

HOME

Login

PDBalert

Personal Databases

Contact

Tool Versions

Imprint

Disclaimer

Help

MAX-PLANCK-GESELLSCHAFT

Show results of job:

Show results

Recent jobs:

Select all Deselect all

Clear sel. Jobs

Delete sel. Jobs

queued

running

done

error

Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

Quickfinder

Search

Alignment

Sequence Analysis

2ary Structure

3ary Structure

Classification

Utils

CS-BLAST

HHblits

HHpred

HHsenser

HMMER3

PatternSearch

ProtBLAST

PSI-BLAST

SimShiftDB

New job

Resubmit

Resubmit_HMM

Resubmit/HHsenser

Realign

Log

Input-params

Delete

HHpred - Results

Job-ID: 3637708

Date: 02:18 on Sep 06 2013

Help

Results

Histogram

Reduced alignment

Representative alignment

Full alignment

Create model

Merge Q/T alignments

Forward to PCoils

Forward HMM

Save

Export

Color alignments

☐ color only SS

☒ color alignments

☐ color alignments

View alignment

10

100

200

220

Resubmit

1xks_A

4g3n_A

1zvt_A

1suu_A

3uc1_A

3uc1_A

3l6v_A

1zvu_A

1wp5_A

1zi0_A

3mny_A

1suu_A

1zi0_A

4g3n_A

3l6v_A

1wp5_A

3no0_A

1zvt_A

3zey_7

3no0_A

1gxr_A

4aow_A

Query

Fri_Sep_06_02:18:42_+0200_2013

(seq=TSNNKYGNTK...QQLIKPQNSF

Len=220

Neff=5.4

Nseqs=97)

Parameters

score

SS:yes

search:local

realign

with

MAP:no

No Hit

Prob

E-value

P-value

Score

SS

Cols

Query

HMM

Template

HMM

☐

1

1xks_A

Nuclear pore complex pr

100.0

2.9E-40

9.1E-45

311.1

21.0

172

10-220

7-187

(450)

☐

2

4g3n_A

DNA gyrase subunit A; D

89.3

3.8

0.00012

36.5

11.2

135

50-205

42-181

(327)

☐

3

1zvt_A

Topoisomerase IV subuni

84.4

3.7

0.00012

35.2

7.9

69

129-204

47-118

(256)

☐

4

1suu_A

DNA gyrase subunit A; t

84.1

2

6.4E-05

37.7

6.3

76

129-211

61-149

(312)

☐

5

3uc1_A

DNA gyrase subunit A; D

82.1

2.8

8.9E-05

37.3

6.5

78

129-211

56-144

(327)

☐

6

3uc1_A

DNA gyrase subunit A; D

81.7

19

0.0006

31.9

11.7

134

50-204

42-184

(327)

☐

7

3l6v_A

GYRA, DNA gyrase subuni

79.9

4

0.00013

37.1

6.7

78

129-211

60-148

(370)

☐

8

1zvu_A

Topoisomerase IV subuni

76.2

4

0.00013

40.6

6.0

76

129-211

517-600

(716)

☐

9

1wp5_A

Topoisomerase IV; broke

75.8

9.3

0.00029

33.8

7.8

67

129-200

53-125

(323)

☐

10

1zi0_A

DNA gyrase subunit A; b

74.5

11

0.00034

32.9

7.8

67

129-200

56-128

(307)

☐

11

3mny_A

MRNA export factor; mRN

73.1

18

0.00056

29.4

8.4

123

53-211

229-357

(368)

☐

12

1suu_A

DNA gyrase subunit A; t

71.3

14

0.00044

32.3

7.7

80

129-219

117-200

(312)

☐

13

1zi0_A

DNA gyrase subunit A; b

68.1

60

0.0019

28.1

11.1

130

50-200

42-176

(307)

☐

14

4g3n_A

DNA gyrase subunit A; D

66.5

18

0.00058

32.1

7.5

67

129-200

56-128

(327)

☐

15

3l6v_A

GYRA, DNA gyrase subuni

65.2

56

0.0018

29.4

10.6

143

50-215

46-195

(370)

☐

16

1wp5_A

Topoisomerase IV; broke

63.8

77

0.0024

27.8

11.1

143

50-215

39-189

(323)

☐

17

3no0_A

DNA gyrase subunit A; D

63.4

27

0.00085

30.0

7.8

65

126-200

80-146

(276)

☐

18

1zvt_A

Topoisomerase IV subuni

63.0

5.8

0.00018

34.0

3.4

41

165-205

27-73

(256)

☐

19

3zey_7

Guanine nucleotide-bind

55.0

75

0.0024

24.5

9.3

100

60-196

36-135

(318)

