

Quickfinder

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		

Help

Create model Merge Q/T alignments Forward to PCoils Forward MSA Save Export

View Alignment

2 724

100 200 300 400 500 600 700

Resubmit section

Protein Domain	Count
5a9q_4	6
3iko_C	4
3cqc_A	4
5a9q_8	4
4xnn_B	4
2qx5_A	3
3f3f_C	3
4xnn_D	3
3bg1_B	3
3fro_A	3
4ycz_B	3
4bz_I_A	2
5a9q_5	2
2pn7_A	2
4ycz_A	2
3nzk_B	1

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
1	5a9q_4	Nuclear pore complex pr	100.0	1E-140	4E-145	1258.0	59.3	689	2-724	145-910	(925)
2	3iko_C	Nucleoporin NUP84; NPC	100.0	1.7E-94	4.8E-99	813.2	40.1	459	1-460	1-460	(460)
3	3cq_c_A	Nuclear pore complex pr	100.0	1.4E-43	3.8E-48	371.2	20.0	216	498-724	4-255	(270)
4	5a9q_8	Nuclear pore complex pr	97.9	0.003	8.3E-08	74.3	27.1	418	9-549	69-522	(656)
5	4xmm_B	Nucleoporin NUP145; str	97.8	0.023	6.4E-07	66.6	31.0	355	71-565	171-553	(652)
6	2qx5_A	Nucleoporin N1C96; mRNA	97.7	0.00021	5.9E-09	89.3	13.4	237	180-468	155-401	(661)
7	73f3f_C	Nucleoporin NUP85; stru	97.5	0.0083	2.3E-07	63.8	22.1	246	180-486	245-549	(570)
8	4xmm_D	Nucleoporin NUP85; stru	97.5	0.0078	2.2E-07	71.4	21.5	285	180-542	216-555	(715)
9	3bg1_B	Nucleoporin NUP145; NPC	97.2	0.037	1E-06	61.9	22.4	276	71-451	120-402	(442)
10	3jro_A	Fusion protein of prote	96.9	0.015	4.1E-07	69.3	16.6	267	71-451	429-711	(753)
11	4ycz_B	NUP85; structural prote	96.3	0.096	2.7E-06	63.1	17.2	321	180-542	223-662	(933)
12	4bzj_A	Protein transport prote	95.9	0.11	3.2E-06	65.8	16.6	209	182-439	512-729	(1273)
13	5a9q_5	Nuclear pore complex pr	95.3	1.3	3.7E-05	53.9	21.8	266	181-488	451-749	(937)
14	2pm7_A	Protein WEB1, protein t	94.7	1.2	3.4E-05	49.1	17.9	215	177-439	143-365	(399)
15	4myz_C	Fusion protein of SEC13	90.3	1.6	4.5E-05	53.0	12.2	250	182-488	465-732	(876)
16	3mzk_B	Protein transport prote	89.4	0.87	2.4E-05	51.0	8.2	87	177-286	150-256	(441)
17	73f3f_C	Nucleoporin NUP85; stru	33.6	79	0.0022	36.5	7.1	96	181-297	332-427	(570)
18	2kw0_A	CCMH protein; oxidoredu	26.0	74	0.0021	27.3	3.9	45	161-206	27-73	(90)
19	4xmm_D	Nucleoporin NUP85; stru	23.8	1.2E+02	0.0033	36.1	6.4	96	181-297	303-398	(715)
20	5cqs_A	Elongator complex prote	22.9	2.6E+02	0.0071	30.9	8.7	84	182-286	126-213	(435)
21	2k6e_A	SVTR protein, uncharac	20.9	1.7E+02	0.0046	21.9	4.7	36	454-489	21-56	(56)

No 1       

>5a9q_4 Nuclear pore complex protein NUP107; transport protein; 23.00A {Homo sapiens}
 Probab=100.00 E-value=1.5e-140 Score=1258.04 Aligned cols=689 Identities=20% Similarity=0.304 Sum probs=0.0

Q ss_pred		CccchhhhhhhhhhhhhhhhhcCccccCCHHHHHHHHHHHHHHHHHHh-----hhhCCHHHHHHHHHH	
Q Fri_Mar_04_23:	2	L5LPTQTERTKFSQDLKKFKKIQNNQNIPDPNIFRFSAAAGLALDLANS-----GDENVISSKDWELEA	72 (726)
Q Consensus	2	-Fa-L- -f- -lv-f- -E-	72 (726)
		+...+.+.+ ++ +.+.+ . .++ + ++ ++++.+.+. . .+.+.+.+ ++ +	
T Consensus	145	-fa-flD-f ic- l-r- -l-1E-	216 (925)
T 5a9q_4	145	DPGEAASMSMFDLQSFLKH-----S-SSTVFDLVEEYENICGSQVNILSKIIVSRATPGLQKFSKTASMLWLLQQEM	216 (925)
T ss_dssp		-----CGGGHHHHHHHHHHHH-----H-HSCSHHHHHHHHHHHHHHHHHHH-----CHHHHHHHHHHHHHHHHH	
T ss_pred		Cccchhhhhhhhhhhhhhhhhc-----C-CcCHHHHHHHHHHHHHHHHHHHhhcccccccccccCHHHHHHHHHHH	

