTEEEEEEECCTTCCSCEECTTSCEEECCSSCCCCEEEEEC-----CSS-
T ss_pred
                  CCCceEEEecCCCcEEEEeccCCccceeccCcceeccCcceEEEEcc------CCC-
Q ss_pred
                  \verb|cccCCCceEEEEECCCceEEEEe|
 Q Fri_Sep_06_02: 121 NSGKFNNGICIINKKNSQFLYFE 143 (220)
O Consensus
               121 ~~~~epGlliV~p~tG~v~yWE 143 (220)
               .-|-++..-..|.++.|.
399 -----q~1~a~q~~q~~~~~
T Consensus
                                       416 (420)
               399 ----SNGEVLEVGKNNFCALYN 416 (420)
T 3v11_A
T ss_dssp
                  ----SSCEEEEETTTEEEEE
                  ----CCCEEEECCCCEEEEE
T ss pred
                            PDB"
PROTEIN DATA BANK
                                      NCBI
No 27
                                               Pub Med
>4gga_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; 2.04A
 {Homo sapiens} PDB: 4ggd _A
Probab=30.93 E-value=2.6e+02 Score=23.74 Aligned cols=69 Identities=10% Similarity=0.237 Sum probs=0.0
Q ss pred
                  CCCEEEEeCCCCCEEEEc---CCeEEEeeCCCCCCCCeEEEECCCccccCCCCceEEEeCCccccccCCCCC
Q Fri Sep 06 02:
                42 THHFEGLVDTALQKALVND---LDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASG 118 (220)
O Consensus
                118 (220)
               T Consensus
               T 4gga A
                   SCEEEEEETTTTEEEEEECTTTCCEEEEETTTCC---EEEEE-----CCCSSCEEEEEECT------
T ss dssp
                   cceeeeecCCCCeEEEEEcCCCc--EEEEE-----cCCCCCEEEEEEcC-----
T ss pred
                  ccccCCCceEEEEECCCceEEEEe
Q ss pred
Q Fri_Sep_06_02:
               119 NINSGKFNNGICIINKKNSQFLYFE 143 (220)
                  ~~~~epGlliV~p~tG~v~yWE 143 (220)
               119
                        +...|+-...+|.|++|.
T Consensus
               375 -----dg~~l~S~s~D~tvriWd 392 (420)
               375 -----DGATVASAAADETLRLWR 392 (420)
T 4gga A
                  ----TSSCEEEETTTEEEEEC
T ss_dssp
 T ss_pred
                   -----CCCEEEEEecCCeEEEE
                             PDB
                                               Pub Med
No 28
>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 2xu7_A* 3gfc_A 3cfs_B 3cfv_B
Probab=29.48 E-value=2.8e+02 Score=23.71 Aligned_cols=60 Identities=12% Similarity=0.205 Sum_probs=0.0
                  Q ss pred
Q Fri_Sep_06_02:
                55 KALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINK 134 (220)
                ++.++.+.
                   +|....++||+.....+.-+..
                                                                            .+.+++..
T Consensus
               247 l-s---dg-i-i-d-----l-tg- 297 (430)
               247 FGSVADDOKI MIWDTRNNNTSKPSHTVDAHTA-----EVNCI SFN------PY-----SEFILATGS 297 (430)
T 2xyi A
```

```
T ss_dssp
                   EEEEETTSEEEEETTCSCSSSCSEEEECCSS-----CEEEEEEC-----SS-----CTTEEEEE
T ss_pred
                   EEEEeCCCeEEEEECCCCCcceeEeecCCC------CeEEEEeC-------CC-------CCCEEEEEe
                   CCceEEEEe
Q ss_pred
 Q Fri_Sep_06_02: 135 KNSQFLYFE 143 (220)
 O Consensus
               135 ~tG~v~yWE 143 (220)
                   .+|.|+.|+
                298 ~dg~v~vwd 306 (430)
T Consensus
T 2xyi_A
               298 ADKTVALWD
                            306 (430)
 T ss_dssp
                   TTSEEEEEE
T ss pred
                   CCCeEEEE
                            SCOP
No 29
                                  PDB"
PROTEIN DATA BANK
                                                            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=28.09 E-value=3e+02 Score=25.05 Aligned_cols=81 Identities=12% Similarity=-0.027 Sum_probs=0.0
                   Q ss pred
 Q Fri Sep_06 02: 20 VTKLSTDLSFLPGSNGNNNTIDTHHFEGLVDTALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFT
                                                                                        99 (220)
Q Consensus
                99 (220)
                          ++.||+.|...+
T Consensus
                                                                                        67 (611)
T 1nr0_A
                 7 TALFPSLPRTAR-----GTAVVLGNTPAGDKIQYCNGTSVYTVPVG-SLTDTEIYT-----EHSHQTTVAKT
                                                                                        67 (611)
 T ss_dssp
                   EEEECCCCCCT------TCCCCCEECTTSSEEEEEETTEEEEEETT-CSSCCEEEC------CCSSCEEEEE
                   ccEECCCCccc------CceeEEeeCCCCEEEEeCCC-CcccCeEec------CCCCceEEEE
T ss_pred
Q ss pred
                   CCcccccccCCCcccccCCCcceEEEEE
Q Fri_Sep_06_02:
               100 SSISSTNNDTANYNNNASGNINSGKFNNGICIINKKNSQFLYFE