☐

20

3no0_A

DNA gyrase subunit A; D

54.4

55

0.0017

28.0

8.2

66

129-200

130-196

(276)

☐

21

1gxr_A

ESG1, transducin-like e

49.0

1E+02

0.0033

24.4

15.8

117

46-200

56-172

(337)

☐

22

4aow_A

Guanine nucleotide-bind

46.7

1.2E+02

0.0037

25.3

9.0

108

55-212

188-295

(340)

☐

23

3zey_7

Guanine nucleotide-bind

33.5

1.7E+02

0.0054

22.4

9.3

73

45-143

241-313

(318)

☐

24

4aow_A

Guanine nucleotide-bind

32.7

1.2E+02

0.0036

25.3

6.7

74

46-143

261-334

(340)

☐

25

4bh6_A

APC/C activator protein

32.6

1.9E+02

0.0059

22.6

11.3

102

53-202

34-135

(308)

☐

26

3v11_A

26S proteasome regulato

32.3

2.3E+02

0.0072

23.5

8.7

81

42-143

335-416

(420)

☐

27

4gga_A

P55CDC, cell division c

30.9

2.6E+02

0.0082

23.7

9.6

69

42-143

321-392

(420)

☐

28

2xyi_A

Probable histone-bindin

29.5

2.8E+02

0.0089

23.7

9.1

60

55-143

247-306


(430)

No 1




Q ss_pred	eEEecCCCCcEEEEecccCceEEEEEccCcEEEEECccccEeEEEEEEeccCCCC	
Q Fri_Sep_06_02:	HVLIDKLKDNIETSTTnCPSGIIITATSLGRVLFITIKDSTGKPKLELKQLKIQNSF	220 (220)
Q Consensus	~~~~~L--g-v-t- -n-ePaG-IlaTS-gRl---itirD~~~~lik~~~~	220 (220)
T Consensus	+++..+ . ++ + + + + + + ++ } + ++ ++ ++++	
T 1xks_A	-ei-----L--E-v-t-l-n-epaGfIlaTStgrl--lsir---Gkp-~-l-----G-	187 (450)
T ss_dssp	TEAFVDSGGDKTYSYFLAVQGGSFILSSSGSQLRLIPIE---SSGKIHQ--HILPQQQM	187 (450)
T ss_pred	EEEECC---CEEEEEEEETTTEEEETTTCEEEEEC---TTSCEEE--EECTCCCC	
T ss_pred	EEEEECccccCceEEEEecCcCeEEEEecceEEEEEc---CCcEEE--EEcCCCCc	

Q ss_pred		E	
Q Fri_Sep_06_02:	205 P	205 (220)	
Q Consensus	205 p	205 (220)	
T Consensus	181 ~	181 (327)	
T 4g3n_A	181 P	181 (327)	
T ss_dssp		B	
T ss_pred		c	

No 3  **PDB** **NCBI** **PubMed**

☐ **>1zvt_A** 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


```
Q ss_pred      EEEEECCCeEEEEccccccccccccccccceEEe--cCCCCCeEEEEecccCce-EEEEccCCEEEEEeCCCCC
Q Fri_Sep_06_02: 129 ICITNKNSQFLYFEDISTINNLTKLSKSAHVLD--LKLKDNENITSTINCEPSG-IITATSLGRVLFITIKDSTGK 204 (220)
Q Consensus    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    47 ll--T--Gr--y-----elp-----r--G--i--i-L--e-Iv-----lll-T--G--Kr-----e-- 118 (256)
T 1zvt_A       47 VVFVDS-TGRS-YAIDPITLPS-----ARGQGEPLTGKLTLPFGATVDHMLMESDDQKLLMASDAGYGFVCTNDLVAR 118 (256)
T ss_dssp      EEEEE-TSEE-EEECGGGSCC-----SSSCCEEggGTCCCTTCCEEEEECCCTTCEEEEBTTSEEEEEGGGGGCC
T ss_pred      EEEEEc-CCeE-EEEEHHHCCC-----cCCCCeEeeeeccccCEEEEEeCCCCCEEEEEcCCeEEEEHHHhccc
```

