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MAX-PLANCK-GESELLSCHAFT

Show results of job:

Show results

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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

ProtBLAST+

PSI-BLAST

PSI-BLAST+

SimShiftDB

New job

Resubmit

Resubmit\_HMM

Resubmit/HHsenser

Realign

Log

Input-params

Delete

HHpred - Results

Job-ID: nup133\_new

Date: 23:24 on Mar 04 2016

Help

Results

Histogram

Reduced alignment

Representative alignment

Full alignment

Create model

Merge Q/T alignments

Forward to PCoils

Forward MSA

Save

Export

Color alignments

View Alignment

color only SS

color alignments

color alignments

42

1100

100

200

300

400

500

600

700

800

900

1000

1100

Resubmit section

5a9q\_3

4q9t\_A

3i4r\_B

1xks\_A

4mhc\_A

5a9q\_A

3no0\_A

1zi0\_A

3i6v\_A

1zvt\_A

4i0o\_A

1wp5\_A

4g3n\_A

1suu\_A

1zvu\_A

4g3n\_A

3f7f\_A

3no0\_A

4xnn\_E

1wp5\_A

3kfo\_A

3cqc\_B

3i5p\_A

4kno\_B

Query

Fri\_Mar\_04\_23:24:12\_+0100\_2016

(seq=MSEKKVHLRL...INYEYNTVEY

Len=1157

Neff=7.1

Nseqs=143)

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

5a9q\_3

Nuclear pore complex pr

100.0

1E-143

3E-148

1404.9

0.8

950

42-1100

56-1141(1156)

2

4q9t\_A

Nucleoporin NUP133; nuc

100.0

1.7E-83

4.8E-88

761.3

42.8

421

48-483

2-449 (459)

3

3i4r\_B

Nuclear pore complex pr

100.0

4.7E-83

1.3E-87

792.3

0.0

552

491-1084

2-614 (644)

4

3kfo\_A

Nucleoporin NUP133; nuc

100.0

1.4E-63

3.9E-68

555.0

17.4

279

878-1157

2-280 (288)

5

1xks\_A

Nuclear pore complex pr

100.0

1.1E-60

3E-65

565.2

39.9

367

59-481

7-413 (450)

6

3cqc\_B

Nuclear pore complex pr

100.0

5.5E-35

1.5E-39

316.8

6.7

190

881-1097

2-207 (227)

7

5a9q\_A

Nuclear pore complex pr

99.3

7.4E-06

2E-10

109.4

66.2

823

67-1046

81-1225 (1391)

8

3i5p\_A

Nucleoporin NUP170; hel

98.1

1.3E-05

3.6E-10

97.3

13.2

179

843-1046

180-367 (525)

9

4mhc\_A

Nucleoporin NUP157; nuc

96.4

0.54

1.5E-05

60.0

26.1

257

67-362

71-367 (826)

10

3no0\_A

DNA gyrase subunit A; D

77.0

26

0.00072

38.8

13.3

111

164-298

130-243 (276)

11

1zi0\_A

DNA gyrase subunit A; b

70.8

34

0.00094

38.6

12.3

111

164-298

56-175 (307)

12

3i6v\_A

GYRA, DNA gyrase subuni

68.4

29

0.00081

40.2

11.4

112

164-296

60-177 (370)

13

1zvt\_A

Topoisomerase IV subuni

68.2

18

0.00049

39.8

9.1

112

164-297

47-161 (256)

14

4i0o\_A

Protein ELYs; beta prop

67.9

94

0.0026

37.4

15.5

116

83-234

34-174 (497)

15

4kmo\_B

Putative vacuolar prote

63.3

2E+02

0.0056

32.6

16.9

134

789-960

35-176 (333)

16

1wp5\_A

Topoisomerase IV; broke

63.2

49

0.0014

37.6

11.7

113

164-298

53-173 (323)

17

4g3n\_A

DNA gyrase subunit A; D

57.8

63

0.0017

36.7

11.4

110

164-297

160-277 (327)