                                                        143 (220)
                100 ~p~s~~d~~~~~s~~~~epGlliV~p~tG~v~yWE
                                        +.-+|+...+|.|+
T Consensus
                68 sp-----dg~lasg~d~vvlWd
68 SP----SGYYCASGDVHGNVRIWD
                                                          87 (611)
T 1nr0 A
                                                          87 (611)
T ss dssp
                   CT----TSSEEEEEETTSEEEEEE
T ss_pred
                      -----CCcEEEEECCCCEEEeE
                             PDB"
No 30
                                                      Pub Med
>3odt_A Protein DOA1; ubiquitin, nuclear protein; HET: MSE MES; 1.35A {Saccharomyces cerevisiae}
Probab=27.69 E-value=2.3e+02 Score=22.07 Aligned_cols=126 Identities=12% Similarity=-0.010 Sum_probs=0.0
                   CCCCEEEEecCCCCEEEEecCCeEEEeecCCCCCCCCCEEEEECCCcccCCCCCCEEEEeCCcccccCCCCCcc
Q ss_pred
Q Fri Sep 06 02: 41 DTHHFEGLVDTALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNI 120 (220)
                41 ~~~~g~iDs~sGyALv~s~~~~VW~Y~s~~~~prac-fplp~~~~~~Pl~~~v~p~s~~d~~~~~~s~~~
O Consensus
               T Consensus
                                                                                       234 (313)
                184 NDVVRHLAVVDDGHFISCSNDGLIKLVDMHTGD---VLRTYEGHES-----FVYCIKLL------FVYCIKLL
T 3odt A
                                                                                      234 (313)
                   SSCEEEEEETTEEEEEETTSEEEEEETTTCC---EEEEEECCSS------CEEEEEEC-------
T ss dssp
                   T ss_pred
Q ss_pred
                   CCCCCCeEEEECCCCeEEEEecccccccccccccceeEecCCCCCCeEEEeeccCCceEEEEeccCceEEEEEeC
Q Fri_Sep_06_02: 121 NSGKFNNGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKD
                                                                                       200 (220)
               121 ~~~~epGlliV~p~tG~v~yWEsIs~a~~l~~~L~~~k~~~~l~L~~qE~vt~l~n~ePaG~IlaTS~qRl~~itirD
Q Consensus
                                                                                       200 (220)
               T Consensus
                                                                                       296 (313)
T 3odt A
               235 ----PNGDIVSCGEDRTVRIWSKENGS-----LKQVITLPAISIWSVDCMSNGDIIVGSSDNLVRIFSQEK
T ss_dssp
                  ----TTSCEEEEETTSEEEEECTTTCC-----EEEEEECSSSCEEEEEECTTSCEEEEETTSCEEEEESCG
T ss_pred
                   CCCCEeEEEeeEE
Q ss_pred
 Q Fri_Sep_06_02: 201 STGKPKLELKQQL 213 (220)
Q Consensus
                201 ~~Gkp~l~~~~l 213 (220)
               .=....++.+
T Consensus
                               309 (313)
T 3odt_A
                297 SRWASEDEIKGEL 309 (313)
                   GGCCC-----
T ss_dssp
T ss_pred
                   Cceeehhhhhhhh
No 31
                                                Pub Med
🗎 >3148_A Outer membrane usher protein PAPC; IG fold, greek KEY, cell outer membrane, fimbrium, transmembrane,
transport, transport protein; 2.10A {Escherichia coli} PDB: 2kt6 _A
Probab=26.53 E-value=28 Score=25.54 Aligned_cols=18 Identities=22% Similarity=0.405 Sum_probs=0.0
Q ss_pred
                   eccCcEEEEEeCCCCCE
Q Fri_Sep_06_02: 188 TSLGRVLFITIKDSTGKP
                                   205 (220)
 Q Consensus
               188 TS~gRl~~itirD~~Gkp 205 (220)
                 |..||-+.|+++.+|+|
4 t~~G~~~ll~l~~~dG~p
                                    21 (94)
T Consensus
                 4 VLKGKRLFAILRLADGSQ
T 3148_A
                                    21 (94)
T ss dssp
                   ---CCCEEEEEETTSCC
                   eEEEEEEEEECCCCC
T ss pred
```

```
PDB<sup>™</sup>
PROTEIN DATA BANK
                                                       Pub Med
>4aez A CDC20, WD repeat-containing protein SLP1; cell cycle, KEN-BOX, D-BOX, APC/C; 2.30A {Schizosaccharomyces
 pombe }
 Probab=26.09 E-value=3.1e+02 Score=23.03 Aligned_cols=106 Identities=11% Similarity=0.045 Sum_probs=0.0
                   CCCCEEEEECCCeEEEeeCCCCCCCCEEEEECCCcccccCCCceEEEECCccccccCCCccccccCCCCccEEE
 Q ss pred
                \tt 51\ TALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGIC
 Q Fri Sep 06 02:
                                                                                        130 (220)
                 51 s-sGyALv-s----VW-Y-s----p----fplp------Pl---v-p-s--d------
                                                                                  ~~epGll 130 (220)
 Q Consensus
                   +....+.+....++||+.....+..
