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MAX-PLANCK-GESELLSCHAFT

Show results of job:

Show results

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

Quickfinder

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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

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Input-params

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HHpred - Results

Job-ID: sec13_new

Date: 23:25 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

1

297

100

200

Resubmit section

2pn7_B

3irp_A

4l9o_A

3bg1_A

4u1e_I

4j87_A

4j73_A

1vqh_C

3f3f_A

1vqh_C

5a9q_7

1got_B

4j87_A

3u15_A

3jro_A

1got_B

4j8w_A

4wju_A

3fn0_A

3ow8_A

4j73_A

5cxb_B

1er_i_A

2pb1_B

3fn0_A

1k8k_C

4bh6_A

3ow8_A

4jsn_D

3frx_A

4lg9_A

4lg9_A

1er_i_A

4wju_A

4wjs_A

4a11_B

4lg8_A

4psw_B

3jan_g

4d6v_A

4gpc_A

4lg8_A

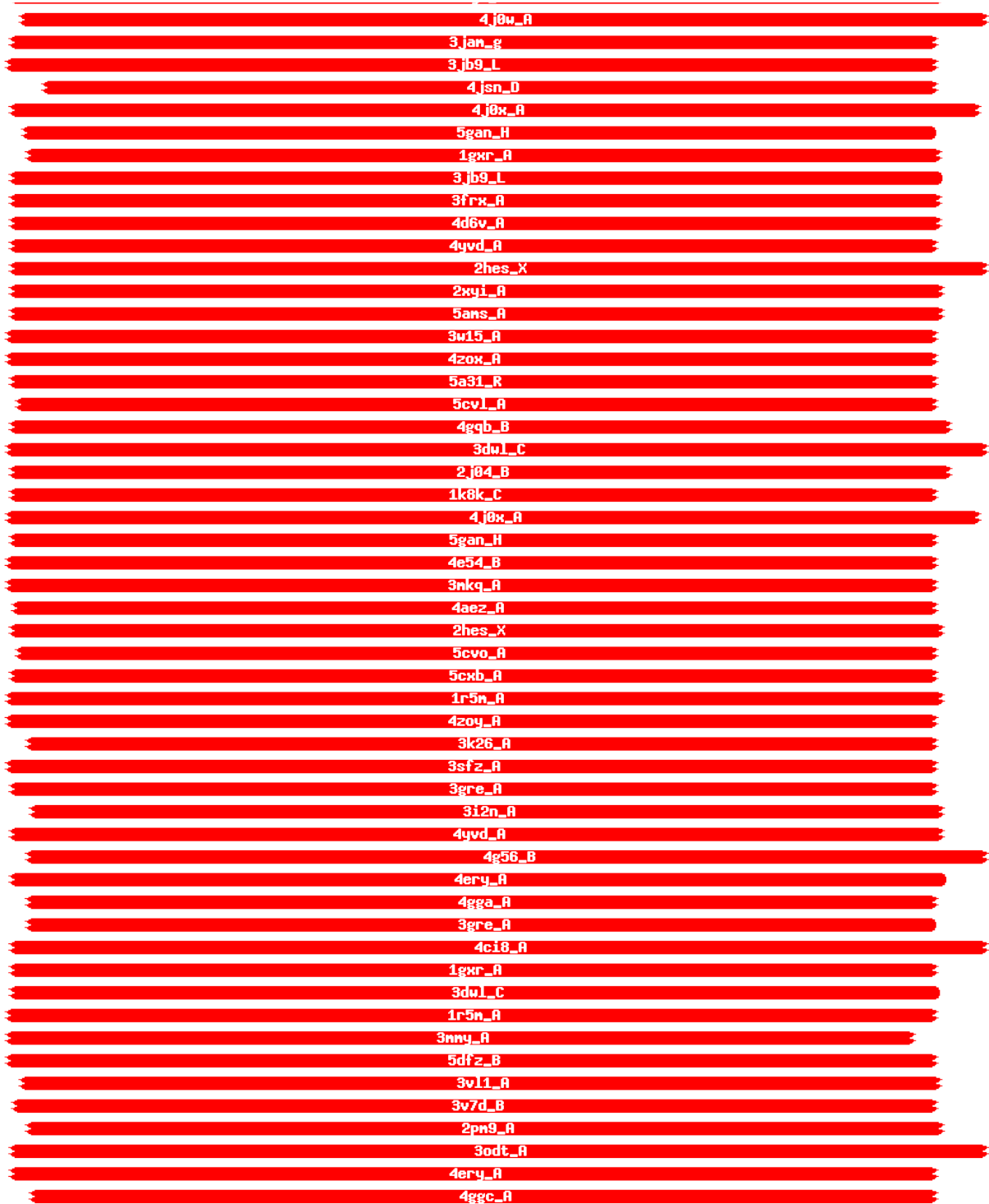
5ans_A

4gga_A

3e13_B

4wjs_A

4xvh_A



Query Fri_Mar_04_23:25:06_+0100_2016 (seq=MVVIANAHNE...KWEPAGEVHQ Len=297 Neff=10.8 Nseqs=172)
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 2pm7_B Protein transport prote	100.0	2.3E-51	6.2E-56	341.2	38.4	297	1-297	1-297 (297)
<input type="checkbox"/>	2 3jrp_A Fusion protein of prote	100.0	2.9E-48	8E-53	333.2	38.9	297	1-297	3-299 (379)