18

1suu\_A

DNA gyrase subunit A; t

57.3

57

0.0016

36.8

10.8

111

164-298

61-180 (312)

19

1zvu\_A

Topoisomerase IV subuni

53.4

34

0.00093

42.9

8.6

113

164-297

517-631 (716)

20

4g3n\_A

DNA gyrase subunit A; D

48.2

1.2E+02

0.0033

34.5

11.6

112

164-296

56-173 (327)

21

3f7f\_A

Nucleoporin NUP120; nuc

47.0

49

0.0014

42.0

8.9

89

210-310

165-259 (729)

22

3no0\_A

DNA gyrase subunit A; D

46.4

1.7E+02

0.0046

32.2

12.2

104

164-298

38-145 (276)

23

4xnn\_E

Nucleoporin NUP120; str

40.4

92

0.0025

41.3

10.2

87

210-310

173-267 (1045)

24

1wp5\_A

Topoisomerase IV; broke

40.0

2.4E+02

0.0065

32.0

12.4

113

164-298

158-276 (323)

25

4uuy\_A

Vacuolar membrane prote

38.5

3.6E+02

0.0099

31.0

13.6

105

89-233

23-130 (349)

26

4bzj\_A

Protein transport prote

35.6

8.1E+02

0.022

33.2

18.5

209

786-1045

511-744 (1273)

27

4gq2\_M

Nucleoporin NUP120; bet

32.2

1.8E+02

0.005

38.2

10.9

90

209-310

174-275 (950)

28

5a9q\_1

Nucleoporin SEH1; trans

30.6

61

0.0017

44.5

6.4

95

211-312

221-324 (1436)

29

1zvt\_A

Topoisomerase IV subuni

29.3

3.5E+02

0.0097

29.4

11.1

109

160-298

1-113 (256)

30

1zi0\_A

DNA gyrase subunit A; b

26.5

3.3E+02

0.0091

30.5

10.6

110

164-298

160-276 (307)

31

3mkq\_B

Coatomer subunit alpha;

24.7

97

0.0027

31.8

5.3

41

780-820

100-140 (177)

32

5cqs\_A

Elongator complex prote

24.0

7.4E+02

0.02

29.1

13.4

126

789-924

128-258 (435)

33

1suu\_A

DNA gyrase subunit A; t

23.5

6.7E+02

0.019

27.9

12.4

112

164-297

165-281 (312)

http://toolkit.tuebingen.mpg.de/hhpred/results/nup133\_new

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No 2

```

Q ss_pred          hhhcccCCCCcEEEcCCCCEEEEcCCCCchhc-----ccCcCeEEEEcCCCCEEEEcCcEEEEcCCCCCCCCc
Q Fri_Mar_04_23:  48 QLRlhSHFDNSKvYFTNNRYIVTLQTPDYSGGF-----SNDELNGYIDMQIGYGLVNDHKKVYIWNHSTQKDPY      119 (1157)
Q Consensus       2  d-vlt-n-Y-Vs-lp-lp-----g-id-sG-Alv-----VW-y-s-----p      119 (1157)
                  ++++++|+|++|+|+|++|+|++|+|++|+|+...++++|+|++|+|+|+++++|+|+|+++++|+|
T Consensus       2  vlt-n-y-V-l-p-l-al-----g-id-sG-Alvv-----l-VW-y-s-----s      81 (459)
T 4q9t_A          2  SLTSNNKYGNTKILTETEKYSVKTLSTDLPSGNSNNNTIDTHHFGVLVDALQVLNLDHIYIWNYSIQKDP      81 (459)
T ss_dssp         -----CEEEECSSEEEEECSSCCCCSC-----CCCCEEETTEEEEECSSEEEECTTSSCCCCC
T ss_pred         ccccccCCCCcEEEEcCCCCEEEEcCCCCcHHHHhhhhccccccCcCcEEEEcCCCCEEEEcCCCCCCCCc