No 4  **SCOP** **PDB** **NCBI** **PubMed**

☐ **>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

```
Q ss_pred      EEEEECCCeEEEEccccccccccccccccceEEe----ecCCCCCeEEEEeccc---CCeEEEEecccCEEEEEeC
Q Fri_Sep_06_02: 129 ICITNKNSQFLYFEDISTINNLTKLSKSAHVLD--DLKLDNENITSTINC-----PSGIIATSLGRVLFITIKD 200 (220)
Q Consensus    129 lliV-p-tG-v-yWESIs-a--l--L--k-----l-L--gE-vt-l-n-----ePaG-IlaTS-grl--itirD 200 (220)
               ++++. .|+ .|+=+.+.+. .+.+.+.+. .+|+|.|.|.|.+.+.+.+. .+..++++|+.|+.+.+.+.+
T Consensus    61 ll--T--G-----ip-----r--G--i--l--l--e-i-----ll--T--G--kr--l-- 133 (312)
T 1suu_A       61 LFMISN-EGKLYLINAYEIK-----DSSRASKQNISELINLGDQEEILTIKNSKDLTDDAYLLLTASGKIARFESTD 133 (312)
T ss_dssp      EEEEE-TSEEEEEGGGSCC-----C-----CBGGTSCCTTCCEEEEEESCCCTTCEEEEBTTSEEEEEGGG
T ss_pred      EEEEEc-CCeEEEEHHHCCC-----CCcCCcChhhccccCCCCCEEEEEeccccCEEEEEeCCcEEEEHHH
```


```
Q ss_pred      C-----CCCeEEEEe
Q Fri_Sep_06_02: 201 S-----TGKPKLELKQ 211 (220)
Q Consensus    201 -----Gkp-l----- 211 (220)
               . .|+.+.+.+.
T Consensus    134 ---r-G---i-L-- 149 (312)
T 1suu_A       134 FKA VKSRGVIVIKLND 149 (312)
T ss_dssp      GCC-----CEECBCCCT
T ss_pred      hhcccCCCCeEEEEcCC
```

No 5  **PDB** **NCBI** **PubMed**

☐ **>3uc1_A** DNA gyrase subunit A; DNA binding protein, topoisomerase, isomerase; HET: DNA; 1.65A {Mycobacterium tuberculosis}
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      EEEEECCCeEEEEccccccccccccccccceEEe--cCCCCCeEEEEecccC---CceEEEEecccCEEEEEeC--
Q Fri_Sep_06_02: 129 ICITNKNSQFLYFEDISTINNLTKLSKSAHVLD--LKLKDNENITSTINC-----PSGIIATSLGRVLFITIKD-- 200 (220)
Q Consensus    129 lliV-p-tG-v-yWESIs-a--l--L--k-----l-L--gE-vt-l-n-e-----PaG-IlaTS-grl--itirD-- 200 (220)
               |+++.. .|+ .|+=+.+.+.+. .+.+.+.+. .+|+|.|.|.|.+.+.+.+. .+..+|+|.|.|.+.+.+.+.+
T Consensus    56 ll-ftT--Gr--y-----lp-----r--G--i--l--l--e-i-----e--v--T--G--iKr--l-- 130 (327)
T 3uc1_A       56 ILFFTT-QGR-VYRAKAYDLPEAS---RTARGQHVANLLAFQPEERIAQVIQIRGYTDAPYLVLAIRNGLVKKSLKLTDFD 130 (327)
T ss_dssp      EEEEE-TSE-EEEEEGGGSCBCC---SSSCCEEHHHTTCCTTCCEEEEEESSTSSSEEEEBTTSEEEEEGGGGC
T ss_pred      EEEEEc-CCe-EEEEHHHCCC---ccCCCEHHHccccCCCCCEEEEEeccccCEEEEEeCCcEEEEHHHh
```

```
Q ss_pred      ---CCCCEEEEEe
Q Fri_Sep_06_02: 201 ---STGKPKLELKQ 211 (220)
Q Consensus    201 -----Gkp-l----- 211 (220)
               . .|+.+.+.+.
T Consensus    131 ---r-G---i-lke 144 (327)
T 3uc1_A       131 SNRSGGIVAVNLRD 144 (327)
T ss_dssp      CCCSSCEESCBCCCT
T ss_pred      cccccceEEEEeCC
```

No 6  **PDB** **NCBI** **PubMed**

☐ **>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      eCCCCEEEEeCCeEEEEccccccccccccccccceEEe--CCcCCCCcCCcEEEEcCccccccccccccccCcccccCCC
Q Fri_Sep_06_02: 50 DTAQKALVNDLHIIYWNYSIQKDTPICKIS---LHDDYSVLSPSPICLFTSSISSTNNDTANYNNNASGNISGKFN 126 (220)
Q Consensus    50 Ds-sGYALV-s---VW-Y-s---p---fp---lp---Pl--v-p-s-d---s---e 126 (220)
               |.....+.+.+.+.+. .+.+.+.+. .|+.....|.|.|.+.+.+.+. .+
T Consensus    42 D---t-d-ll-ftT-----Gr-y---lp---r--G--i--l--l--e-i-----e 109 (327)
T 3uc1_A       42 DIVAHFPVCSTHDLILFFTT-----QGRVYRAKAYDLPEASRTARGQHVANLLAF-QPEERIAQVIQIRGYTD-----A 109 (327)
T ss_dssp      GCEEEEEEBTTSEEEET-----TSEEEEEGGGSCBCCSSSCCEEHHHTTC-CTTCEEEEEESSTTS-----S
T ss_pred      CEEEEEEeCCCCEEEEeC---cCEEEEEHHHccccCCCCcCEHHHcccC-CCCCEEEEEEeccccC-----C
```

```
Q ss_pred      ceEEEEeCCcCeEEEEccccccccccccccccceEEe--cCCCCCeEEEEecccC-CceEEEEecccCEEEEEe--C--
Q Fri_Sep_06_02: 127 NGICITNKNSQFLYFEDISTINNLTKLSKSAHVLD--LKLKDNENITSTINC--PSGIIATSLGRVLFITIK--D-- 200 (220)
Q Consensus    127 pGlliV-p-tG-v-yWESIs-a--l--L--k-----l-L--gE-vt-l-n-e-PaG-IlaTS-grl--itir--D-- 200 (220)
               +-++++. .|.|=--=. .+.+.+.+. .+|+|.|.|.+.+.+.+. .+..++++|.|.|.++++.+- +
```