                                                   .+...-.++-.+
                -~~~1 149 (401)
 T Consensus
                102 SNLNVVAVALERNVYVWNADSGSVSALAET-----DESTYVASVKWSH-----DGSFL
 T 4aez A
                                                                                         149 (401)
                   CTTSEEEEETTTEEEEEETTTCCEEEEEEC-----TSSEE
 T ss dssp
 T ss pred
                   cccceeeeeccccceeeeec-----cccceeeeecc-----ccccee
 Q ss_pred
                   EEECCCceEEEEeccccccccccccceeEEecCCCCceEEEeEccCCceEEEEeccCc
 Q Fri_Sep_06_02: 131 IINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDST
                                                                                  202 (220)
 O Consensus
                131 iV-p-tG-v-yWEsIs-a--l---k----k----l-L--gE-vt-l-n-ePaG-IlaTS-gRl--itirD--
                                                                                  202 (220)
                T Consensus
                                                                                  207 (401)
                150 SVGLGNGLVDIYDVESQT-----KLRTMAGHQARVGCLSW-NRHVLSSGSRSGAIHHHDVRIAN
 T 4aez A
                                                                                  207 (401)
 T ss_dssp
                   EEEETTSCEEEEETTTCC-----EEEEECCCSSCEEEEE-ETTEEEEEETTSEEEEETTSSS
                   EEECCCCeEEEEECcCCe------EEEEecCCCCceEEEEE-CCCEEEEECCCCCEEEEeccCCC
 T ss_pred
                             PDB<sup>N</sup>
PROTEIN DATA BANK
                                       NCBI Pub Med
->4gga_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; 2.04A
 {Homo sapiens} PDB: 4ggd A
 Probab=26.00 E-value=1.7e+02 Score=24.85 Aligned_cols=61 Identities=8% Similarity=0.072 Sum_probs=0.0
                   CCCCEEEEEcCCeEEEeeCCCCCCCCEEEEECCCccccCCCceEEEeC-CccccccCCCcccccCCCCceE
 Q Fri_Sep_06_02:
                51 TALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTS-SISSTNNDTANYNNNASGNINSGKFNNGI
                                                                                         129 (220)
 O Consensus
                51 s~sGyALv~s~~~~VW~Y~s~~~~pp-~~fplp~~~~~~Pl~~v~-p~s~~d~~~~~s~~~~~epGl 129 (220)
                    +.++.--+.-+.+||+......+--|
                                                                                    + - -+
                114 S--n-lAvgld-tV-lWd--tg-----V-sv-fsp-
 T Consensus
                                                                                    -dg~~
                114 SSGNVLAVALDNSVYLWSASSGDILQLLQM------EQPGEYISSVAWIK------EGNY
 T 4gga A
                                                                                         161 (420)
 T ss_dssp
                   CTTSEEEEEETTTCCEEEEEC-----CSTTCCEEEEEECT-----TSSE
                   CCCCEEEEeCCCEEEEEECCCCCEEEEEEe------CCCCCEEEEEECC------CCCC
 T ss_pred
 Q ss_pred
                   EEEECCCceEEEEe
 Q Fri_Sep_06_02: 130 CIINKKNSQFLYFE 143 (220)
 O Consensus
                130 liV~p~tG~v~yWE 143 (220)
                    |++...+|.|+.|+
                162 lasgs~Dg~v~iWd 175 (420)
 T Consensus
 T 4gga_A
                162 LAVGTSSAEVQLWD 175 (420)
 T ss_dssp
                   EEEEETTSCEEEEE
                   EFFECCCOFFFEFF
 T ss pred
                             PDB"
PROTEIN DATA BANK
                                       NCBI
 No 34
                                                      Pub Med
>4kt3_B Putative lipoprotein; glycoside hydrolase, hydrolase, PFL_3036; HET: MSE; 1.44A {Pseudomonas protegens}
 Probab=25.50 E-value=70 Score=25.26 Aligned_cols=39 Identities=10% Similarity=0.119 Sum_probs=0.0
                   CCCCCCeEEEECCCccccCCCCceEEEEeCCccccccccCCCCcccccCCCCcceEEEEE
 Q ss pred
                 72 IQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINKKNSQFLYFE
 Q Fri Sep 06 02:
                 72 ~~~p~~~fplp~~~~~Pl~~~v~p~s~~d~~~~~s~~~~epGlliv~p~tG~v~yWE
 Q Consensus
                   +...|-++.|.+-.+
                                          + | +++
                                                         . . .
