

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

ProtBLAST+

PSI-BLAST

PSI-BLAST+

SimShiftDB

New job

Resubmit

Resubmit_HMM

Resubmit/HHsenser

Realign

Log

Input-params

Delete

HHpred - Results

Job-ID: nup120_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

Need help on how to interpret your results? Click here.

2

1037

Resubmit section

4xnn_E

3f7f_A

5a9q_1

4fhn_B

4gq2_H

4u1e_I

4j87_A

4jsn_D

3as5_A

1na8_A

4cgv_A

2dba_A

2p12_A

3as5_A

3vtx_A

1elw_A

4cgw_A

5a9q_A

3q49_B

1hxi_A

2hr2_A

4d10_B

2fo7_A

2vqi_A

2q7f_A

4gco_A

4qvq_C

4yvo_A

4xi0_A

4nrh_B

2xcb_A

2ckk_A

2vgx_A

3uq3_A

3upv_A

1na3_A

4gcn_A

2lni_A

3sz7_A

4g4o_A

2vqi_A

1elr_A

2ho1_A

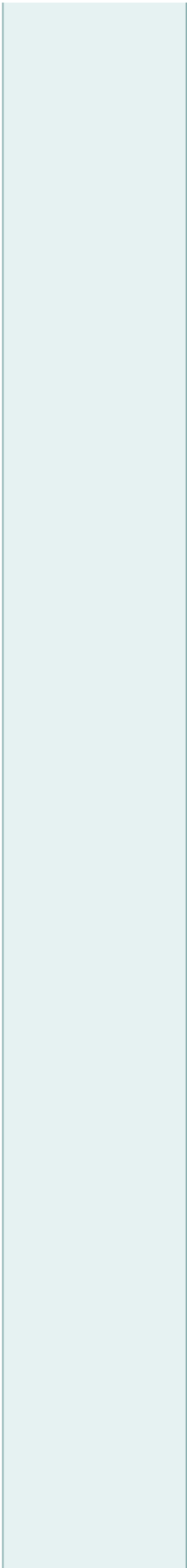
2c2l_A

1xnf_A

3na5_A





1hh8_A

3g4z_A



Query Fri_Mar_04_23:23:54_+0100_2016 (seq=MACLSRIDAN...TDLRDELRLGL Len=1037 Neff=7.0 Nseqs=160)
Parameters score SS:yes search:local realign with MAP:no

No Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
<input type="checkbox"/>	1 4xmm_E Nucleoporin NUP120; str	100.0	4E-209	1E-213	1966.2	72.0	1036	2-1037	10-1045(1045)
<input type="checkbox"/>	2 3f7f_A Nucleoporin NUP120; nuc	100.0	9E-142	2E-146	1305.7	61.0	729	1-729	1-729 (729)
<input type="checkbox"/>	3 5a9q_1 Nucleoporin SEH1; trans	100.0	7E-127	2E-131	1249.5	75.4	921	16-1036	52-1189(1436)
<input type="checkbox"/>	4 4fhn_B Nucleoporin NUP120; pro	100.0	4E-125	1E-129	1202.4	68.1	904	20-1036	21-1118(1139)
<input type="checkbox"/>	5 4gq2_M Nucleoporin NUP120; bet	100.0	1.3E-94	3.6E-99	915.5	75.4	781	19-889	18-950 (950)
<input type="checkbox"/>	6 4ycz_C NUP120; structural prot	100.0	3.8E-34	1E-38	311.9	8.5	150	873-1036	22-274 (313)
<input type="checkbox"/>	7 3as5_A MAMA; tetratricopeptide	93.3	1.4	3.8E-05	44.3	14.0	124	715-894	39-163 (186)
<input type="checkbox"/>	8 1na0_A Designed protein CTPR3;	93.2	0.68	1.9E-05	42.5	10.7	92	750-894	5-96 (125)
<input type="checkbox"/>	9 4cgw_A Spaghetti, RNA polymera	92.2	3.1	8.5E-05	37.8	13.8	131	709-895	2-136 (136)
<input type="checkbox"/>	10 2dba_A Smooth muscle cell asso	92.2	1.5	4.3E-05	41.7	12.1	92	750-894	24-118 (148)
<input type="checkbox"/>	11 2pl2_A Hypothetical conserved	91.8	3	8.3E-05	43.1	14.6	154	714-894	1-170 (217)
<input type="checkbox"/>	12 3as5_A MAMA; tetratricopeptide	91.6	1.8	4.9E-05	43.6	12.2	108	731-894	22-129 (186)
<input type="checkbox"/>	13 3vtx_A MAMA; tetratricopeptide	91.5	1.7	4.8E-05	43.2	11.9	138	731-894	19-160 (184)
<input type="checkbox"/>	14 1elw_A TPRI-domain of HOP; HOP	91.4	1.5	4.1E-05	39.4	10.4	90	752-894	2-91 (118)
<input type="checkbox"/>	15 4cgw_A Spaghetti, RNA polymera	91.3	1.5	4E-05	39.0	10.2	92	750-894	14-105 (117)
<input type="checkbox"/>	16 5a9q_A Nuclear pore complex pr	91.3	2.4	6.7E-05	56.7	16.0	236	724-1006	823-1125(1391)
<input type="checkbox"/>	17 3q49_B STIP1 homology and U bo	91.1	1.9	5.4E-05	39.5	11.1	93	749-894	4-96 (137)
<input type="checkbox"/>	18 1hxi_A PEX5, peroxisome target	91.0	1.4	4E-05	39.8	10.0	84	758-894	21-104 (121)