T Consensus 110 ---v--T--G-iKr--l-----r-G--i-lke-D-lv-----d-ill-T--G--rf-----eip 180 (327)
 T 3uc1_A 110 PYLVLATR-NGLVKKSKLTD-----FDSNRSGGIVAVNLRDNDLGVAVLCSAGDDLLVLSANGQSIKRSATDEALR 180 (327)
 T ss_dssp SEEEEET-TSEEEEEEGGG-----GCCCSSESCBCCTTCCEEEEEETTCCEEEEEETTSCEEEEECTTTSC
 T ss_pred CEEEEc-CCEEEEHHH-----hhccccCceEEEECCCCCEEEEEeCCCEEEEECCCEEEEECCCCc

Q ss_pred CCCC
 Q Fri_Sep_06_02: 201 STGK 204 (220)
 Q Consensus 201 --Gk 204 (220)
 .+||
 T Consensus 181 --gr 184 (327)
 T 3uc1_A 181 PMGR 184 (327)
 T ss_dssp CCCC
 T ss_pred cCCc

No 7      

☐ >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

Q ss_pred EEEEECCCeEEEEccccccccccccccccceEEe--cCCCCCeEEeEcc---CCceEEEEccCCEEEEEeC--
 Q Fri_Sep_06_02: 129 ICIINKNKSQFLYFEDISTINNLTKLSKSKAHVLD--LKLKDNENITSTINC---EPGIIATSLGRVLFITIKD-- 200 (220)
 Q Consensus 129 lliV-p-tG-v-yWESis-a--l--L--k-----l-L--gE-vt-l-n---ePaG-IlaTS-gRl--itirD-- 200 (220)
 |+++.. .|++ ||=.+...+.+ -+.+...+. ++|+|||.+.+.+. +..-++++|..|.+.+.+.+
 T Consensus 60 ll-ft--G--v--eip-----r-a-G-i-ll-L--e-Iv-----ll--T--G-vKrt-l-e-- 134 (370)
 T 316v_A 60 LLTFTS-SGKV-FWLPVHQLPEAG---SNARGRPILINWIPLESGERVQAVLPVREYADNRYVFMATRNKGTVKKTPLESEFA 134 (370)
 T ss_dssp EEEEE-TSEE-EEEEGGGSCBCC---TSCCEBGGGSCCCTTCCEEEEEESCCCTTCCEEEEEETTSCEEEEEGGGGC
 T ss_pred EEEEE-CCeE-EEEEHHHCcCCC---cccCCcChhhccCCCCCEEEEEeCCCCCEEEEECCCEEEEEHHHHh

Q ss_pred ---CCCCeEEEEe
 Q Fri_Sep_06_02: 201 ---STGPKLELKQ 211 (220)
 Q Consensus 201 ---Gkp-l----- 211 (220)
 ..|+-.+.+++
 T Consensus 135 ---G--ai-L-- 148 (370)
 T 316v_A 135 FRLARGKIAINLDE 148 (370)
 T ss_dssp SCCTTCESCCCT
 T ss_pred cccCCcEEEEeCC