<input type="checkbox"/>	3 419o_A Protein transport prote	100.0	1.6E-46	4.3E-51	319.0	40.5	288	2-297	62-349 (349)
<input type="checkbox"/>	4 3bg1_A Protein SEC13 homolog;	100.0	5.2E-45	1.4E-49	305.6	30.9	278	1-297	5-305 (316)
<input type="checkbox"/>	5 4ule_I Eukaryotic translation	100.0	2.3E-41	6.3E-46	287.1	36.9	252	3-284	4-323 (347)
<input type="checkbox"/>	6 4j87_A Coatomer subunit alpha;	100.0	7.4E-41	2E-45	281.5	36.8	268	1-297	3-299 (327)
<input type="checkbox"/>	7 4j73_A Coatomer subunit beta';	100.0	9.2E-41	2.5E-45	278.0	35.3	251	1-282	5-256 (301)
<input type="checkbox"/>	8 1vyh_C Platelet-activating fac	100.0	2.9E-41	8E-46	292.8	33.2	247	1-282	142-408 (410)
<input type="checkbox"/>	9 3f3f_A Nucleoporin SEH1; struc	100.0	4E-40	1.1E-44	279.8	39.2	277	1-297	3-349 (351)
<input type="checkbox"/>	10 1vyh_C Platelet-activating fac	100.0	6.4E-41	1.8E-45	290.6	33.1	246	2-282	101-366 (410)
<input type="checkbox"/>	11 5a9q_7 Nucleoporin SEH1; trans	100.0	7.4E-40	2E-44	279.2	37.9	281	1-295	4-319 (360)
<input type="checkbox"/>	12 1got_B GT-beta; complex (GTP-b	100.0	7.6E-40	2.1E-44	277.0	35.8	249	2-282	48-298 (340)
<input type="checkbox"/>	13 4j87_A Coatomer subunit alpha;	100.0	4.6E-39	1.3E-43	270.6	37.8	251	2-284	46-327 (327)