```

Q ss_pred		EEeCCCCcCCCCCcEEEc-CCcccccccccCCC----	CCCeEEEECCCCe--eecccchhhhcccchhc	
Q Fri_Mar_04_23:	120	TIVPRSDNDNIIAIPARCLITP-ATMDSPALNPNDQ---	ETGGILIKGSKAI--YYEDINSINLKNFKSE	190 (1157)
Q Consensus	120	--pLP-----ltp-----s-----	pGLviv-pTG--yWeSI--a_lgl-l-	190 (1157)
		++    ++.+++++ + ++  ++ +.+++++ +++	++   + +.  +    + +++++ .l.+	
T Consensus	82	--LP-s-----spvl-----s-----	pGLviv-tGVryWeSI-----sl-l-	160 (459)
T 4q9t_A	82	CKISLI-DYSLVSSPPICLFPTSSISSSTNNDTANYNNNASGNISNGKFNNGICINKKNSQLFYFDISTINLNLYTKLSK		160 (459)
T ss_dssp		EEEECC-----CCCEEEEECCC-----	CEEEECTTTCEEEESCSCSSCCCC-----	
T ss_pred		EEECcC-CccccCcCCcEEEcCCccccccccccccccccccccCCCCcEEEECCcCcEEEcCccccccccccccchhc		



No 4






                 

☐ >3kfo\_A Nucleoporin NUP133; nuclear pore complex, yeast, proteolysis, structural genomics, PSI2, protein structure initiative; HET: MSE; 1.90A [Saccharomyces cerevisiae]  
 Probab=100.0 E-value=1.4e-63 Score=554.95 Aligned cols=279 Identities=100% Similarity=1.381 Sum\_probs=0.0

[illegible]

[illegible]

No 6

>3cqc\_B Nuclear pore complex protein NUP133; nucleoporin, mRNA transport, nucleus, phosphoprotein, protein transport, translocation; 2.53A {Homo sapiens} PDB: 3cqc\_B  
Probab=100.00 E-value=5.5e-35 Score=316.80 Aligned\_cols=190 Identities=13% Similarity=0.174 Sum\_probs=0.0

Q ss\_pred cccCcc

Q Fri\_Mar\_04\_23: 881 KYGHVAWITQGLDGSYADAMNTLNKTIVDSDKKGSLSECELHLNVAKLSLLV-EKDNDINTLRKIQLYNLDTDAEKN 959 (1157)

Q Consensus 881 l--lSWI-dl---y--As-tLA-lA--lk--LSLaKla-LA--l-i--lQe-L-li-iQe- 959 (1157)  
.++|||+|.++.+||+|+++..+. +.++|+||+|||+|+|+ +++...+.+++|++|++|+

T Consensus 2 l--lSWI-dl---y--Aa-tLA-lA--e-----l--lk--LSLaKla-LA--l~i--lQe-L-li-iQe- 78 (227)

T 3cqc\_B 2 ASHMLSLWEHSIQELEKAHATLLGLANME--TRYFAKKTLLGLSKLAALASDFSEDMLQEKEEMAEQERFLHQET 78 (227)

T ss\_dssp -CCTTHHHHHHTTCCHHHHHHHHHHHHC---CSCCHHHHHHHHHHHHHHSCCCCHHHHHHHHHHHHHHHHHHHHT

T ss\_pred CCCcccHHHHHHhCCHHHHHHHHHHhhc---cc

Q ss\_pred HHHHHhhhhhhHHHHhhccHHHHHHHHHHHHhhcCCcCHHHHHHHhhccc---chHHHHHHHHHHhhhhccCCCCHHHH

Q Fri\_Mar\_04\_23: 960 ISNKLKKGVEQICKRFKNGSIREVFNLVVELKSTTVVNLSDLVLYLSMLD---DEESLFIPRLRLSVDGNNLNFYVKK 1035 (1157)

Q Consensus 960 L-----l-----a-----l-----L-eIdlltLl-d-----F-AL-vl-----e----- 1035 (1157)  
+++++. .|. ++++++|+||+|+|+++ ++||+|+|+|+++++.++ .++

T Consensus 79 l-----l-----eIdllt-----F-AL-vl----- 138 (227)

