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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

HMNER3

PatternSearch

ProtBLAST

ProtBLAST+

PSI-BLAST

PSI-BLAST+

SimShiftDB

New job

Resubmit

Resubmit\_HMM

Resubmit/HHsenser

Realign

Log

Input-params

Delete

HHpred - Results

Job-ID: nup85\_new

Date: 23:23 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

☐ color only SS

☒ color alignments

☐ color alignments

View Alignment

41

100

200

300

400

500

600

700

744

Resubmit section

4xnn\_D

3f3f\_C

5a9q\_8

4ycz\_B

4xnn\_B

5a9q\_5

3bg1\_B

2qx5\_A

4ycz\_A

3jro\_A

5a9q\_4

2pn7\_A

4lct\_A

3iko\_C

4ady\_A

4bz\_A

3mkq\_B

3nzk\_B

4bz\_A

2pn7\_A

5cqr\_A

5cqr\_A

2wvp\_A

2n81\_A

5cqs\_A

4d0p\_A

5cqs\_A

5ft9\_A

Query

Fri\_Mar\_04\_23:23:42\_+0100\_2016

(seq=MTIDDSNRLL...LNFKLCQAFM Len=744 Neff=6.6 Nseqs=153)

Parameters

score SS:yes search:local realign with MAP:no

No Hit

1

4xnn\_D

Nucleoporin NUP85; stru

100.0

3E-159

8E-164

1398.7

54.4

704

41-744

12-715

(715)

2

3f3f\_C

Nucleoporin NUP85; stru

100.0

2E-129

5E-134

1120.7

46.4

570

1-570

1-570

(570)

3

5a9q\_8

Nuclear pore complex pr

100.0

5.1E-97

1E-101

866.6

36.4

611

37-744

1-648

(656)

4

4ycz\_B

NUP85; structural prote

100.0

3E-94

8.3E-99

848.5

33.7

579

142-744

115-925

(933)

5

4xnn\_B

Nucleoporin NUP145; str

98.4

6.7E-05

1.8E-09

88.3

26.1

312

177-572

170-512

(652)

6

5a9q\_5

Nuclear pore complex pr

97.9

0.00031

8.4E-09

85.8

19.5

341

155-571

366-769

(937)

7

3bg1\_B

Nucleoporin NUP145; NPC

97.8

0.0019

5.2E-08

72.8

21.1

295

179-552

121-441

(442)

8

2qx5\_A

Nucleoporin NIC96; mRNA

97.7

0.0058

1.6E-07

72.3

24.6

362

246-659

156-568

(661)

9

4ycz\_A

Fusion protein of SEC13

97.7

0.0003

8.2E-09

85.8

14.2

330

149-571

391-752

(876)

10

3jro\_A

Fusion protein of prote

97.2

0.019

5.1E-07

68.5

21.0

308

179-552

430-750

(753)

11

5a9q\_4

Nuclear pore complex pr

97.1

0.0036

9.9E-08

76.6

14.3

283

245-584

346-704

(925)

12

2pn7\_A

Protein WEB1, protein t

95.3

2.1

5.7E-05

47.7

22.2

212

242-511

143-376

(399)

13

3iko\_C

Nucleoporin NUP84; NPC,

95.2

0.12

3.3E-06

58.7

11.8

191

245-484

180-431

(460)

14

4bzj\_A

Protein transport prote

95.1

0.75

2.1E-05

58.6

20.2

205

247-504

512-740

(1273)

15

3mkq\_B

Protein transport prote

90.8

5.8

0.00016

44.7

16.4

196

247-491

155-381

(441)

16

4bzj\_A

Protein transport prote

85.8

29

0.00081

44.2

19.8

201

391-649

512-723

(1273)

17

2pn7\_A

Protein WEB1, protein t

70.3

61

0.0017

35.9

13.9

139

387-571

144-283

(399)

18

4lct\_A

COP9 signalosome comple

65.4

1.7E+02

0.0047

31.4

22.0

205

517-743

89-319

(348)

19

4ady\_A

RPN2, 26S proteasome re

60.3

1.6E+02

0.0044

36.5

16.2

226

485-742

17-275

(963)

20

4d10\_D

COP9 signalosome comple

59.8

2.3E+02

0.0064

31.0

20.0

156

500-672

66-235

(410)

21

5cqr\_A

Elongator complex prote

58.6

1.2E+02

0.0033

35.6

14.1

145

392-568

223-369

(622)