                                                                 -=|+.-|+|+||.|
 T Consensus
                 56 ~p~hpGyysF~vqyd-----sp-taG----a~d-----wqlfSVs~~TGdi--WE
                                                                                   94 (137)
 T 4kt3 B
                 56 KPPHPGYYDFSLGYN DP-KAG ATE YWGLFSVSLNTGDT-WE
                                                                                   94 (137)
                   SCSSTTEEEEEEEC------CT-TSS-----BCE-----EEEEEEEETTTCCE--EE
 T ss dssp
                   CCCCCceeEeeccc------CC-CCC------ccc---eeEEEEecCCCCCe--ee
 T ss pred
                              PDB<sup>™</sup>
PROTEIN DATA BANK
 No 35
                                       NCBI Pub Med
           repeat-containing protein 61; structural genomics consortium, SGC, transcriptio; 2.30A {Homo sapiens}
  Probab=24.80 E-value=2.5e+02 Score=21.47 Aligned_cols=74 Identities=7% Similarity=0.084 Sum_probs=0.0
                   Q ss pred
 Q Fri Sep 06 02:
                 36 NNNTIDTHHFEGLVDTALQKALVNDLDH-IYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTS-SISSTNNDTANYN 113 (220)
                 Q Consensus
                                                                                        113 (220)
                T Consensus
                                                                                         300 (321)
                243 TLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVWDVGTRT---CVHTFFDHOD------OVWGVKYNG-------
 T 3ow8 A
                                                                                        300 (321)
 T ss_dssp
                   EECCCSSCEEEEECTTSSEEEEEETTSCEEEEETTTTE---EEEEECCCSS------CEEEEEECT------
                   EeecCCCceEEEEEcCCCCEEEEEecCCceEEEEECCCc---EEEEEECCCC--------CEEEEEEcC------
 T ss pred
 Q ss_pred
                   CCCCccccCCCCceEEEECCCceEEEE
 Q Fri Sep 06 02:
                114 NNASGNINSGKFNNGICIINKKNSOFLYFE 143 (220)
                114 ~~~s~~~~epGlliV~p~tG~v~yWE 143 (220)
 Q Consensus
                            +...|+...+|.|+.|+
 T Consensus
                       -----g~~l~s~s~Dg~l~iWD 318 (321)
 T 3ow8_A
                301 ----NGSKIVSVGDDQEIHIYD 318 (321)
                   ----TSSEEEEETTCCEEEE
 T ss_dssp
                   -----CCCEEEEEeCCCeEEEE
 T ss pred
```

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No 36
                                      PDB"
                                              NCBI
                                                          Pub Med
                               SCOP
>1mwz_A PYP, photoactive yellow protein; PAS, LOV, GAF, domains fold, signaling protein; HET: HC4; 0.82A
 {Halorhodospira halophila} SCOP: d.110.3.1 PDB: 1kou _A* 1ot9 _A* 1otb _A* 1s4r _A* 1s4s _A* 1ts0 _A* 1ts6 _A* 1ts7
1uwn _X* 1uwp _X* 2d01 _A* 2phy _A* 2pyp _A* 2pyr _A* 2qj5 _A* 2qj7 _A* 2qws _A* 2zoh _A* 2zoi _A* ...
Probab=24.73 E-value=50 Score=25.40 Aligned_cols=14 Identities=14% Similarity=0.439 Sum_probs=0.0
 Q ss_pred
                    eeeeeecccceeee
 Q Fri_Sep_06_02: 128 GICIINKKNSQFLYF
                                  142 (220)
                 128 GlliV~p~tG~v~yW
 Q Consensus
                                   142 (220)
                 |++++.+ +|+|.||
29 Gii~lD~-~g~I~~~
 T Consensus
                                    42 (125)
 T 1nwz A
                 29 GAIOLDG-DGNILOY
                                    42 (125)
 T ss dssp
                    EEEEET-TCBEEEE
 T ss pred
                    eEEEECC-CCEEEEE
 No 37
                               PDB
                                                   Pub Med
                                         S NCBI
>4gn4_B Obody AM2EP06; beta barrel, OB-fold, protein-protein complex, novel scaffol muraminidase, enzyme
 inhibition, engineered binding protein inhibitor; 1.86A {Pyrobaculum aerophilum} PDB: 4glv _B* 4gn5 _A* 4gla _C 4gn3 _B
 Probab=24.68 E-value=56 Score=23.96 Aligned cols=21 Identities=24% Similarity=0.531 Sum probs=0.0
                    cccceeeeee
 Q ss pred
 Q Fri_Sep_06_02: 189 SLGRVLFITIKDSTGKPKLEL 209 (220)
                189 S~gRl~~itirD~~Gkp~l~~
                                        209 (220)
 Q Consensus
                 ..|.+.|+.|||..|.-.+.+
33 ~~q~~Fi~LrD~~q~~q~~~
 T Consensus
                                         53 (108)
 T 4gn4_B
                 33 DYGRVKIVKVSDREGGAAVPV
                                         53 (108)
 T ss_dssp
                    ECSSEEEEEESSTTCCCEEE
 T ss_pred
                    cccceeeeeccccceeee
                               PDB"
PROTEIN DATA BANK
 No 38
                                         NCBI
                                                         Pub Med
- >3frx A
        Guanine nucleotide-binding protein subunit beta- like protein; RACK1, WD40, beta propeller, ribosome,
 translation, acetylation; 2.13A {Saccharomyces cerevisiae} PDB: 3izb a 3o2z T 3o30 T 3u5c g 3u5g g 3rfg A 3rfh
  1trj A 3jyv R*
 Probab=24.22 E-value=2.8e+02 Score=22.62 Aligned cols=74 Identities=7% Similarity=-0.032 Sum probs=0.0
 Q ss_pred
                    Q Fri_Sep_06_02:
                 45 FEGLVDTALQKALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGK 124 (220)
 Q Consensus
                 ....+.+...+..+.+.+.||.+.