No 1    

>4xmn_E Nucleoporin NUP120; structural protein, immune system, transport protein-immune complex; 7.38A
{Saccharomyces cerevisiae S288C} PDB: 4xmn_E
Probab=100.00 E-value=4.5e-209 Score=1966.19 Aligned_cols=1036 Identities=100% Similarity=1.483 Sum_probs=0.0

Q ss_pred
Q Fri Mar 04 23: 2 ACLSRDI¹ANL²LQY³EK⁴PE⁵NP⁶NT⁷VD⁸LY⁹VN¹⁰SN¹¹NN¹²GN¹³KK¹⁴GD¹⁵K¹⁶IS¹⁷TP¹⁸VP¹⁹PG²⁰SE²¹YS²²NC²³LL²⁴SN²⁵SE²⁶YI²⁷CH²⁸FS²⁹SR³⁰ST³¹LL³²TF³³ 81 (1037)

[illegible]

No 2

> **357f_A** Nucleoporin NUP120; nuclear pore complex, macromolecular assembly, membrane coat, nucleocytoplasmic transport, beta-propeller; 2.60Å [Saccharomyces cerevisiae] PDB: **3h7n_A** **3hxr_A**
 Probab=100.00 E-value=9e-142 Score=1305.70 Aligned_cols=729 Identities=100% Similarity=1.465 Sum_probs=0.0

[illegible][illegible]





Q ss_pred		CeEEEEECcCCcEeecccccccccccccCccChhHHHHHhhheEEEEEcCCcEEEEEEecCCCeEeeeccccC			
Q Fri_Mar_04_23:	241	CHLKIWDLTSFTLIQDYDMVQSQSDSPSHFRKVEAVGEYLSLYNNLTLLPLENGLFMGTLLVDSSGILTYTFQNIP	320	(1037)	
Q Consensus	241	-LRlWsl-t-1-dL-----1-vlylp-g-F-1-l-1-ip	320	(1037)	
		+ ++ + ++++ +++.....++ ++++ + +++ + + +++ + + +.++++++.++ +++			
T Consensus	241	-LRlWsl-t-1-dL-----1-r-1-vlylp-g-F-1-l-1-ip	320	(729)	
T 3f7_f_A	241	CHLKIWDLTSFTLIQDYDMVQSQSDSPSHFRKVEAVGEYLSLYNNLTLLPLENGLFMGTLLVDSSGILTYTFQNIP	320	(729)	
T ss_dssp		CEEEEEETTTTTEEEEEETTSTSCSSCCSSCCSSCCCEESSSEEEETTTEEEEEEC-----CEECECEEE			
T ss_pred		CEEEEEECcCCcEeecccccccccccccCccChhHHHHHhhHEEEEBcCCcEEEEEEEcCCcEeeccccC			