22

5cqr\_A

Elongator complex prote

55.8

1.1E+02

0.0031

35.9

13.2

140

482-651

233-375

(622)

23

3mkq\_B

Coatomer subunit alpha;

53.3

20

0.00055

35.0

5.4

50

518-571

20-69

(177)

24

2wvp\_A

GET4, UPF0363 protein Y

53.1

2.7E+02

0.0074

29.7

16.6

161



















389-595

16-195

(312)

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No 3                  

☐ [5a9q\\_8 Nuclear pore complex protein NUP85](#); transport protein; 23.00A {Homo sapiens}  
Probab=100.00 E-value=5.1e-97 Score=866.61 Aligned cols=611 Identities=17% Similarity=0.222 Sum\_probs=0.0

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No 5                                   








[illegible]



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




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No 9       

☐ >4ycz\_A Fusion protein of SEC13 and NUP145C; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein; 4.10A {Thielavia heterothallica}  
Probab=97.68 E-value=0.0003 Score=85.83 Aligned cols=330 Identities=12% Similarity=0.133 Sum\_probs=0.0

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No 12        

☐ >2pm7\_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces cerevisiae} PDB: 2pm6\_A 3mzl\_B

Probab=95.35 E-value=2.1 Score=47.66 Aligned cols=212 Identities=9% Similarity=0.069 Sum\_probs=0.0

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>4ady A RPN2, 26S proteasome regulatory subunit RPN2; protein binding, PC repeat; 2.70A {Saccharomyces



No 20     

No 21       

[illegible]

T ss\_pred HHHHHHcCCcHHHHHHHHccchHHHHHHHHhhHHHHH---HHhh-----CcHHHHHHHHHH

Q ss\_pred hhhccCCcchHHHHHHHHcCCcchHHHHHHHHhccCCCCcHHHHHHHHHHhC-CcHHHHHHHHHHHHHHCC

Q Fri\_Mar\_04\_23: 472 ELCSLGDKELWPAIGLIALSATGTRSAKMKVIAELLPHPVNTDDIEWMLSCVQWR-LPEIAKEIYTTLGQMLSAH 550 (744)

Q Consensus 472 -l-l---LW-vai-YL--c---g---r-r-i-eL-r-pl-t---ek-L-iC---L---a-I---g---l-g 550 (744)

T Consensus 285 -L---g---eAa--Y-kag---kAie-y-a-----w-A-la--l---l---lA--l---g 350 (622)

T 5cqr\_A 285 HLM---QHMYEPAGLMFARCGAHE---KALSAFLTC---GNWQALCVAAQLNFTKDQLVGLGRTLAKGLVEQR 350 (622)

T ss\_dssp HHH---TTTCHHHHHHHHHHTTCHH---HHHHHHHT---TCHHHHHHHHTTTCCHHHHHHHHHHHHHHTTT

T ss\_pred HHH---HCCCcHHHHHHHHcCCcH---HHHHHHHc-----cCHHHHHHHHcCCcchHHHHHHHHHHHHHCC

Q ss\_pred CHHHHHHHHH-cCCHHHH

Q Fri\_Mar\_04\_23: 551 NIIESIANFSR-AGKYELV 568 (744)

Q Consensus 551 -g-AL---r-A-d---V 568 (744)

T Consensus 351 -eA-----l-d---A 369 (622)

T 5cqr\_A 351 KHIDAAMVLEECADQYEEA 369 (622)

T ss\_dssp CHHHHHHHHHHSCCHHHH

T ss\_pred CHHHHHHHHHHcCCHHHH

No 22      

☐ >5cqr\_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 3.02A {Homo sapiens}  
Probab=55.77 E-value=1.1e+02 Score=35.89 Aligned\_cols=140 Identities=16% Similarity=0.169 Sum\_probs=0.0

Q ss\_pred hHHHHHHHHhCCcchHHHHHHHHHHhccCCCCcHHHHHHHHHHhCCcHHHHHHHHHHHHHHHHHHHHHHHH

Q Fri\_Mar\_04\_23: 482 WPVAIGLIALSATGTRSAKMKVIAELLPHPVNTDDIEWMLSCVQWR-LPEIAKEIYTTLGQMLSAHNIIESIANFSR 561 (744)

Q Consensus 482 W-vai-YL--c---g---r-r-i-eL-r-pl-t---ek-L-iC---L---a-I---g---l-g-g-AL---r 561 (744)