                 241 ----sp----la-----i-v----
                                                             ·~~~v~~~~sp-----
 T Consensus
                                                                                            296 (319)
 T 3frx A
                 241 FSLAFSPNRYWLAAATATGIKVFSLD-PQYLVDDLRPEFAGYSKAAEPHAVSLAWSA-----
 T ss dssp
                    EEEEECSSSSEEEEETTEEEEEEETTEEEEEEECCCTTCCGGGCCCEEEEECT-------
 T ss_pred
                    EEEEEcCCCCEEEEEcCCCceeeeccCccccccCcCcceeEEEECC-------
 Q ss_pred
                    CCceEEEECCCceEEEEe
 Q Fri_Sep_06_02: 125 FNNGICIINKKNSQFLYFE
                                      143 (220)
                125 ~epGlliV~p~tG~v~yWE 143 (220)
                     +...|+...+|.|+.|+
                297 -da~~l~sq~~Dq~i~vWd 314 (319)
 T Consensus
                297 -DGQTLFAGYTDNVIRVWQ
 T 3frx A
                                      314 (319)
 T ss_dssp
                    -TSSEEEEEETTSCEEEEE
 T ss_pred
                    -CCCEEEEeecCceEEEE
                               PDB"
 No 39
                                                         Pub Med
        Protein DOA1; ubiquitin, nuclear protein; HET: MSE MES; 1.35A {Saccharomyces cerevisiae}
 Probab=24.00 E-value=2.7e+02 Score=21.64 Aligned_cols=100 Identities=7% Similarity=0.092 Sum_probs=0.0
                    EEEEECCCeEEEeeCCCCCCCCEEEEECCCccccCCCceEEEeCCcccccccCCCcceEEEECCCccccccCCCCccEEEEEC
 Q ss pred
 Q Fri_Sep_06_02:
                 55 KALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINK 134 (220)
                 .+..-...+++|+
                                                                                   +..+++..
 T Consensus
                 ._____1~~~~
                                                                                            162 (313)
                 117 VISGSWDKTAKVWK----EGSLVYNLOAHN----ASVWDAKVVSF------SENKFLTAS
 T 3odt A
                                                                                            162 (313)
                    EEEEETTSEEEEEE....-TTEEEEEEECCS----SCEEEEEEET------TTTEEEEEE
 T ss_dssp
                    EEEEeCCCCEEEEc----CCCEEEeccCC-----CceeEEEEccC-------CCCEEEEEE
 T ss_pred
 Q ss pred
                    CCceEEEEecccccccccccceeEEecCCCCCceEEEeeccCcceEEEEeccCc
 Q Fri_Sep_06_02: 135 KNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPSGIIIATSLGRVLFITIKDST 202 (220)
                135 ~tG~v~yWEsIs~a~~l~~~k~~~~l~L~~gE~vt~l~n~ePaG~IlaTS~gRl~~itirD~~
 Q Consensus
                    .+|.|+.|+
                                     -----i-----dg-i-i-d-----
 T Consensus
                                                                                  216 (313)
 T 3odt_A
                163 ADKTIKLWQ-----NDKVIKTFSGIHNDVVRHLAVVDDGHFISCSNDGLIKLVDMHTGD 216 (313)
 T ss dssp
                    TTSCEEEE-----TTEEEEEECSSCSSCEEEEEEETTEEEEEETTSEEEEEETTTCC
                    CCCCEEEEe-----CCceEEEEeccCccEEEEEccCCceEEEEccCchh
 T ss pred
                              PDB NCBI Pub Med
>3v11 A 26S proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A (Saccharomyces
```

```
cerevisiae} PDB: 3acp _A
Probab=23.70 E-value=3.3e+02 Score=22.52 Aligned cols=122 Identities=7% Similarity=-0.051 Sum probs=0.0
                  {\tt EEEEEeCCCC-EEEEEcC-CeEEeeeCCCCCCCCeEEEECCCccccCCCCceEEEeeCCcccccCCCCccccc}
0 ss pred
 Q Fri_Sep_06_02:
                {\tt 45~FEGLVDTALQ-KALVNDL-DHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINS}
                                                                                    122 (220)
                45 ~~g~iDs~sG-yALv~s~-~~~VW~Y~s~~~~profplp~~~~~Pl~~~v~p~s~~d~~~~
 Q Consensus
                                                                                    122 (220)
                  ....+++... +.++.+. ..++||+....-..+.