No 8      

☐ >1zvuv_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 EEEEECCCeEEEEccccccccccccccccceEEe--cCCCCCeEEeEccCCe-EEEEccCCEEEEEeCCC--
 Q Fri_Sep_06_02: 129 ICIINKNKSQFLYFEDISTINNLTKLSKSKAHVLD--LKLKDNENITSTINCPSG-IITATSLGRVLFITIKDST-- 202 (220)
 Q Consensus 129 lliV-p-tG-v-yWESis-a--l--L--k-----l-L--gE-vt-l-n-ePaG-IlaTS-gRl--itirD-- 202 (220)
 ++++.. .|++ ||=.+...+.+ .+.+...+. ++|+|||.+.+.+. +..-++++|..|.+.+.+.+
 T Consensus 517 ll-ft--Gr--y-----lp-----G--i-ll-l--e-i-----l--T--G-vk--l-- 589 (716)
 T 1zvuv_A 517 VVVFDS-TGRS-YAIDPITLPS-----ARGQGEPLTGKLTLPAGATVDHMLMESDDQKLLMASDAGYGFVCTFNDLVARN 589 (716)
 T ss_dssp EEEEE-TSEE-EEECTTSCC-----CC---CBSTTSCCTTCCEEEEECCCTTCCEEEEEBTSEEEEEGGGGCCCS
 T ss_pred EEEEE-CCeE-EEEEeccc-----cccCCcChhhccCCCCCEEEEEeCCCeEEEECCeEEEEHHHHccc

Q ss_pred --CCEeEEEEe
 Q Fri_Sep_06_02: 203 --GPKLELKQ 211 (220)
 Q Consensus 203 --Gkp-l----- 211 (220)
 |+-.+.+++
 T Consensus 590 --g--ai-L-- 600 (716)
 T 1zvuv_A 590 RAGKALITLPE 600 (716)
 T ss_dssp TTCEECBCCT
 T ss_pred cccEEEEeCC

No 9      

☐ >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

Q ss_pred EEEEECCCeEEEEccccccccccccccccceEEe--cCCCCCeEEeEccC---CceEEEEccCCEEEEEeC
 Q Fri_Sep_06_02: 129 ICIINKNKSQFLYFEDISTINNLTKLSKSKAHVLD--LKLKDNENITSTINC---PSGIIATSLGRVLFITIKD 200 (220)
 Q Consensus 129 lliV-p-tG-v-yWESis-a--l--L--k-----l-L--gE-vt-l-n-e---PaG-IlaTS-gRl--itirD 200 (220)
 |+++.. .|++ ||=.+...+.+ -+.+...+. ++|+|||.+.+.+. +..-++++|..|.+.+.+.+
 T Consensus 53 ll-ft--Gr--eip-----r-a-G-i--i-L--e-Iv-----ll--T--G-iKrt-l-e 125 (323)
 T 1wp5_A 53 LLLFTN-KGNY-LYCPVHELDIR---WKDLGQHIANIIPIDRDEEIIKAIPINDFELNGYLFVTRNGMVKKTELKH 125 (323)
 T ss_dssp EEEEE-TSEE-EEEEGGGSCBCC---TSCCEBGGGSCCCTTCCEEEEEESCTTSCCEEEEEETTSCEEEEEGGG
 T ss_pred EEEEE-CCeE-EEEEHHHCcCCC---CCCCCcChhhccCCCCCEEEEEeccccCCcCEEEEECCCEEEEEHHH

No 10      

☐ >1zi0_A DNA gyrase subunit A; beta pinwheel, topoisomerase, spiralling beta pinwheel, DNA wrapping, isomerase, DNA binding 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

Page 5 of 15

Page 6 of 15

Page 7 of 15

T ss_pred EEEEECCcEEEECCcEEEECCCCcEEEEccccC----CCcEEEEEC-----

Q ss_pred CcEEEECCcEEEEccccccccccccccceEEcCCCCCCEEEEcCCcEEEEccCEEEEEEC

Q Fri_Sep_06_02: 126 NNGICINKNKNSQFLYFEDISTINNLTKLSKSAHVLDLKLKDNENITSTINCEPSGIIATSLGRVLFITIKD 200 (220)

Q Consensus 126 epGlliv-p-tG-v-yWEsIs-a-l-L-k-----l-L-gE-vt-l-n-ePaG-IlaTS-gRl-~itirD 200 (220)

T Consensus 108 ~-l~-d~-i~-d-----1-----1-----dg-v~-d----- 172 (337)

T 1qxr_A 108 DGCTLIIVGGEASTLSIWDLAA-----PTPRIKAEILTSSAPACYALAI SPDSKYCFSCCDGNI AVWDLHN 172 (337)

T ss_dssp TSSEEEEESSSEEEEECC-----C-----EEEEECSSSCEEEECTTSSEEEETTSCSEEEETT

T ss_pred CCCEEEECCcEEEECC-----CcEEEEccCCcCEEECCCCCEEEECcCCcEEEECC

No 22      

☐ >4aow_A 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

Q ss_pred EEEEECCcEEEECCCCCCCCcEEEECCccccCCcCEEECCccccccccccccCCccccCCcCEEEEEC

Q Fri_Sep_06_02: 55 KALVNDLHDHIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSKFNNGICINLK 134 (220)