<input type="checkbox"/>	14	3w15_A	Peroxisomal targeting s	100.0	8.4E-40	2.3E-44	279.6	32.7	252	8-282	61-365 (368)
<input type="checkbox"/>	15	3jro_A	Fusion protein of prote	100.0	1E-39	2.8E-44	303.4	32.0	297	1-297	1-297 (753)
<input type="checkbox"/>	16	1got_B	GT-beta; complex (GTP-b	100.0	1.4E-38	3.8E-43	269.4	34.3	249	2-282	90-340 (340)
<input type="checkbox"/>	17	4j0w_A	U3 small nucleolar RNA-	100.0	2E-38	5.5E-43	268.7	34.0	247	1-284	6-274 (343)
<input type="checkbox"/>	18	4wju_A	Ribosome assembly prote	100.0	2.5E-38	6.9E-43	282.1	34.2	249	2-282	179-514 (515)
<input type="checkbox"/>	19	3fm0_A	Protein CIA01; WDR39,SG	100.0	1.9E-37	5.4E-42	262.6	37.2	258	2-283	8-281 (345)
<input type="checkbox"/>	20	3ow8_A	WD repeat-containing pr	100.0	7.8E-38	2.2E-42	262.5	33.7	249	1-282	24-276 (321)
<input type="checkbox"/>	21	4j73_A	Coatomer subunit beta';	100.0	1.3E-37	3.6E-42	259.0	34.1	249	2-280	48-298 (301)
<input type="checkbox"/>	22	5cxb_B	Ribosome biogenesis pro	100.0	1.1E-37	3E-42	266.7	33.7	254	1-282	13-369 (369)
<input type="checkbox"/>	23	1erj_A	Transcriptional repress	100.0	1.7E-37	4.7E-42	267.7	34.9	247	7-283	121-387 (393)
<input type="checkbox"/>	24	2pbi_B	Guanine nucleotide-bind	100.0	2.1E-37	5.9E-42	263.4	34.4	252	2-282	57-354 (354)
<input type="checkbox"/>	25	3fm0_A	Protein CIA01; WDR39,SG	100.0	7.7E-37	2.1E-41	258.9	37.5	262	3-284	55-334 (345)
<input type="checkbox"/>	26	1k8k_C	P40, ARP2/3 complex 41	100.0	3.9E-37	1.1E-41	262.4	35.1	270	2-297	1-287 (372)
<input type="checkbox"/>	27	4bh6_A	APC/C activator protein	100.0	2.1E-37	5.7E-42	258.6	32.5	249	2-286	55-307 (308)
<input type="checkbox"/>	28	3ow8_A	WD repeat-containing pr	100.0	4.8E-37	1.3E-41	257.8	34.8	249	2-285	73-321 (321)
<input type="checkbox"/>	29	4jsn_D	Target of rapamycin com	100.0	2.4E-37	6.6E-42	260.1	33.0	258	1-282	34-298 (326)
<input type="checkbox"/>	30	3frx_A	Guanine nucleotide-bind	100.0	8.7E-37	2.4E-41	255.8	34.8	247	2-284	10-266 (319)
<input type="checkbox"/>	31	4lg9_A	F-box-like/WD repeat-co	100.0	1.1E-36	2.9E-41	263.3	35.8	241	7-282	109-397 (400)
<input type="checkbox"/>	32	4lg9_A	F-box-like/WD repeat-co	100.0	6.5E-37	1.8E-41	264.6	34.2	249	2-282	48-356 (400)
<input type="checkbox"/>	33	1erj_A	Transcriptional repress	100.0	1.2E-36	3.3E-41	262.4	34.1	246	2-282	57-338 (393)
<input type="checkbox"/>	34	4wju_A	Ribosome assembly prote	100.0	1.8E-37	4.9E-42	276.6	29.8	250	1-282	135-472 (515)
<input type="checkbox"/>	35	4wjs_A	RS4; ribosome assembly	100.0	1.3E-36	3.6E-41	269.1	34.6	250	2-282	150-484 (485)
<input type="checkbox"/>	36	4all_B	DNA excision repair pro	100.0	2.5E-36	7E-41	261.6	35.1	258	1-284	35-364 (408)
<input type="checkbox"/>	37	4lg8_A	PRE-mRNA-processing fac	100.0	2.7E-36	7.4E-41	256.7	34.6	247	2-283	107-354 (354)
<input type="checkbox"/>	38	4psw_B	Histone acetyltransfera	100.0	1.1E-36	3E-41	263.3	32.0	249	2-284	111-383 (401)
<input type="checkbox"/>	39	3jam_g	RACK1; eukaryotic trans	100.0	3.9E-36	1.1E-40	252.6	34.5	247	2-282	11-271 (326)
<input type="checkbox"/>	40	4d6v_A	GIB2, G protein beta su	100.0	6E-36	1.6E-40	250.1	35.1	249	2-282	8-260 (314)
<input type="checkbox"/>	41	4ggc_A	P55CDC, cell division c	100.0	7.1E-36	2E-40	250.4	34.4	247	2-282	60-312 (318)