                                                       .+...++..+.+
               294 -----l--g--dg-i-vwd------v----v----
T Consensus
                                                                                    344 (420)
               294 NSLTVDGNNANYIYAGYENGMLAQWDLRSPECPVGEFL-----INEGTPINNVYFA-----
T 3vl1 A
                                                                                    344 (420)
                  EEEEECSSCTTEEEEEETTSEEEEEETTCTTSCSEEEE.-----ESTTSCEEEEEEE.-----
T ss_dssp
T ss_pred
                  eeEEEeCCCCCEEEEEeCCCccchhhhh------ccCCCcceEEEeC------
                  Q ss pred
Q Fri Sep 06 02: 123 GKFNNGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLDLKLKDNENITSTINCEPS---GIIIATSLGRVLFITIK
                                                                                    199 (220)
               123 ~~\text{$\sim$-epGlliV-p-tG-v-yWEsIs-a-l---k---k----l-L--gE-vt-l-n-ePa---G-IlaTS-gRl--itir}
                                                                                    199 (220)
O Consensus
                     +..+++....+|.|+.|+---..... +...... +.-..++.-....+..
               T Consensus
                                                                                    418 (420)
               345 ---AGALFVSSGFDTSIKLDIISDPESERP--AIEFETPTF-LVSNDDAVSQFCYVSDDESNGEVLEVGKNNFCALYNLS
T 3vl1 A
                                                                                    418 (420)
                  ---TTEEEEEETTTEEEEEEECCTTCCSC--EECTTSCEE-ECCSSCCCCEEEEECCSSSSCEEEEEETTTEEEEEEESC
T ss_dssp
T ss_pred
                  Q ss_pred
                  CC
Q Fri_Sep_06_02: 200 DS 201 (220)
               200 D~ 201 (220)
Q Consensus
               |.
419 ~~
                     420 (420)
T Consensus
               419 NP 420 (420)
T 3vl1 A
T ss dssp
                  C-
                  CC
T ss_pred
                                                            Pub Med
                            SCOP
-> lmzu A PPR; photoactive yellow protein, PAS, PYP, signaling protein; HET: HC4; 2.00A {Rhodospirillum centenum}
 SCOP: d.110.3.1
Probab=23.22 E-value=56 Score=25.42 Aligned_cols=14 Identities=7% Similarity=0.221 Sum_probs=0.0
Q ss pred
                  eeeeeecccceeee
Q Fri_Sep_06_02: 128 GICIINKKNSQFLYF
                                142 (220)
Q Consensus
               128 GlliV~p~tG~v~yW 142 (220)
                   |++++.+ +|+|.||
                34 GiivlD~-dg~I
T Consensus
                                 47 (129)
T 1mzu_A
                34 GAIQVDG-SGVIHRY
                                 47 (129)
T ss dssp
                  EFFERET-TCREEF
T ss pred
                  eEEEECC-CCeEEEE
                                                     Pub Med
>3fm0 A Protein CIAO1; WDR39,SGC,WD40,CIAO1, nucleus, WD repeat, biosynthetic prote structural genomics,
 structural genomics consortium; 1.70A {Homo sapiens}
Probab=22.98 E-value=2.6e+02 Score=23.05 Aligned_cols=66 Identities=9% Similarity=0.042 Sum_probs=0.0
                  Q Fri_Sep_06_02:
                55 KALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINK 134 (220)
                Q Consensus
                  ++++|+-..
                                                                      -----laS~s
T Consensus
T 3fm0 A
               267 LATACGDDAIRVFOEDPNSDPOOPTFSLTAHLHOAHSODVNCVAWNP-----K----EPGLLASCS
T ss dssp
                  EEEEETTSCEEEEEECTTSCTTSCCEEEEEEETTSSSSCEEEEEECS-----STTEEEEEE
T ss_pred
                  Q ss_pred
                  CCceEEEEe
 Q Fri_Sep_06_02:
               135 KNSQFLYFE 143 (220)
Q Consensus
               135 ~tG~v~yWE 143 (220)
                  .+|.|++|+
               324 ~Dg~v~~W~
                           332 (345)
T Consensus
T 3fm0_A
               324 DDGEVAFWK
                           332 (345)
                  TTSCEEEEE
 T ss_dssp
                  CCCCEEEEE
T ss pred
No 43
                            SCOP
->1pgu_A Actin interacting protein 1; WD repeat, seven-bladed beta-propeller, protein binding; 2.30A
 {Saccharomyces cerevisiae} SCOP: b.69.4.1 b.69.4.1 PDB: 1pi6 _A
Probab=22.29 E-value=4.1e+02 Score=23.13 Aligned_cols=85 Identities=6% Similarity=0.020 Sum probs=0.0
Q ss_pred
                  Q Fri_Sep_06_02:
                {\tt 21~TKLSTDLSFLPGSNGNNNTIDTHHFEGLVDTALQKALVNDLDHIYIWNYNSIQKD-TPICKISLHDDYSVLSSPP-ICLF}
                                                                                     98 (220)
 Q Consensus
                98 (220)
                               ....-.+++...+.++....+.||+.....|.-+..