Q Consensus 55 yALV-s-----VW-Y-s-p-fplp-----Pl-v-p-s-d-----s-----epGlliv-p 134 (220)

T Consensus 188 l-s~-d~-v-iwd-----h~-v~-sp-----dg~-l~-s~- 234 (340)

T 4aow_A 188 IVSCGWDKLVKVVNLANCK-----LKTNHIGHTGYLNTVTVSP-----DGS LCASGG 234 (340)

T ss_dssp EEEEEETTSCEEEETTTE-----EEEEECCSSCEEEECT-----TSSSEEEEE

T ss_pred EEEcCCcCEEEECcCC-----eeEEcCCcCEEEEC-----CCCEEEEC

Q ss_pred CCcEEEEccccccccccccccceEEcCCCCCCEEEEcCCcEEEEccCEEEEECCCCCEEEEEEC

Q Fri_Sep_06_02: 135 KNSQFLYFEDISTINNLTKLSKSAHVLDLKLKDNENITSTINCEPSGIIATSLGRVLFITIKDSTGPKLELKQK 212 (220)

Q Consensus 135 -tG-v-yWEsIs-a-l-L-k-----l-L-gE-vt-l-n-ePaG-IlaTS-gRl-~itirD-Gkp-l-~ 212 (220)

T Consensus 235 ~-dg~-iwd-----v~-l~-iwd-----s----- 295 (340)

T 4aow_A 235 KDQGLMWDLNE-----GKHYLTLDGGDIINALCFSPNRYWLCAATGP--SIKIWDLEKIIIVDELKQ 295 (340)

T ss_dssp TTCEEEETT-----TTEEEECSSCEEEECTSSSEEEETT-----EEEEETTTEEEEC

T ss_pred CCCEEEECC-----CcEEECcCCcCEEECCCCCEEEECcC-----cEEECcCCcEEhhhc

No 23      

☐ >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 EEEEECCCCEEEECCcEEEECCCCCCCCcEEEECCccccCCcCEEECCccccccccccccCCccccCC

Q Fri_Sep_06_02: 45 FGLVDLTALQKALVNDLHDHIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSK 124 (220)

Q Consensus 45 ~-g-iDs-sGyALV-s-----VW-Y-s-p-fplp-----Pl-v-p-s-d-----s----- 124 (220)

T Consensus 241 ~-d~-i~-d-----v~-l~-s----- 295 (318)

T 3zey_7 241 NQICFSPNRYWMAATEKGRIFDL--ENKDIIVELAPEHQSGKKIVPECVSIAWSA----- 295 (318)

T ss_dssp EEEECSSSEEEEEETTEEEETT-----TTEEEECSSCCSSCCCEEEECT-----EEEEETTTEEEEC

T ss_pred eeeeecccccccccCEEEEC-----CCCCEEECcCccCccccCEEEEC-----

Q ss_pred CCcEEEECCcEEEE

Q Fri_Sep_06_02: 125 FNNGICINKNKNSQFLYF 143 (220)

Q Consensus 125 -epGlliv-p-tG-v-yWE 143 (220)

T Consensus 296 ~-dg~-l~-sg~-Dg-v-iwd 313 (318)

T 3zey_7 296 -DGSTLYSGYTDNVI RVWG 313 (318)

T ss_dssp -TSCEEEESSCEEEEC

T ss_pred -CCCEEEECcCEEEEC

No 24      

☐ >4aow_A Guanine nucleotide-binding protein subunit beta-2; receptor, WD-repeat, beta-propeller; 2.45A {Homo sapiens} PDB: 3j3a_g 2zkq_a 3j38_g
 Probab=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 EEEECcCCcEEEECCcEEEECCCCCCCCcEEEECCccccCCcCEEECCccccccccccccCCccccCC

Q Fri_Sep_06_02: 46 EGLVDLTALQKALVNDLHDHIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSK 125 (220)

Q Consensus 46 ~-g-iDs-sGyALV-s-----VW-Y-s-p-fplp-----Pl-v-p-s-d-----s----- 125 (220)

T Consensus 261 ~-sp~-l~-i~-iwd-----v~-l~-sp----- 316 (340)

T 4aow_A 261 ALCFSPNRYWLCAATGPSIKIWDLEKIIIVDELKQEVISTSKAEPQCTSLAWSA----- 316 (340)