<input type="checkbox"/>	42	4lg8_A	PRE-mRNA-processing fac	100.0	5.3E-36	1.5E-40	254.9	34.1	241	8-282	67-311 (354)
<input type="checkbox"/>	43	5ams_A	SQT1, ribosome assembly	100.0	5.6E-36	1.5E-40	261.1	34.2	254	1-282	57-339 (431)
<input type="checkbox"/>	44	4gga_A	P55CDC, cell division c	100.0	1E-35	2.9E-40	258.7	34.6	247	2-282	140-392 (420)
<input type="checkbox"/>	45	3ei3_B	DNA damage-binding prot	100.0	1E-35	2.9E-40	255.6	33.7	258	2-284	66-381 (383)
<input type="checkbox"/>	46	4wjs_A	RS4; ribosome assembly	100.0	6.4E-36	1.8E-40	264.7	33.0	253	1-282	106-442 (485)
<input type="checkbox"/>	47	4xyh_A	Kinetochore protein MIS	100.0	1.9E-36	5.2E-41	264.2	28.5	257	2-284	124-413 (430)
<input type="checkbox"/>	48	4j0w_A	U3 small nucleolar RNA-	100.0	5.6E-36	1.5E-40	253.6	30.2	259	5-297	63-334 (343)
<input type="checkbox"/>	49	3jam_g	RACK1; eukaryotic trans	100.0	5.9E-35	1.6E-39	245.4	36.1	247	2-282	59-321 (326)
<input type="checkbox"/>	50	3jb9_L	PRE-mRNA-splicing facto	100.0	2E-37	5.4E-42	262.2	20.5	253	1-282	42-297 (340)
<input type="checkbox"/>	51	4jsn_D	Target of rapamycin com	100.0	8.5E-36	2.3E-40	250.7	30.4	243	12-282	3-248 (326)
<input type="checkbox"/>	52	4j0x_A	Ribosomal RNA-processin	100.0	1.5E-35	4.1E-40	259.3	33.0	266	2-295	25-392 (451)
<input type="checkbox"/>	53	5gan_H	U4/U6 small nuclear rib	100.0	3.3E-36	9E-41	265.2	28.5	246	6-282	215-465 (465)
<input type="checkbox"/>	54	1gxr_A	ESG1, transducin-like e	100.0	8.3E-35	2.3E-39	244.8	35.6	241	7-283	95-335 (337)
<input type="checkbox"/>	55	3jb9_L	PRE-mRNA-splicing facto	100.0	5.1E-37	1.4E-41	259.7	21.5	251	2-284	86-340 (340)
<input type="checkbox"/>	56	3frx_A	Guanine nucleotide-bind	100.0	1.3E-34	3.6E-39	242.7	35.5	246	2-283	58-315 (319)
<input type="checkbox"/>	57	4d6v_A	GIB2, G protein beta su	100.0	1.3E-34	3.5E-39	242.0	34.9	250	2-283	56-312 (314)
<input type="checkbox"/>	58	4yvd_A	Pleiotropic regulator 1	100.0	1.6E-34	4.3E-39	246.9	35.9	244	2-282	57-300 (374)
<input type="checkbox"/>	59	2hes_X	YDR267CP; beta-propelle	100.0	4.9E-34	1.4E-38	238.9	38.0	270	2-297	7-291 (330)
<input type="checkbox"/>	60	2xyi_A	Probable histone-bindin	100.0	1.5E-35	4.2E-40	258.4	29.9	263	2-284	121-409 (430)
<input type="checkbox"/>	61	5ams_A	SQT1, ribosome assembly	100.0	9.2E-35	2.5E-39	253.4	34.4	247	2-284	102-430 (431)
<input type="checkbox"/>	62	3w15_A	Peroxisomal targeting s	100.0	5E-35	1.4E-39	250.1	32.1	254	1-282	2-305 (368)
<input type="checkbox"/>	63	4zox_A	Ribosome assembly prote	100.0	1.5E-34	4.2E-39	247.0	34.9	258	1-282	7-289 (381)
<input type="checkbox"/>	64	5a31_R	The anaphase-promoting	100.0	5.6E-35	1.5E-39	251.4	32.3	244	2-282	124-372 (386)
<input type="checkbox"/>	65	5cvl_A	WD repeat-containing pr	100.0	3.6E-35	1E-39	266.0	32.4	248	4-282	40-295 (598)
<input type="checkbox"/>	66	4gqb_B	Methylosome protein 50;	100.0	8.1E-35	2.2E-39	246.0	32.4	253	2-286	75-332 (344)
<input type="checkbox"/>	67	3dwl_C	Actin-related protein 2	100.0	1.1E-36	3E-41	260.5	21.0	268	1-297	3-292 (377)
<input type="checkbox"/>	68	2j04_B	YDR362CP, TAU91; beta p	100.0	4.7E-36	1.3E-40	268.0	25.5	258	2-286	200-518 (524)
<input type="checkbox"/>	69	1k8k_C	P40, ARP2/3 complex 41	100.0	6.8E-35	1.9E-39	248.5	31.5	256	2-282	45-358 (372)