Q ss_pred		CCCCCCCc eEeeEeE ccccccccCcc EEEEEE EcCc EEEEEE EccccCCCC eee ccccCCCCCCCCCCCCCCC		
Q Fri_Mar_04_23:	321	T NLSASATWSIVDLVLRPLNLNVEASYLNILVLWKSGTASLKQLINVNDESFKNYEWIESVNSKSLVDLQSEHDLDIVTK	400	(1037)
Q Consensus	321	T NLSASATWSIw-LDF-l-p -l-Lw-LWks -v-l W-v-1 e- w -l-e- + . . . ++++++ . ++++++	400	(1037)
		+ + + + + + + + + + + . + + + + + + + + + + + + + + + + + . + + + + + + + . + + + + + + +		
T Consensus	321	T NLSASATWSIw-LDF-l-p -l-Lw-LWks -v-l W-v-1 e- w -l-e- + . . . ++++++ . ++++++	400	(729)
T 3f7f_A	321	T NLSASATWSIVDLVLRPLNLNVEASYLNILVLWKSGTASLKQLINVNDESFKNYEWIESVNSKSLVDLQSEHDLDIVTK	400	(729)
T ss_dssp		CCCTTC TPCEEEEEEE SCCCSCSCSS EEEEEEEE TT EEEEEEEE SCSSST EEEEEE CSCCHHHHHHTTCCSSC		
T ss_pred		CCCCCCCc eEeeEeE ccccccccCcc EEEEEE EcCc EEEEEE EccccCcCc Ee ccccCCCCCCCCCCCCCCC		

Page 7 of 44






Page 8 of 44

Page 9 of 44

No 5    

☐ >4fqg2_M Nucleoporin NUP120; beta propeller alpha helical, component of nuclear pore COMP transport protein; 2.40A {Schizosaccharomyces pombe} PDB: 4fhm_B

Probab=100.00 E-value=1.3e-94 Score=915.47 Aligned_cols=781 Identities=13% Similarity=0.123 Sum_probs=0.0

No 6     

☐ **4yczc_C** NUP120; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein; 4.10Å {Thielavia heterothallica}

Probab=100.00 E-value=3.8e-34 Score=311.89 Aligned cols=150 Identities=19% Similarity=0.303 Sum_probs=0.0

Page 12 of 44

No 13

No 14

No 15

Q ss_pred CCCHHHHHHHHHHH-ccchHHHHHHHHHHHCCcccCCChHHHHHHHHHHHHHCCHHHHHHHHHHHHhhccccccchHH

Q Fri_Mar_04_23: 715 TENSFFMTFFRSYII-ENTSHKNIRFLENVECPFYLRHNEVQEFMFAMTLFCGNFDQSYEIFQLHDYPEAINDKLPTE 793 (1037)

Q Consensus 715 np-----l--vi--q-----f1-i--p-----f1--l-----A-pa-----F-a-----lp-pa----- 793 (1037)

T Consensus 54 p-----la-----A-p-----a1-----p-----lq-----q-----A-a----- 117 (243)

[illegible]

Page 25 of 44

No 50

>4apo_A AH receptor-interacting protein; signaling protein-peptide complex, ARYL hydrocarbon receptor; HET: 12P;
1.90A {Homo sapiens} PDB: 4aif_A
Probab=86.79 E-value=3.5 Score=39.88 Aligned_cols=100 Identities=9% Similarity=-0.014 Sum_probs=0.0

T Consensus

Q ss_pred

Q Fri_Mar_04_23:

Q Consensus

T Consensus

T 4apo_A

T ss_dssp

T ss_pred

Q ss_pred

Q Fri_Mar_04_23:

Q Consensus

T Consensus

T 4apo_A

T ss_dssp

T ss_pred

Page 26 of 44

Page 29 of 44

No 64


```

Q ss_pred          hhhhhhhhhhhhhhhhhhhhhcchhhH
Q Fri_Mar_04_23:  870  THYLLNLIHFRMFEEVDVLRGLGE      894 (1037)
Q Consensus        870  -----T-----F-----L-----a      894 (1037)
                    |..+-----|+++|
T Consensus        185  -----L-----1-----A-----A      201 (225)
T 2vq2_A           185  -----LLLGWKTAKALGNAQAA      201 (225)
T ss_dssp          -----HHHHHHHHHTTCHHHH
T ss_pred          -----HHHHHHHHHcCCHHHH