T 3cqc\_B 79 LPQLQA-----EQOL-----NLSAMPVLTAQPLIGLYICENRRANYDPFKALDLPIDEEED-ININ 138 (227)

T ss\_dssp CCTTHNH-----HTTC-----CSSSSCCCCHHHHHHHSTCTTCTTCCHHHHHHHHTTTTTC-----CSH



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```

Q ss_pred          EEEEECCCCe-eeccccchhhccchccCceEEEEeCCCCCceEEEEeeCCc-eEEEEccccEEEEeCCCCCee
Q Fri_Mar_04_23: 164 LIIKGSKAI-YYEDINSINLNFKLSKFSHELELPINSSGGKCDLMLNCEPA-GIVLSTNMGRIFITIRNSMGKPK 241 (1157)
Q Consensus        164 lviV-p-tG-yWesI--a~lg1-l~-----l-L~---gE-vt-l-n-epa-g-IlaTS-gRl~lslrd--Gkp- 241 (1157)
                    +++++. .|+ ||=.+...+.| -++..+...-++|. .||.+.+...+. -++++|..|.+.+.+.
T Consensus        47 ll--T--G-----eip-----r-g-v~li-L~---e-IV-----ll--T--G~Krt-l~----- 113 (256)
T 1zvt_A           47 VVFVDS-TGRSYAIDPITLPSAR--GQGEPLTGKLTLP--PGATVDHMLMESDDQKLLMASDAGYGFVCTFN----- 113 (256)
T ss_dssp          EEEEE-TSEEEEGGGSSCCSS--SCCEGGGTCCCC--TCCEEEEECCTTCEEEEBTTSEEEEEGG-----
T ss_pred          EEEEEc-CCeEEEEhhCCCC--CCceeeEECCC--CCCEEEEEeCCCCEEEEeCCCCEEEEHH-----

```

```

Q ss_pred          eEehhhccC-ccCccchhhcCCCCeEEEcCCCCcccEEEEEECCCEEEEEe
Q Fri_Mar_04_23: 242 LKLGKLLNKP-FKLGIVSKIFNTNSSVSLRNGPILGKTRLVYITNKGIFQTWQL 297 (1157)
Q Consensus        242 l-----L-k-----g-----i-----I-si-g-----g-r-i-ilt--g-lq-W~ 297 (1157)
                    +|-+. .+|. .+....-|+++... .+.|+++|.+.+.+.
T Consensus        114 -----r-g~i~l~---d-v-----i-l-T--G~lrf-- 161 (256)
T 1zvt_A           114 ----DLVARNRAGKALITL-EPENAHVMPVPIED---ASDMLLAITQAGRLMPFV 161 (256)
T ss_dssp          -----GGCCSTTCEECB-CCCTTCBCCCECC--TTCEEEETTSEEEEEG
T ss_pred          ----HccccCcCceEEE-EeCCCCEEEEEEecC--CCCEEEEEeCCCCEEEEHH

```

No 14      

☐ **4i0o\_A** Protein Elys; beta propeller, structural protein, nuclear pore complex, WD repeat, mRNA transport; 1.90A {Mus musculus}  
 Probab=67.89 E-value=94 Score=37.42 Aligned\_cols=116 Identities=12% Similarity=0.113 Sum\_probs=0.0

```

Q ss_pred          CCeEEEECC-CCEEEEcCCeEEEcCCCCCCCCeEEEcCCCCCCCCCceEEEc-CCCCccccccccCCCC
Q Fri_Mar_04_23: 83 DDELNGYIDMQ-IGYGLVNDHKYVIWNHSTQKDPYITVPFRSDNDDEIAVAPRCILTF-PATMDESLALNPNQDQE 160 (1157)
Q Consensus        83 -----g-id--sG-Alv-----VW-y-s--p-----pLp-----pl~l~p-----s- 160 (1157)
                    .+.+.+.+. .|+|. .+...+.|+|+... -...+.+. .+ .+.+.+.+. .|...
T Consensus        34 -----g~g~g~aw~s-L-V~tg~e~F-----I-av-efp----- 93 (497)
T 4i0o_A           34 ESVLRGKFAAGKNGLACGPOLLEVNSLTG--ERLSAYRFS-GV--NEQPPVVLAVKEFSWHK----- 93 (497)
T ss_dssp          SCCCEEEECSSSSSEEEETTEEEETTTT---CEEEEECC-CT--TSSCEEEEEEETTT-----
T ss_pred          hhhcCcEeCCceEEEEeCcEEEEecCC--CEEEEEcc-CC--CCcCceEEEEcCCccc-----

```