T ss_dssp EEEECSSSEEEEEETTEEEETT-----TTEEEECcC-----CCCCEEEEECT-----

T ss_pred EEECCCCcEEEECCcEEEECCcEEhhhccccccccCCcCEEEEC-----

Q ss_pred CcEEEECCcEEEE

Q Fri_Sep_06_02: 126 NNGICINKNKNSQFLYF 143 (220)

Q Consensus 126 epGlliv-p-tG-v-yWE 143 (220)

T Consensus 317 dg~-l~-sg~-Dg-v-vW- 334 (340)

T 4aow_A 317 DGQTLFAGYTDNLVRVWQ 334 (340)

T ss_dssp TSSEEEETTSCSEEEEC

T ss_pred CCCEEEEcCCCCEEEC

Page 9 of 15

No 35      

☐ >3ow8_A WD repeat-containing protein 61; structural genomics consortium, SGC, 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          cccccCCCcEEEEeCCCCEEEEeCCe-EEEEeCCCCCCCCeEEEECCCCccccCCCcEEEEc-Cccccccccccc
Q Fri_Sep_06_02:  36  NNNTIDTHHfEGLVDLTALQALVNDLDH-IYIWNYSIQKDTPICKISLHDDYSVLSPPICLFTS-SISSTNNDTANYN  113 (220)
Q Consensus        36  ~~~~g-1Ds~sGYAlv~s~~~~VW-Y~s~p~~~~fplp~~~~Pl~v~p~s~d~~~~  113 (220)
T Consensus        243  ~~~~~v~~~~~l~sgs~Dg~i~iwd~~~~~l~H~~~~~v~l~s~-----  300 (321)
T 3ow8_A           243  TLSGHASWVLNVAFCPDTHFVSSSSDKSVKVDVGTRT---CVHTFFDQHD-----QVWGVKYNG-----  300 (321)
T ss_dssp          EECSSSCSEEEEECTTSSSEEEETTSCEEEETTTT-----EEEECCCSS-----CEEEETCT-----
T ss_pred          EeECcCCcEEEEEcCCCCEEEEeCCcEEEEECCCCc---EEEEECCCCC-----CEEEEEcC-----

Q ss_pred          cCCCccccccCCCcEEEEeCCCCeEEEEe
Q Fri_Sep_06_02:  114  NNASGNISGKfNNGICIIINKNSQFLYFE  143 (220)
Q Consensus        114  ~~~s~~~~~epGlliiv~p~tG~v~yWE  143 (220)
T Consensus        301  -----g~l~s~s~Dg~I~iWD  318 (321)
T 3ow8_A           301  -----NGSKIVSVDGQIEIHIYD  318 (321)
T ss_dssp          -----TSSEEEEETTCCEEEEE
T ss_pred          -----CCCEEEEEeCCcEEEEEe
  
```

Page 12 of 15

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

```

Q ss_pred      EEEEECCCC-EEEEcC-CeEEEECCCCCCCCeEEECcCcccccCCcCeEEEEcCccccccccccccCCCCcccc
Q Fri_Sep_06_02: 45 FEGLVDTALQ-KALVNDL-DHIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINS 122 (220)
Q Consensus    45 --g-iDs-sG-yALv-s-----VW-Y-s---p-----fplp-----Pl--v-p-s--d-----s----- 122 (220)
               ...+++... +.++.+. ..++| |+.-----+.+. .+...+.+.+|
T Consensus    294 -----1-g~dg~i~vwd-----v----- 344 (420)
T 3v11_A       294 NSLTVDGNNANYIYAGYENGMLAQWDLRSPECPVGEFL-----INEGTPINNYYFA----- 344 (420)
T ss_dssp      EEEECSSCTTEEEETTSEEEETTCTTSCSEEE-----ESTTSEEEEEEE-----
T ss_pred      eEEEECCCCEEEEeCCeEEEEeCCcCchhhh-----ccCCCCeEEEEc-----

Q ss_pred      cCCCeEEEECCcCeEEEEccccccccccccccceEEecCCCCCCEEEEcCCcC---eEEEEccCCEEEEEe
Q Fri_Sep_06_02: 123 GKFNNGICITINKKNSQFLYFEDISTNNLYTKLSKSKAHVLDLKLKDNENITSTINCEPS---GITATSLGRVLFITIK 199 (220)
Q Consensus    123 ---epGlliv-p-tG-v-yWEsIs-a--l---L---k-----l-L-gE-vt-l-n-ePa--G-IlaTS-gRl--itir 199 (220)
               +.+++++...|.|.+.+---..... +..... +.-.++-.....+.+. -+++.+.|.+.+...+.
T Consensus    345 -----l-s--d--v-iw-----s-----g-l-a-g--g----- 418 (420)
T 3v11_A       345 ---AGALFVSSGFDTSIKLDIISDPESERP--AIEFETPTF-LVSNDDAVSQFCYVSDDESNGEVLVKGNNFCALYNLS 418 (420)
T ss_dssp      ---TEEEEETTTEEEEEECCTTCCSC--EECTTSCEE-ECCSSCCCEEEEECCSSSSCEEEEEETTTEEEESC
T ss_pred      ---CCEEEEeCCcCeEEEEccCCCCcc--ceecCccE-EccCccEEEEEcCCCCcCeEEEEcCCeEEEEcc