-----v~~~~spdg~1~~~~v~v~v~~~~~~h~~.
                                                                              + +.++
                                                                     ~~h~~-
                                                                                     70 (615)
T Consensus
                 8 EIIPPQPSTQR-----NFTTHLSYDPTTNAIAYPCGKSAFVRCLDDGDSKVPPVVQFTGHGS-----SVVTTV
T 1pgu_A
                                                                                     70 (615)
 T ss dssp
                  EEECCCCCCT-----TCCCCCEEETTTTEEEEEETTEEEEEECCSSCCSSCSEEEECTTTT-----SCEEEE
                  hccCCCCCcc------ceeEEEECCCCCEEEEECCCCcccccceEEecCCC-----ceEEEE
T ss pred
```

```
Q ss pred
                                eCCccccccccCCCcccccCCCceEEEEECCCceEEEE
 Q Fri_Sep_06_02:
                            99 TSSISSTNNDTANYNNNASGNINSGKFNNGICIINKKNSOFLYFE
                                                                                                 143 (220)
 O Consensus
                            99 v~p~s~-d~~~~s~~~epGlliV~p~tG~v~yWE
                                                                                                143 (220)
                                                         ..+
                                                                     +..+|+...+|.|+.|+
                                                                    -----l~s~~~dg~v~vw~
 T Consensus
                                                        -p~~---
                            71 KFS-----PIK-----GSQYLCSGDESGKVIVWG
 T 1pgu A
                                                                                                  94 (615)
 T ss_dssp
                                EEC-----SST----TCCEEEEETTSEEEEE
                                EEC-----CCCEEEEecCCCEEEEe
 T ss_pred
                                                 PDB<sup>™</sup>
PROTEIN DATA BANK
                                                                NCBI
                                                                                Pub Med
>2pm9 A Protein WEB1, protein transport protein SEC31; beta propeller; 3.30A {Saccharomyces cerevisiae}
 Probab=22.17 E-value=1.9e+02 Score=23.82 Aligned cols=65 Identities=11% Similarity=0.065 Sum probs=0.0
 Q ss_pred
                                Q Fri_Sep_06_02:
                            55 KALVNDLDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFN-NGICIIN 133 (220)
 O Consensus
                            55 yALv-s----VW-Y-s----p----fplp-----------Pl----v-p-s--d-------e-pGlliV- 133 (220)
                                .+-.-..++||+....+..+..-...+...++-..|
                                                                                                                                  + ..+++..
                          129 l~s~~~dg~v~iwd~~~~~
                                                                                 ~~~~v~~~
 T Consensus
                                                                                                                                                  184 (416)
 T 2pm9_A
                          129 LASGGNNGEIFIWDMNKCTESPSNYTPLTPGQSMSSVDEVISLAWNQ-----
                                                                                                                          ----SLAHVFASA
                                                                                                                                                 184 (416)
                                EEEECSSSCEEBCBTTTTSSCTTTCCCBCCCCSCCSCCCCEEECS-----SCTTEEEEE
 T ss_dssp
                                T ss pred
                                CCCceEEEe
 Q ss pred
 Q Fri_Sep_06_02: 134 KKNSQFLYFE
                                               143 (220)
                          134 p~tG~v~yWE 143 (220)
                          ..+|.|+.|+
185 ~~dg~v~iwd
 T Consensus
                                               194 (416)
 T 2pm9_A
                          185 GSSNFASIWD
                                               194 (416)
 T ss_dssp
                                SSSSCEEEEE
 T ss_pred
                                CCCCCEEEE
 No 45
                                                  PDB"
                                                                NCBI
                                                                                Pub Med
              CAFIA usher, F1 capsule-anchoring protein; transport protein; 1.60A {Yersinia pestis}
 Probab=21.76 E-value=47 Score=23.55 Aligned_cols=15 Identities=47% Similarity=0.804 Sum_probs=0.0
 Q ss pred
                                CcEEEEEeCCCCCE
 Q Fri_Sep_06_02: 191 GRVLFITIKDSTGKP
                                                       205 (220)
                          191 gRl~~itirD~~Gkp
 Q Consensus
                             | | -+. | + | ++. + | + |
1 G~~~1~~1~~~dG~~
 T Consensus
                                                         15 (89)
                             1 GGRLFLHLKRSDNKP
 T 2xet A
                                                        15 (89)
 T ss_dssp
                                CEEEEEEEETTSCB
                                CEEEEEEECCCCCC
 T ss pred
 No 46