```

Q ss_pred          CCeEEE-EECCCCe---eeccccchhhccchccCceEEEEeCCCCCceEEEEeCC-----c
Q Fri_Mar_04_23: 161 TGGLII-IKGSKAI--YYEDINSINLNFKLSKFSHELELPINSSGGKCDLMLNCEP-----A 217 (1157)
Q Consensus        161 -pGLvi-V-p-tG--yWesI--a~lg1-l~-----l-L~---gE-vt-l-n-ep-----a 217 (1157)
                    ..|+++ +...+|- +| +++ . .-.+.++ +.||+.+.+. .
T Consensus        94 ~-LLVgle-----L-l~di-----srvv~i~ip-----IT~l-----s~l~L~f-g 157 (497)
T 4i0o_A           94 RTGLLIGLEADGSLCLY-DLGI-----SRVVKAVVLP--GRVTAIEPIINHGGASASTQHLPLSLRWLFG 157 (497)
T ss_dssp          EEEEEEEECSSSEEEEEE-ETTT-----TEEEEEES---SCEEEEEEECSSSCGGGTTSCHHHHTSSS
T ss_pred          cccEEEEeCCCCEEEE-EcCC-----CcEEEEeCC--CcEEEEeCCcCCCCccchhhHhccCc

```

```

Q ss_pred          eEEEEccccEEEEe
Q Fri_Mar_04_23: 218 GIVLSTNMGRIFITIR 234 (1157)
Q Consensus        218 g-IlaTS-gRl~lslr 234 (1157)
                    -+|+|.+.|+++++.
T Consensus        158 vLAVGt~G~vLiLiDL~ 174 (497)
T 4i0o_A           158 VAAVVTDVGIILLIDLC 174 (497)
T ss_dssp          EEEEEETTCEEEEEC
T ss_pred          eEEEEeCCCCEEEEec

```

No 15      

☐ **4kmo\_B** Putative vacuolar protein sorting-associated PROT; membrane trafficking, SM protein, HOPS complex, thermophile, transport protein; 2.60A {Chaetomium thermophilum}  
 Probab=63.26 E-value=2e+02 Score=32.61 Aligned\_cols=134 Identities=10% Similarity=0.112 Sum\_probs=0.0

```

Q ss_pred          HHHHHHCCChHHHHHHHHhCCHHHHHHHHHhccccchHHHHHHHHHHhchHHHHHHHHhC-----CCHHHHHh
Q Fri_Mar_04_23: 789 NHVLCKVNLKEQCIQAEFYKDLGLVQTLQTLQDQSDTTVSLYETFFNEFPKFSFTLFYLLKH-----KKLNDLIF 862 (1157)
Q Consensus        789 i~L~g~e~A~LAeKy-Df-sLvel-----rl~Yf-kfg-FA~lf~yi-----g~LL- 862 (1157)
                    +..|++|.+.+.|=|=+.|+.+.+.+.+.+.+.+.+. .+..+. .+..+.+.+.
T Consensus        35 VpLLL-m-e~AL-kAi-SgD-dLI~VLi-L~l~f~f~l~p~a~l~y~----- 104 (333)
T 4kmo_B           35 VPLLlSMEEDELALDKAIESGDTDLIYFVIHQRLRLPLA--SFFRVVSS--RPTASAMVEALARNSDGDGND----- 104 (333)
T ss_dssp          HHHHHHTTCTTHHHHHHHHTCHHHHHHHHHHHHSCHH--HHHHHT--SHHHHHHHHTC-----C-----
T ss_pred          HHHHHcCCcHHHHHHHHHHhCCChHHHHHHHHHHhCCHH--HHHHHHh--CchHHHHHHHHHHhccccccC-----

```