Q ss_pred      CC
Q Fri_Sep_06_02: 200 DS 201 (220)
Q Consensus    200 D- 201 (220)
               |.
T Consensus    419 -- 420 (420)
T 3v11_A       419 NP 420 (420)
T ss_dssp      C-
T ss_pred      CC
  
```

No 41          

☐ >lmzu_A PPR; photoactive yellow protein, PAS, PYP, signaling protein; HET: HC4; 2.00Å {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      eEEEECCcCeEEEE
Q Fri_Sep_06_02: 128 GICITINKKNSQFLYF 142 (220)
Q Consensus    128 Glliv-p-tG-v-yW 142 (220)
               |+++++. +|+|.|
T Consensus    34 GllivD~dg~I~ 47 (129)
T lmzu_A       34 GAIQVDG~SGVIHRY 47 (129)
T ss_dssp      EEEEEET~TCBEEEE
T ss_pred      eEEEECC~CCeEEEE
  
```

No 42          

☐ >3fm0_A Protein CIA01; WDR39,SGC,WD40,CIA01, nucleus, WD repeat, biosynthetic prote structural genomics, structural genomics consortium; 1.70Å {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 ss_pred      EEEECcCeEEEECCCCCCCCeEEECcCcccccCCcCeEEECcCccccccccccccCCCCccccCCcCeEEEEc
Q Fri_Sep_06_02: 55 KALVNDLHDIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINS 134 (220)
Q Consensus    55 yALv-s-----VW-Y-s---p-----fplp-----Pl--v-p-s--d-----epGlliv-p 134 (220)
               .|-.....+.| |+.-----+.....+...+.++---+| . +++++|+...
T Consensus    267 l-s--d--i~vw-----h---V-v~p-----laS-s 323 (345)
T 3fm0_A       267 LATACGDDAIRVFQEDPNSDPQQPTSLTAHLQHAHQSDVNCVAWNPN-----K-----EPGLLASCS 323 (345)
T ss_dssp      EEEEEETTSCEEEEEETTSCTTSCCEEEEEETTSSTSSCEEEEEECs-----S-----STTEEEEE
T ss_pred      EEEEECCcCeEEEECCCCCCCCeEEECcCcccccCCcCeEEECc-----C-----CceEEEEc
  
```

```

Q ss_pred      CCcEEEEe
Q Fri_Sep_06_02: 135 KNSQFLYFE 143 (220)
Q Consensus    135 -tG-v-yWE 143 (220)
               .+|. |++|+
T Consensus    324 -Dg-v~W~ 332 (345)
T 3fm0_A       324 DDGEVAFWK 332 (345)
T ss_dssp      TTSCEEEEE
T ss_pred      CCCeEEEE
  
```

No 43          

☐ >lpgu_A Actin interacting protein 1; WD repeat, seven-bladed beta-propeller, protein binding; 2.30Å

{Saccharomyces cerevisiae} SCOP: **b.69.4.1 b.69.4.1** PDB: **lpi6_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      EECcCCChhhhhhhcccccccCCcCEEEEECCCCEEEEcCCeEEEECCCCCCCC~CCeEEEECCCCccccCCcC~eEEF
Q Fri_Sep_06_02: 21 TKLSTDLSPGSGNGNNITDTHHFEGLVDLTKALVNDLHDIYIWNYSIQKDTPICKISLHDDYSVLSSPPICLF 98 (220)
Q Consensus    21 s-l--p--l-----g-iDs-sGyALv-s---p-----fplp-----P-l-- 98 (220)
               ..+|. |.... .+++++.+++++. | |+.-----+.+. .+...+.+.+
T Consensus    8 -----v-----spdg-----l-----v-----h-----V----- 70 (615)
T lpgu_A       8 ELIPQPSTQR-----NFTTHLSYDPTTNAIAYPCGKSAFVRCLDDGDSKVPPVQFTGHGS-----SVVTTV 70 (615)
T ss_dssp      EEECCCCCCT-----TCCCCCEETTTTTEEEETTTEEEECSSCCSSCEEEECTTTT-----SCEEEE
T ss_pred      hccCCCCCc-----CcEEEEECCCCEEEEcCCeEEEECCCCCCCCccccEEecCCC-----ceEEEE
  
```


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