                                                                                           Pub Med
>2k50_A Replication factor A related protein; uncharacterized protein, structural genomics, PSI-2; NMR
  {Methanothermobacterthermautotrophicus str}
 Probab=21.59 E-value=76 Score=23.10 Aligned_cols=43 Identities=23% Similarity=0.227 Sum_probs=0.0
 Q ss pred
                                CCCCCCEEEEeEccCCceEEE--EeccC---cEEEEEEeCCCCCEEEEE
 Q Fri_Sep_06_02: 166 KLKDNENITSTINCEPSGIII--ATSLG---RVLFITIKDSTGKPKLELK
                                                                                                        210 (220)
 Q Consensus
                          166 ~L~~gE~vt~l~n~ePaG~Il--aTS~g---Rl~~itirD~~Gkp~l~~~
                                                                                                        210 (220)
                               T Consensus
                                                                                                         59 (115)
                            12 KLEEGAETPVTGRVMKISSPRTFTTRKGREGKLANVIIADDTG--ELRAV
 T 2k50 A
                                                                                                         59 (115)
                                TCCTTCEEEEEEEECCCEECCCTTSSCCEEEEEEETTE--EEEEE
 T ss dssp
                                HCCCCCEeEEEEEECCCCceEEEcCCCCEEEEEEEEECCC--eEEEE
 T ss pred
 No 47
                                                  PDB"
                                                                                           Pub Med
              Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 3.00A
  {Escherichia coli}
 Probab=21.41 E-value=1.5e+02 Score=29.49 Aligned_cols=79 Identities=13% Similarity=0.169 Sum_probs=0.0
                                CGERERECCCGERERECGCGGGGGGGGGGGGGGGEREC-CCCCCCGERERECG--CCGERERECGCGGERERECC--
 Q ss pred
 Q Fri_Sep_06_02: 126 NNGICIINKKNSQFLYFEDISTINNLYTKLSKSKAHVLD-LKLKDNENITSTINC--EPSGIIIATSLGRVLFITIKD--
                          126 \ \ epGlliV-p-tG-v-yWEsIs-a-cl-c-k-c-c-l-L-cgE-vt-l-n--ePaG-IlaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-llaTS-gRl-citirD--ePaG-ll
 Q Consensus
                                                                                                                                                 200 (220)
                          635 (716)
 T Consensus
                          564 DDOKLLMASDAGYGFVCTFND-----LVARNRAGKALITLPENAHVMPPVVIEDASDMLLAITQAGRMLMFPVSDLP 635 (716)
 T 1zvu A
                                TTCEEEEEBTTSEEEEEEGGG-----GCCCSTTCEECBCCCTTCCBCCCEECCCTTCEEEEEETTSEEEEEESTTSC
 T ss dssp
                                CCCEEEEECCCCEEEEEcHHH------hcccCccceEEEeeCCCCEEEEEEeCCCCEEEEEEHHHCC
 T ss pred
 Q ss_pred
                                CCCCEEEEEeeEEec
 Q Fri Sep 06 02: 201 STGKPKLELKQQLIK 215 (220)
                          201 ~~Gkp~l~~~~lik
                                                      215 (220)
 Q Consensus
                                .+|| .--+ +.+|
 T Consensus
                                ~~gr-~~GV--~~i~
                          636 QLSK-GKGN--KIIN 647 (716)
 T 1zvu A
 T ss_dssp
                                BCSS-BSCE--ESSC
 T ss_pred
                                ccCc-ccCe--EEEE
```

```
PDB"
No 48
                                                     PubMed
>4ggc_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; HET:
MRD; 1.35A {Homo sapiens}
Probab=20.02 E-value=3.3e+02 Score=21.21 Aligned_cols=70 Identities=11% Similarity=0.218 Sum_probs=0.0
                   Q ss pred
Q Fri_Sep_06_02:
               41 DTHHFEGLVDTALQKALVND---LDHIYIWNYNSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNAS
                41 ~~~~~g~iDs~sGyALv~s---~~~VW~Y~s~~~~pp~~~fplp~~~~~~Pl~~~v~p~s~~d~~~~~~~s~~117 (220)
                   .....+
                                                            ..|...=.++-.+|
               240 ---v----sq--d--i-iwd-------1--------qH---V--l--sp-------
T Consensus
                                                                                      294 (318)
               240 HSQVCSILWSPHYKELISGHGFAQNQLVIWKYPTMAKVAEL-----KGHTSRVLSLTMSP------
T 4ggc A
                                                                                      294 (318)
T ss_dssp
                   SSCEEEEEETTTTEEEEEECTTTCCEEEEETTTCCEEEEE.-----CCCSSCEEEEEECT------
                   eeeeeeeeccccceEEEEEcCCCEEEEEE.-----cCCCCCEEEEEEcc------
T ss_pred
                  cccccCCceEEEEECCCceEEEEe
Q ss_pred
Q Fri_Sep_06_02: 118 GNINSGKFNNGICIINKKNSQFLYFE 143 (220)
Q Consensus
               118 ~~~~epGlliV~p~tG~v~yWE 143 (220)
                         +..+|+-...+|.|+.|.
T Consensus
               295 ----dg~~l~S~s~D~~v~iWd 312 (318)
               295 -----DGATVASAAADETLRLWR 312 (318)
T 4ggc_A
                   ----TSSCEEEEETTTEEEEEC
T ss_dssp
                   -----CCCEEEEEecCCeEEEE
T ss_pred
```

Done!

Please cite as appropriate:

HHpred: Söding, J. (2005) Protein homology detection by HMM-HMM comparison. Bioinformatics 21: 951-960.

PSIPRED: Jones, D.T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. JMB 292: 195-202.

PDB: Bourne, PE. et al. (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.

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