```







Q ss_pred          ccchhhHHHHHHHHhCCcccCchHHHHhCCHHHHHHHHHhccccCCHHHHHHHHHHHHHhC-C-CCccc
Q Fri_Mar_04_23: 863 RFPQOHDLVLIQFFQESAPKYGHVAVIQIILDGYSADAMNLTKNITVDSDSKGESLSECEHLNVAKLSSLLV-E-KDNL 940 (1157)
Q Consensus        863 -----L~FL-----p-----lsWI-dI~y~As-tL~lA-----l~kk~LSLaKLa-LA----- 940 (1157)
                    .+|.|.+. .+++.|+.....|... .+++.|-|.|. . . . . .
T Consensus        105 -----L~d~y~q-----d~e~a-----L~a----- 156 (333)
T 4kmo_B           105 ----TALLKDLIYQ~-----DDRRLDGASVFIREALQ~---PETRTASDKLDLAA---NLLQGNQKEH 156 (333)
T ss_dssp          -----HHHHHHHHHH-----TTCHHHHHHHHHHTTC-----SSHHHHHHHHHH-----HHHSSCTTC
T ss_pred          -----HHHHHHHHHH-----cCHHHHHHHHHHHhC--CCHHHHHHHHHHH-----HHhhccccC

```

```

Q ss_pred          hHHHHHHHHHHHHHHHH
Q Fri_Mar_04_23: 941 INTLRKIQYNLDITDAEKNI 960 (1157)
Q Consensus        941 ~-l~i~L~li~iQe-L 960 (1157)
                    .-.+.++++.+.+.|+.|
T Consensus        157 -----Ll~Q~L 176 (333)
T 4kmo_B           157 VFELGALKEAKMLRMQETF 176 (333)
T ss_dssp          HHHHHHHHHHHHHHHHHHH
T ss_pred          HHHHHHHHHHHHHHHHHHH







```

**No 16**      

☐ **>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=63.16 E-value=49 Score=37.60 Aligned\_cols=113 Identities=12% Similarity=0.215 Sum\_probs=0.0

Q ss\_pred EEEEECCCCe-eeccccchhhccchhccCceEEEE--EecCCCCCceEEEEeeCC---ceEEEEccccEEEEeeCC  
 Q Fri\_Mar\_04\_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELE--LPINSSGGKCDLMLNCEP---AGIVLSTNMGRIFFTIRNS 236 (1157)  
 Q Consensus 164 lviV-p-tG--yWesI--a--lgl-l-----l-L---gE-vt-l-n-ep---ag-IlaTS-gRl--lsrld- 236 (1157)  
 +++++. .|+ ||=. +.+.+.+. -+.+.+.+. ++|. .|||. +.+.+.+. -++++|..|. +.+.+.+.  
 T Consensus 53 ll-ft--G-----elp-----r-a-G--i-li-l-----e-Iv-----ll--T--G-iKrt-l--- 124 (323)  
 T 1wp5\_A 53 LLLFTN-KGNLYCPVHELDIR---WKDLGQHIANIIPID--RDEEIIKAIPINDFELNGYFLFVTRNGVMKKTELK-- 124 (323)  
 T ss\_dssp EEEEE-TSEEEEEEGGSCBCC---TSCCEEggTSCCC--TCCEEEEEEECTTSSCEEEEEETTSSEEEEEGG--  
 T ss\_pred EEEEEc-CCEEEEEhhCcCCC---CccCCcCHhccCCC---CCCEEEEEeeccccCCcCEEEEECCCCEEEEeHH--







Q ss\_pred CCCeeEehhhccCc-cCccchhhccCCCCeEEecCCCCCccEEEEEECCCEEEEEee  
 Q Fri\_Mar\_04\_23: 237 MGKPOLKLGKLLNKP-FLGIWSKIFNTNNSVSLRNGPILGKGTRLVYITNKGIFQTWQLS 298 (1157)  