T Consensus 233 -eeAl-y-g---g---Al-l-----g-y-AleLa-----i---A-L---g---eAa--Y-k 301 (622)

T 5cqr\_A 233 YEKAIHLSKSGPEYFPECLNLKID---KNLYNEALKLYSP--SSQYQDISIAYGEHLMQEHMYEPAGLMFAR 301 (622)

T ss\_dssp HHHHHHHHTTSCSSSHHHHHHHHH---HTCHHHHTTSCST--TCHHHHHHHHHHHHHHTTCHHHHHHHHH

T ss\_pred HHHHHHHHHccchHHHHHHHHH-----hHHHHHHHHhh--CcHHHHHHHHHHHHHHHHHHHHHHHH

Q ss\_pred cCCHHHHHHHHHHHHHHHhCCCCCC-HHHHHHHHHccccccccccchHHHHhhhhcHHHHHHHHHHHHHHHHHHhC-

Q Fri\_Mar\_04\_23: 562 AGKYELVKYSWLLFEASCMGQKLD-DPVLNAIVSKNSPAEDDVIPQDILDCVVTNSMRQTLAPYAVLSQFYELDR- 639 (744)

Q Consensus 562 A-d--V--i--l--sl-g---D--l--iv-----p-le-----l--Ls-ya-lreF----- 639 (744)

T Consensus 302 ag---kA-----ie-y-a---w-A-la-l-----l--lA--l---g---eAa--Y-k 362 (622)

T 5cqr\_A 302 CGAHEKA-----LSAFLTCG---NWQALCVAAQLNF-----TKDQLVG--LGRTLAGLKVLEQRKHIDAAMVLEEC 362 (622)

T ss\_dssp TTCHHHH-----HHHHHTT--CHHHHHHHHTTTC-----CHHHHH--HHHHHHHHHTTCHHHHHHHHH

T ss\_pred cCCHHHH-----HHHHHc---CHHHHHHHHHcCC-----ChHHHH--HHHHHHHHHCCCHHHHHHHHH

Q ss\_pred -CcHHHHHHHHHH

Q Fri\_Mar\_04\_23: 640 -EDWGQALRLLL 651 (744)

Q Consensus 640 -g---Aa--Lv- 651 (744)

T Consensus 363 l-d---AI-l-l-- 375 (622)

T 5cqr\_A 363 AQDYEEAVLLLLLE 375 (622)

T ss\_dssp SCCHHHHHHHHHH

T ss\_pred cCCHHHHHHHHH

No 23      

☐ >3mkq\_B Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces cerevisiae}  
Probab=53.31 E-value=20 Score=35.00 Aligned\_cols=50 Identities=8% Similarity=0.058 Sum\_probs=0.0

Q ss\_pred HHHHHHHHHHcCCHHHHHHHHHHHHHHHcCCHHHHHHHHHcCCHHHHHHH

Q Fri\_Mar\_04\_23: 518 DIEWMLSCVQWR-LPEIAKEIYTTLGQMLSAHNIIESIANFSRAGKYELVSKY 571 (744)

Q Consensus 518 -ek-L-iC---L---a-I---g---l-g-g-AL---rA-d--V-i 571 (744)

T Consensus 20 -l-A--a---W-La--AL--l-lAe--y---d--l--L 69 (177)

T 3mkq\_B 20 NLDAALDEAKKL---NDSITWERLIQELAQGNASLAEMIYQHSFDFKLSFL 69 (177)

T ss\_dssp CHHHHHHHHHH---CCHHHHHHHHHHHHTCHHHHHHHHHHTCHHHHHHH

T ss\_pred CHHHHHHHHHc---CCHHHHHHHHHHHcCCHHHHHHHHHcCCHHHHHHH

No 24      

☐ >2wpv\_A GET4, UPF0363 protein YOR164C; golgi-ER trafficking, tail-anchored protein, protein binding GET4; 1.99A {Saccharomyces cerevisiae} PDB: 5bwk\_E 3lku\_A 5bw8\_C 4pwx\_E\*  
Probab=53.15 E-value=2.7e+02 Score=29.70 Aligned\_cols=161 Identities=12% Similarity=0.122 Sum\_probs=0.0

Q ss\_pred HHHHHHHHHHcCCHHHHHHHHHcChH-----HHHHHHHHHhCccccccccccccccccccccchhhhhcc

Q Fri\_Mar\_04\_23: 389 DWEQPCVDIISGKIHSILPVMSLDS-----TAAFTAMICEAKGLIENIFEGEKNSSDDYSNEDNEMLEDFLS 456 (744)

