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MAX-PLANCK-GESELLSCHAFT

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

Quickfinder

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Sequence Analysis

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CS-BLAST

HHblits

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HHsenser

HMMER3

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New job

Resubmit

Resubmit_HMM

Resubmit/HHsenser

Realign

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HHpred - Results

Job-ID: 1681421

Date: 23:55 on Aug 29 2012

Help

Results

Histogram

Show query alignment

Create model

Merge Q/T alignments

Forward to PCoils

Save

Export

Color alignments

☐ color only SS

☒ color alignments

☐ color alignments

View alignment

Note: Corrupted alignments are the most common source of high-scoring false positives. Check the query alignment by clicking Show Query Alignment above. To check the template alignments use the logos.



HHpred has detected hits to coiled coil-containing proteins. You may consider running a PCOILS prediction on your query.

Query Wed_Aug_29_23:55:05_+0200_2012 (seq=STMQLNDIIS...IESSSGRISW Len=145 Neff=2.4 Nseqs=13)

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	4ds7_E Spindle POLE BODY compo	100.0	1.1E-30	3.9E-35	176.5	6.4	54	92-145		2-55	(55)
<input type="checkbox"/>	2	2o60_B CAM, peptide correspond	36.6	28	0.001	19.5	2.5	22	98-119		3-24	(26)
<input type="checkbox"/>	3	3d5p_A Putative glucan synthe	19.8	40	0.0014	23.6	1.4	19	47-71		19-37	(144)
<input type="checkbox"/>	4	3twe_A Alpha4H; unknown functi	12.5	1.2E+02	0.0042	17.5	1.9	14	126-139		14-27	(27)
<input type="checkbox"/>	5	3gn4_A Myosin-VI; unconvencion	12.3	3.2E+02	0.011	20.7	4.8	29	102-130		24-52	(148)
<input type="checkbox"/>	6	2prv_A Uncharacterized protein	11.9	85	0.003	22.1	1.4	19	47-71		28-46	(153)
<input type="checkbox"/>	7	1yhn_B RILP, RAB interacting l	11.7	2.9E+02	0.011	18.7	4.0	38	5-45		22-59	(65)
<input type="checkbox"/>	8	2icg_A LIN2918 protein; hypoth	11.1	91	0.0032	22.0	1.4	18	47-70		31-48	(160)
<input type="checkbox"/>	9	2bcx_B Ryanodine receptor 1; E	10.9	97	0.0035	18.1	1.2	7	109-115		19-25	(30)
<input type="checkbox"/>	10	2pag_A Hypothetical protein; n	10.2	1E+02	0.0037	21.8	1.4	18	47-70		26-43	(135)

No 1



☐ >4ds7_E Spindle POLE BODY component 110; protein binding, metal binding, structura; 2.15A {Saccharomyces cerevisiae S288C}

Probab=99.96 E-value=1.1e-30 Score=176.48 Aligned_cols=54 Identities=100% Similarity=1.531 Sum_probs=0.0

Q ss_pred

Q Wed_Aug_29_23:

Q Consensus

T Consensus

T 4ds7_E

T ss_dssp

T ss_pred

ccccccccc

RGPFYFERRLSFKTVALLVLACVRMKRIAFYRRSDNRLRILDRIESSSGRISW

-----kltFKtvAlfVLAcVRmk-r-a-k-r-d~Rl~Lr~ki~drItw

+++++|||||+++++|||+|||+|||+|||+|||

2-----FKTVALLVLACVRMK~a~RwD-qRi-yLqrKI~drItW

2RGPFYFERRLSFKTVALLVLACVRMKRIAFYRRSDNRLRILDRIESSSGRISW

-----CTCC

CCchhhcccch

No 2



☐ >2o60_B CAM, peptide corresponding to calmodulin binding binding domai neuronal nitric oxide synthase; protein-peptide complex, metal binding protein; 1.55A {Gallus gallus}

Probab=36.64 E-value=28 Score=19.55 Aligned_cols=22 Identities=23% Similarity=0.268 Sum_probs=0.0

Q ss_pred

Q Wed_Aug_29_23:

Q Consensus

T Consensus

T 2o60_B

T ss_pred

cCcc

RRLSFKTVALLVLACVRMKRIA

~kltFKtvAlfVLAcVRmk-r-a

+++.|||.|||=+.-+.-+

3r~fK-la-AV-fss-Lm-ka

3RAIGFKKLAIAVKFSAKLMGQX

chhh

No 3



☐ >3d5p_A Putative glucan synthesis regulator of SMI1/KNR4; STR genomics, joint center for structural genomics, JCSG; HET: MSE; 1.45A {Bacteroides fragilis nctc 9343}

Probab=19.81 E-value=40 Score=23.57 Aligned_cols=19 Identities=32% Similarity=0.478 Sum_probs=0.0

```

Q ss_pred          HHHHHHHhCCCCCCCCccccchh
Q Wed_Aug_29_23:   47 DTRKGEHSLNLSLPDDDELDRDYNN 71 (145)
Q Consensus        47 D--KL-----i-----Y-n 71 (145)
                   ||.++|.+.+.+.+.+.+.+.+.
T Consensus        19 -I---E--Lgi-LP-----dYk~ 37 (144)
T 3d5p_A           19 SIDDVKEKLLNTTLPK-----QYKS 37 (144)
T ss_dssp          HHHHHHHHHHTSCCH-----HHHH
T ss_pred          HHHHHHHHHCCCCCH-----HHHH

```

No 4      

☐ >3twe_A Alpha4H; unknown function; HET: PGE; 1.36A {Synthetic} PDB: 3twe_A* 3twf_A*
 Probab=12.48 E-value=1.2e+02 Score=17.52 Aligned_cols=14 Identities=43% Similarity=0.733 Sum_probs=0.0

```

Q ss_pred          HHHHHHHHHHHhcc
Q Wed_Aug_29_23:   126 DNRRLRLRLRIESS 139 (145)
Q Consensus        126 --RL--Lr-ki--- 139 (145)
                   ++||+.|.|.+.+.
T Consensus        14 qerlrklrkklrsg 27 (27)
T 3twe_A           14 QERLRLRLRLRSG 27 (27)
T ss_dssp          HHHHHHHHHHHHC-
T ss_pred          HHHHHHHHHHHhCC

```

No 5      

☐ >3gn4_A Myosin-VI; unconventional myosin, motility, lever ARM, 3-helix bundle, actin-binding, ATP-binding, calmodulin-binding, coiled coil; 2.70A {Sus scrofa}
 Probab=12.34 E-value=3.2e+02 Score=20.65 Aligned_cols=29 Identities=21% Similarity=0.354 Sum_probs=0.0

```

Q ss_pred          HHHHHHHHHHHHHHHHHHHHHHHHHHH
Q Wed_Aug_29_23:   102 FKTVALLVLACVRMKRIAFYRSDNRLR 130 (145)
Q Consensus        102 FKtVAlfVLAcVRmkR-a-k-r-d--RL- 130 (145)
                   ++.+.---||+|+++++.+.+.+.+.+.
T Consensus        24 WrK-q---lsvIKLKnKI-yR---i-iQ 52 (148)
T 3gn4_A           24 WKVQWCSLSVILKKNKIKYRAEACIKMQ 52 (148)
T ss_dssp          HHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred          HHHHHHHHHHHHHHHHHHHHHHHHHHH

```

No 6       

☐ >2prv_A Uncharacterized protein YOBK; structural genomics, joint center for structural genomics, J protein structure initiative, PSI-2; HET: MSE; 1.30A {Bacillus subtilis} SCOP: d.369.1.1
 Probab=11.94 E-value=85 Score=22.08 Aligned_cols=19 Identities=26% Similarity=0.426 Sum_probs=0.0

```

Q ss_pred          HHHHHHHhCCCCCCCCccccchh
Q Wed_Aug_29_23:   47 DTRKGEHSLNLSLPDDDELDRDYNN 71 (145)
Q Consensus        47 D--KL-----i-----Y-n 71 (145)
                   +|.++|.+.+.+.+.+.+.+.+.
T Consensus        28 -I---E--Lgi-LP-----dYk~ 46 (153)
T 2prv_A           28 NIGRIEENLQCDLPN-----SYKW 46 (153)
T ss_dssp          HHHHHHHHHHTSCCH-----HHHH
T ss_pred          HHHHHHHHHCCCCCH-----HHHH