 Q Consensus 237 -Gkp-l-----L-k-----g-----i-si-g-----g-r-i-ilt--g-lq-W--- 298 (1157)  
 +|-. .++ +. |+-. -+.+.+.+.+. .+.+.|++|. ++|. +.+.+.+.  
 T Consensus 125 -----e-----r-----i-l-e-d-lv-----i-l-T--G--irf--- 173 (323)  
 T 1wp5\_A 125 -----HYK-AQRYSKPLTGINKDDQVVDVHLT---DGMNELFLVTHNGYALWFDSE 173 (323)  
 T ss\_dssp -----GGC-CSCSSCECSCCTTCCEEEEEE---CSCSEEEEEETTSSEEEEEGG  
 T ss\_pred -----Hhc-ccccCCcCEEEEECCCCEEEEEE---CCCEEEEECCCEEEEEehh

**No 17**      

☐ **>4g3n\_A** DNA gyrase subunit A; DNA gyrase C-terminal domain, beta-propeller, topoisomerase isomerase; HET: DNA; 1.40A {Mycobacterium tuberculosis} SCOP: **b.68.10.0** PDB: **3uc1\_A\***  
 Probab=57.75 E-value=63 Score=36.71 Aligned\_cols=110 Identities=9% Similarity=0.045 Sum\_probs=0.0

Q ss\_pred EEEEECCCCe-eeccc-cchhhccchhccCceEEEE--EecCCCCCceEEEEeeCCce-EEEEccccEEEEeeCCC  
 Q Fri\_Mar\_04\_23: 164 LIIIKGSKAI-YYED--INSINNLNFKLSEKFSHELE--LPINSSGGKCDLMLNCEPAG--IVLSTNMGRIFFTIRNSM 237 (1157)  
 Q Consensus 164 lviV-p-tG--yWesI--a--lgl-l-----l-L---gE-vt-l-n-epag--IlaTS-gRl--lsrld- 237 (1157)  
 +++++. .|+ ||=. ....+.| +.+.+. ++|. .|||. +.+.+.+. +++++|..|. +.+.+.+.  
 T Consensus 160 l-l-T--G--r-----i-g-----r-a-Gv-i-L--d-vv-----ll--T--G--Krt-l--- 227 (327)  
 T 4g3n\_A 160 LLLVSA-NGQIRFSATDEALRPMG---RATSGVQGMRFN---IDRLLSLVNVRGTYLLVATSGGYAKRTAIE-- 227 (327)  
 T ss\_dssp EEEEE-TSEEEEECCCTTSCBCC-----SSSCCESSCCCC--TTCCEEEEECCCTTCEEEEEETTSSEEEEEGG--  
 T ss\_pred EEEEEc-CCEEEEEccccccccCCC-----ccccceEEecC---CCCEEEEEeeCCCCEEEECCCCEEEEHH--






Q ss\_pred CCCeeEehhhccCc-cCccchhhccC-CCEEEecCCCCCccEEEEEECCCEEEEEee  
 Q Fri\_Mar\_04\_23: 238 GKPOLKLGKLLNKP-FLGIWSKIFNTNNSVSLRNGPILGKGTRLVYITNKGIFQTWQLS 297 (1157)  
 Q Consensus 238 Gkp-l-----L-k-----g-----i-si-g-----g-r-i-ilt--g-lq-W--- 297 (1157)  
 ++... .+.|+.-+... .+++++... .+.|+++|. +.+.+.+.  
 T Consensus 228 -----e-----R-gkG-----lv-----v-----i-l-t--G--ir--- 277 (327)  
 T 4g3n\_A 228 -----EYPVQGRGGKGLVTVMYDRRGRVLGALIVD---DSELYAVTSGGGVIRTA 277 (327)  
 T ss\_dssp -----GSCBCTTSCCESSCCCTTCCEEEEEEc---TTCCEEEEESSCEEEEEEG  
 T ss\_pred -----HhcccccCCcCEEEEEcccccCCEEEEEc---CCCEEEEECCCEEEEEehh

**No 18**      

☐ **>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=57.34 E-value=57 Score=36.82 Aligned\_cols=111 Identities=17% Similarity=0.129 Sum\_probs=0.0