Q Consensus 389 -E-----i-egd---vL--l--ld-w-----aHladlL--g-L-----dl-- 456 (744)

T Consensus 16 -l-r1---i--G-yEAHQ--RT---Ry-----eAidlL--gA--l1--Q--s----- 71 (312)

T 2wpv\_A 16 FLQRFENKIKAGDYEAHQTLRTIANRVRSKSYHAIEILISQALSFLLKAKQGGs----- 71 (312)

T ss\_dssp HHHHHHHHHHTCHHHHHHHHHHHHHHTTCHHHHHHHHHHHHTTCHHHH-----

T ss\_pred HHHHHHHHHcCCHHHHHHHHHHHhccCHHHHHHHHHHHHHHCCcC-----





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☐ **>3lpz\_A** GET4 (YOR164C homolog); protein targeting, tail-anchored protein biogenesis, GET PAT GET5 binding, protein transport; 1.98A {Chaetomium thermophilum}.  
 Probab=32.94 E-value=3.8e+02 Score=28.93 Aligned\_cols=80 Identities=14% Similarity=0.094 Sum\_probs=0.0



No 41



Q ss_pred		HHCCCH-HHHHHHHHHHChHHHHHHHHHH	
Q Fri_Mar_04_23	397	IISGKI-HSILPVMSEDLSCATAFTAMICE	425 (744)
Q Consensus	397	I-egd---vL--l--ld-w-aHladLl- -L[.+. . .+.+.  .+.  +. +.+. .	425 (744)
T Consensus	266	--L--s-l-v--sWED-LW~l	295 (460)
T 3iko_C	266	YLSGAIPNQEVLYQSDWESDLHIHLNQILQ	295 (460)
T ss_dssp		HHHTSCCCHHHTTCCCHHHHHHHHHHHHH	
T ss_pred		HHHCcchhhhccccCCHHHHHHHHHHHHHH	

Q ss_pred		HHHHHHhhCCCCHHHHHHhh-----hhHHHH-HHHHHheeCCChC-----hHHHHHHHHhhhCCCCCCCHHHHH		
Q Fri_Mar_04_23:	332	TEDFLV-ILGGNQKRLIQYS--RTWYES-FCGFLLGYIPTSLE---LSAEYLQMSLEANVVDTINDWEQP	393	(744)
Q Consensus	332	L-l~l-VL-Gd~-T-s-WYe-I-a-l-y-Pt-----l-y~~~~~E-	393	(744)
		++..+  +. .+..+..+ .  . .= ++ + .  + ... ..+.... .....+..+.. .		
T Consensus	347	--if~llR-G-g-e-elc-qg-WRAAsL-G-l-dp-----Gn-r-LWK-cl-la----yERA	426	(925)
T 5a9_q_4	347	LKYLFTLIRAGMTTEAQRCLKRCQGAWRAATLEGWKLHYDHPNVNGGTGLEPVEGNPYRRRIKWISCRMADEFLFNRYERA	426	(925)
T ss_dssp		HHHHHHHHHTCTHHHHHHHHHHHTCTHHHHHHHTTSBCBCTTCCTTCSSCBSBSCHHHHHHHHHHHHCSSSCHHHHH		
T ss_pred		HHHHHHHHHHCCCCHHHHHHHHHCcHHHHHHccchhcCcCCCcccccccCcHHHHHHHHHHHHHHHHCCCCCHHHHH		

[illegible]

```
Q ss_pred          HHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHCCCHHHHHHHHHHc
Q Fri_Mar_04_23:  517 DDLEWVSLSCIVFWLPLAIKFIYITGLNGMSLAHNILIESIANFSRA    562 (744)
Q Consensus       517 -ek-L-l-iC-L-a-a-g- -l-g- -g-L- -a- -a- -rA           562 (744)
                  +-+..+++.+-+...-++..|.+...|+++.|-+|-+|
T Consensus       113 -al- -a- -a- -a- -a- -a- -a- -a- -a- -a- -a- -a-      158 (165)
T 4yvo_A          113 QYHSMLVAISKRESDSGITEAYGAIAADCYTELGDFLEAKGFYDVTY     158 (165)
T ss_dssp          HHHHHHHHHHHHTTCCTTHHHHHHHHHHHHHHTTCHHHHHHHHHH
T ss_pred         HHHHHHHHHHHHCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
```



Release-2.18.5