```

No 7       

☐ >1yhn_B RILP, RAB interacting lysosomal protein; protein transport; HET: GTP; 3.00A {Homo sapiens} SCOP: h.1.34.1
 Probab=11.73 E-value=2.9e+02 Score=18.72 Aligned_cols=38 Identities=5% Similarity=0.286 Sum_probs=0.0

```

Q ss_pred          HhhHHHHHHHHHHHHHHHHHHHHHHHH
Q Wed_Aug_29_23:   5 LNDIISYYKLYHSEVVRHNDLKVINDYLNKVLALGTRRLR 45 (145)
Q Consensus        5 Lqdei-YYklKY-dev--nNDLkvmn-ylnrvl--Ssq-lk 45 (145)
                   +|+.|.||+. .+.+.+++.+++.+.+.+.
T Consensus        22 lqeEL-yY-----e-l-----p--ll-a-k-aikkqr--ik 59 (65)
T 1yhn_B           22 LKEELAYFQ---RELLTDHRVPSLLLEAMKVAVRKQRKKIK 59 (65)
T ss_dssp          HHHHHHHHH---HHHSSTTCCCCHHHHHHHHHHHHHHHHHHH
T ss_pred          HHHHHHHHH---hccCCccccHHHHHHHHHHHHHHHHHHHH

```

No 8       

☐ >2icg_A LIN2918 protein; hypothetical protein, structural genomics, PSI- protein structure initiative, joint center for structural G JCSG; 1.65A {Listeria innocua} SCOP: d.369.1.1
 Probab=11.15 E-value=91 Score=22.02 Aligned_cols=18 Identities=17% Similarity=0.279 Sum_probs=0.0

```

Q ss_pred          HHHHHHHhCCCCCCCCccccchh
Q Wed_Aug_29_23:   47 DTRKGEHSLNLSLPDDDELDRDYNN 70 (145)
Q Consensus        47 D--KL-----i-----Y- 70 (145)
                   +|.++|.+.+.+.+.+.+.+.
T Consensus        31 -I---E--Lg--LP-----Yk 48 (160)
T 2icg_A           31 LKITYQDALGNFPE-----TYK 48 (160)
T ss_dssp          HHHHHHHHHHTCCCH-----HHH
T ss_pred          HHHHHHHHHCCCCCH-----HHH

```

No 9













☐ >2bcx_B Ryanodine receptor 1; EF-hand, type-2 turn, calcium binding protein; 2.00A {Gallus gallus}
Probab=10.90 E-value=97 Score=18.11 Aligned_cols=7 Identities=71% Similarity=1.341 Sum_probs=0.0

Q ss_pred	HHHHHHH	
Q Wed_Aug_29_23:	109 VLACVRM	115 (145)
Q Consensus	109 VLACVRm	115 (145)
	. .	
T Consensus	19 Vvacfrm	25 (30)
T 2bcx_B	19 VVACFRM	25 (30)
T ss_dssp	HHHHHHH	
T ss_pred	HHHHHHh	

No 10















☐ >2pag_A Hypothetical protein; nysgx, target 10412I, novel fold, structural genomics, PSI-2 structure initiative; 1.60A {Pseudomonas syringae PV} SCOP: d.369.1.1
Probab=10.16 E-value=1e+02 Score=21.76 Aligned_cols=18 Identities=22% Similarity=0.193 Sum_probs=0.0

Q ss_pred	HHHHHHHhCCCCCCCCccccchh	
Q Wed_Aug_29_23:	47 DTRKGEHSLNISLPDDDELDRDY	70 (145)
Q Consensus	47 D--KL-----i-----Y-	70 (145)
	+ .+.+.+.+.+.+.+.+.+	
T Consensus	26 -I---E--Lgi-fP-----dYk	43 (135)
T 2pag_A	26 QLVEIEQLFINIPF-----VFK	43 (135)
T ss_dssp	HHHHHHHHHTCCCCCH-----HHH	
T ss_pred	HHHHHHHHHCCCCCH-----HHH	

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.