Q ss\_pred EEEEECCCCe-eeccccchhhccchhccCceEEEE-----eCCCCCceEEEEee---CCceEEEEccccEEEEee  
 Q Fri\_Mar\_04\_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELE--LPINSSGGKCDLMLNCEPAG--IVLSTNMGRIFFTIRNSM 234 (1157)  
 Q Consensus 164 lviV-p-tG--yWesI--a--lgl-l-----l-L---gE-vt-l-n-epag--IlaTS-gRl--lsrld- 234 (1157)  
 +++++. .|+ ||=. +.+.+.+. -+.+.+.+. ++|. .|||. +.+.+.+. -++++|..|. +.+.+.+.  
 T Consensus 61 ll--T--G-----ip-----r-----G--i-li-l-----e-Iv-----ll--T--G--ikr--- 132 (312)  
 T 1suu\_A 61 LFMISN-EGKLYLINAYEIKDSSR---ASKGQNISEILNLG--DQEEILTIKNSKDLTDAYLLLTASGKIAFEST 132 (312)  
 T ss\_dssp EEEEE-TSEEEEEEGGSCC-----CBGGTSCCC--TTCCEEEEEESCCCTTCEEEEEETTSSEEEEEEG  
 T ss\_pred EEEEEc-CcEEEEEEHHCCCCc---cCCcCHhccCCC---CCCEEEEEeeccccCCcCEEEEECCCCEEEEHH

Q ss\_pred CCCCeeEehhhccCcCccchhhccCCCCeEEecCCCCCccEEEEEECCCEEEEEee  
 Q Fri\_Mar\_04\_23: 235 NSMGKPOLKLGKLLNKPFLGIWSKIFNTNNSVSLRNGPILGKGTRLVYITNKGIFQTWQLS 298 (1157)  
 Q Consensus 235 d--Gkp-l-----L-k-----g-----i-si-g-----g-r-i-ilt--g-lq-W--- 298 (1157)  
 +|. .++..|+---+.+.+.+. +.+.|+++|. +.+.+.+.  
 T Consensus 133 -----e-----G--i-l--D-lv-----i-l-T--G--r--- 180 (312)  
 T 1suu\_A 133 -----DFK-AVKSRRGIVIKLNDKDFVTSAEIVF---KDEKVICLSKKGSATFNRSR 180 (312)  
 T ss\_dssp -----GGC-C---CEBCBCTTCCEEEEEEc---TTCCEEEEEETTSSEEEEEEG  
 T ss\_pred -----Hcc-hhccCceEEEEcCCCCEEEEEEc---CCCEEEEECCCEEEEEehh

**No 19**     

☐ **>1zvu\_A** Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 3.00A {Escherichia coli}  
 Probab=53.41 E-value=34 Score=42.95 Aligned\_cols=113 Identities=14% Similarity=0.192 Sum\_probs=0.0

Q ss\_pred EEEEECCCCe-eeccccchhhccchhccCceEEEEcCCCCCceEEEEeeCCc-eEEEEccccEEEEeeCCCCee  
 Q Fri\_Mar\_04\_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGKCDLMLNCEPAG--GIVLSTNMGRIFFTIRNSMGKPKQ 241 (1157)  
 Q Consensus 164 lviV-p-tG--yWesI--a--lgl-l-----l-L---gE-vt-l-n-epag--IlaTS-gRl--lsrld--Gkp- 241 (1157)  
 +++++. .|+ ||=. +.+.+.+. -+.+.+.+. ++|. .|||. +.+.+.+. -++++|..|. +.+.+.+.  
 T Consensus 517 ll-ft--G--y-----iP-----G--i--l-l-----e-i-----l--aT--G-vKrt-l----- 583 (716)

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☐ >lvzt\_A Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 1.70A {Escherichia coli} PDB: 4mn4\_A\*



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