```

```
Q ss_pred          hHcCCHHHHHHHHHHHHHhhcccccccccchHHHHHHHHHHHHHHHHHHHHhhcchhhh
Q Fri_Mar_04_23: 833 dRNNsqQEFAFKICKISAKSEYSLKEIQTEELQDFKQKHIIHYLNLLIFRMFEVFLDVLRLGHE 894 (1037)
Q Consensus        i33 e---l--a-Ai-----l--F--L-L-----a 894 (1037)
                   ...|.++.|++...+|.+-+... .. |.++.....|+|+.
T Consensus        48 -g-g-a-l-p-----a-----lg-g-a- 90 (213)
T lhh8_A           48 TILKNMTEAEKAFTSRINRDKHLA-----VA-----YFORGLMYQTKEYDYLA 90 (213)
T ss_dssp          HHTTCHHHHHHHHHHHHHCTTCCH-----HH-----HHHHHHHHHHHTTCHHH
T ss_pred          hHccCCHHHHHHHHHHHhhCcCCH-----HH-----HHHHHHHHHHCCCHHH
```

Q ss_pred		HhCC#####ccccccccc#####-----cchhhH	
Q Fri_Mar_04_23:	833	DNNNS QFALCKISKASYSLEIKIIEELQDFEKQHIIYLNLLIHFRMFEEVLDV-----LRIGHE	894 (1037)
Q Consensus	833	e---al-aAl-----e- _{low med high} -l_i-F-L-l-----a	894 (1037)
		. . . + . + . . + + + . . + + + + .	
T Consensus	50	--g-A--Al-p-----lg-----g-g-	103 (217)
T 2pl2_A	50	LKLGVLNPALENGKTlWARTPYL----GG-----YMLSEAYVALYRQAEDRERKGYLEQA	103 (217)
T ss_dssp		HHHTTC#####CTTCH-----HH-----#####TCSS#####	
T ss_pred		HhCCCC#####CtCcH-----HH-----#####cccccccC#####	

```
Q ss_pred          -----cchHHHHHHhhhhccccccccccccchhhccCccHHHHHHHHHHHHhhcCCHHHHHHHHHHHhhcccccccccc
Q Fri Mar 04 23: 789 -----KLTPTLELDKSENHYGDSLWKDLCTFTVTPYRHSAPFYOLSLFLDRNNSOPALKCISKSAEYSLKTIOTFLDQF 864 (1037)
```



```
Q ss_pred          hhhhhhhhhhhhhhhhhhhhhhhhccccch-----HH
Q Fri_Mar_04_23:   865 KEKQIHYYLNLIIHFRMFEEVLDVLRLG-----HE      894 (1037)
Q Consensus        865 .....-1-.....F--L-1-----a      894 (1037)
                   ..|.++....+|+|+|.
T Consensus        235 -----1-----g-----a-----A      259 (382)
T 2h6f_A           235 ---SV-----WGORYPVISNTTGYNDRAVLERE    259 (382)
T ss_dssp          ---HH-----HHHHHHHHHTTCSCSHHHHHHH
T ss_pred          ---HH-----HHHHHHHHHHccccchHHHHHHHH
```

```

Q ss_pred          HHHHHHHHHHHHHHHHHHHHHHHHcchHHH
Q Fri_Mar_04_23:  867  KQHlHYLNLlHFRMFEEVLdVLRlRlGE      894 (1037)
Q Consensus        867  .....-l.....F.....-l.....a      894 (1037)
                   .+ .      |..+=.....|+++.|
T Consensus        286  .....-g.....-g.....-g.....      305 (327)
T 3cv0_A           286  RSM-----WDFPRMLLNVMNRpDLV      305 (327)
T ss_dssp          HHH-----HHHHHHHHHHTTCaHHH
T ss_pred          HHH-----HHHHHHHHHHCcCHHHH

```

Q ss_pred		EEEECCCCcEEeEc	
Q Fri_Mar_04_23:	244	KIWLDTSTFTLQDYD	258 (1037)
Q Consensus	244	RiWdL-t- + +++++.+	258 (1037)
T Consensus	281	-vWd- - - - - -	295 (327)
T 4j87_A	281	RVWDLNRRTAVQTFR	295 (327)
T ss_dssp		EEEETTTCCEEEEEE	
T ss_pred		EEEECCCCchhhhhh	

[illegible]

Q ss_pred hhhhhhhhhHHHHHHHHHHhhcchhhh
Q Fri_Mar_04_23: 870 IHYLNLLIHFRMFEEVLDVLRIGHE 894 (1037)
Q Consensus 870 l l l l l i i i F l l l l l a 894 (1037)

Page 38 of 44

No 94                               

No 95                  

No 96      

Page 41 of 44

No 100      

[illegible]

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.