Q ss pred HHHHHHHHHHhccC-CCcccccc--ccCCCCHHHHHHHHHhCCHHHHHHHHHHHHHHHHhCC--CCCCcccc---ccc

Q ss_pred HHH-----HHhhccccccCCcchHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhccccHHHHHHHHHHHHHHhCCcccH

[illegible]

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






















No 6      

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No 8

No 9      

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No 10                          

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T ss_pred

HHHHHH-HhCCCHHH---HHHHhhHHH---HHHHHHhheCC-----CchhHHHHHHHHHHhCCCCCcHHH

Q ss_pred

HHHHHHHCCcChhhcccccCHHHHHHHHHHHHHHHHHHH

Q Fri_Mar_04_23:

261

RAIYSYLSGAIPNQEVLYQSDWESDLHTLNQILQTE

297 (726)

Q Consensus

261

rAiY--LsG-l-----v-c-sWeD-Lwa--n-ll---

297 (726)

T Consensus

363

-----i-egd---vL--l--ld-w-aAhladLL---

398 (715)

T 4xmm_D

363

QPCVDIISGKIHSILPV-MESLDSCTAAFTAMICEAK

398 (715)

T ss_dssp

HHHHHHHTTCCCSCHHH-HHHHCCHHHHHHHHHHHHHHH

T ss_pred

HHHHHHHCCCHHHHHHH-HhhcChHHHHHHHHHHHHhC

No 20



>5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A {Saccharomyces cerevisiae}

Probab=22.92 E-value=2.6e+02 Score=30.88 Aligned_cols=84 Identities=14% Similarity=0.076 Sum_probs=0.0

Q ss_pred

HHHHHHHCCCHHHHHHHHHhCcHHHHHHHccCcccccCccccccccccccccCchhHHHHHHHHHHhCCCCcHHHH

Q Fri_Mar_04_23:

182

KYIYELLAGAIDEALEEAKLSDNISICMILCGIYEYLPVLDQTIANEFNTQQGIKKHSLWRRTVYSLSQAGLDPYER

261 (726)

Q Consensus

182

---f-llR-G---eA--lc---gq-wrAasL-G-----dp--d-----G---r-LWk--c--la-----yEr

261 (726)

T Consensus

126

eA---Y-kag---kAie-y-a-w--al-la-----l-----l---la--l-----g---

184 (435)

T 5cqs_A

126

DAAVAYEMLGKLKAMGAYQSAKRWRREAMSIAVQ---KFP-----EEVESVAEELISSLTF---EHRYVD

184 (435)

T ss_dssp

HHHHHHHTTCHHHHHHHHHHTTCHHHHHHHHH---TCT-----TTHHHHHHHHHHH---TTCCHH

T ss_pred

HHHHHHHCCCHHHHHHHHHccCHHHHHHHHH---cCh-----HHHHHHHHHHHH---CCCHH

Q ss_pred

HHHHHH--cCCcChhhccc--cCCCHHHHH

Q Fri_Mar_04_23:

262

AIYSYL--SGAIPNQEVLY--QYSDWESDL

286 (726)

Q Consensus

262

AiY--L--sG-l-----v--c-sWeD-L

286 (726)

T Consensus

185

A--ly-----d---AI--l-----eA-

213 (435)

T 5cqs_A

185

AADTQLLEYLDNVKEAVLYCKAYRYDIAS

213 (435)

T ss_dssp

HHHHHHHHHCCCHHHHHHHHHHTTCHHHHH

T ss_pred

HHHHHHHhCCHHHHHHHHHHCCCHHHHH

No 21



>2kel_A SVTR protein, uncharacterized protein 56B; homodimer, ribbon-helix-helix, transcription repres; NMR {Sulfolobus islandicus rod-shaped virus}

Probab=20.86 E-value=1.7e+02 Score=21.89 Aligned_cols=36 Identities=6% Similarity=0.091 Sum_probs=0.0

Q ss_pred

CHHHHHHHHHHHHcCCCHHHHHHHHHHHHHhccc

Q Fri_Mar_04_23:

454

DPQVRKKQITINFLRLPASNILLRRTQRFVDETEQ

489 (726)

Q Consensus

454

d--eR---L-la---gldv--i-k--ve-i-----

489 (726)

T Consensus

21

--e---l---a---g-s-Se-ir-ai---l---g

56 (56)

T 2kel_A

21

DKDLKTRLKVYCAKNLQLTQALIEEAIKEYLQKRNG

56 (56)

T ss_dssp

HHHHHHHHHHHHHSCCHHHHHHHHHHHHHHHHHHHCC

T ss_pred

CHHHHHHHHHHHHcCCCHHHHHHHHHHHHHhCC

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.