<input type="checkbox"/>	70	4j0x_A	Ribosomal RNA-processin	100.0	1.2E-35	3.4E-40	259.9	27.5	265	1-295	106-444 (451)
<input type="checkbox"/>	71	5gan_H	U4/U6 small nuclear rib	100.0	2.9E-35	7.9E-40	259.2	29.9	249	2-282	168-423 (465)
<input type="checkbox"/>	72	4e54_B	DNA damage-binding prot	100.0	5.5E-36	1.5E-40	261.4	25.1	254	1-282	111-384 (435)
<input type="checkbox"/>	73	3mkq_A	Coatomer beta'-subunit;	100.0	5.8E-35	1.6E-39	273.8	33.6	248	1-282	5-256 (814)
<input type="checkbox"/>	74	4aez_A	CDC20, WD repeat-contai	100.0	1.2E-34	3.3E-39	250.6	32.2	246	3-282	128-377 (401)
<input type="checkbox"/>	75	2hes_X	YDR267CP; beta-propelle	100.0	3.6E-34	9.9E-39	239.7	33.8	258	2-284	49-327 (330)
<input type="checkbox"/>	76	5cvo_A	WD repeat-containing pr	100.0	7.3E-35	2E-39	266.3	31.9	248	4-282	25-280 (677)
<input type="checkbox"/>	77	5cxb_A	Ribosome biogenesis pro	100.0	9.5E-35	2.6E-39	258.9	31.8	250	2-282	123-436 (514)
<input type="checkbox"/>	78	1r5m_A	SIR4-interacting protei	100.0	2.4E-34	6.7E-39	249.4	33.2	254	1-284	100-424 (425)
<input type="checkbox"/>	79	4zoy_A	SQT1; chaperone, riboso	100.0	7.7E-34	2.1E-38	250.4	36.7	253	1-282	7-408 (491)
<input type="checkbox"/>	80	3k26_A	Polycarb protein EED; W	100.0	2.1E-34	5.7E-39	244.7	31.7	248	7-282	67-363 (366)
<input type="checkbox"/>	81	3sfz_A	APAF-1, apoptotic pepti	100.0	2.8E-34	7.8E-39	280.1	36.6	249	1-282	607-910 (1249)
<input type="checkbox"/>	82	3gre_A	Serine/threonine-protei	100.0	2.5E-35	6.8E-40	257.2	26.2	254	2-282	55-356 (437)
<input type="checkbox"/>	83	3i2n_A	WD repeat-containing pr	100.0	9E-35	2.5E-39	247.6	28.6	251	8-284	64-352 (357)
<input type="checkbox"/>	84	4yvd_A	Pleiotropic regulator 1	100.0	1.8E-33	5E-38	240.3	36.3	246	2-284	99-352 (374)
<input type="checkbox"/>	85	4g56_B	MGC81050 protein; prote	100.0	2.3E-34	6.4E-39	244.5	30.3	260	7-297	92-355 (357)
<input type="checkbox"/>	86	4ery_A	WD repeat-containing pr	100.0	1.4E-33	3.9E-38	235.1	33.7	253	2-285	58-312 (312)
<input type="checkbox"/>	87	4gga_A	P55CDC, cell division c	100.0	7.9E-34	2.2E-38	246.9	32.8	244	7-282	103-350 (420)
<input type="checkbox"/>	88	3gre_A	Serine/threonine-protei	100.0	7.6E-35	2.1E-39	254.1	26.2	247	7-282	109-437 (437)
<input type="checkbox"/>	89	4ci8_A	Echinoderm microtubule-	100.0	8.9E-34	2.4E-38	259.7	34.4	265	2-297	292-622 (655)
<input type="checkbox"/>	90	1gxr_A	ESG1, transducin-like e	100.0	3E-33	8.3E-38	235.2	34.6	247	2-282	44-293 (337)
<input type="checkbox"/>	91	3dwl_C	Actin-related protein 2	100.0	2.9E-35	8E-40	251.6	22.0	259	2-283	48-377 (377)
<input type="checkbox"/>	92	1r5m_A	SIR4-interacting protei	100.0	6.3E-34	1.7E-38	246.8	30.6	249	1-282	35-358 (425)
<input type="checkbox"/>	93	3mmy_A	MRNA export factor; mRN	100.0	4.7E-34	1.3E-38	244.1	29.3	248	1-275	31-336 (368)
<input type="checkbox"/>	94	5dfz_B	Serine/threonine-protei	100.0	1.2E-36	3.4E-41	295.8	15.0	250	1-282	1061-1363 (1460)
<input type="checkbox"/>	95	3v11_A	26S proteasome regulato	100.0	1.1E-33	3.2E-38	245.4	31.9	245	5-283	92-362 (420)
<input type="checkbox"/>	96	3v7d_B	Cell division control p	100.0	2.6E-33	7E-38	246.7	34.5	242	3-282	115-378 (464)
<input type="checkbox"/>	97	2pm9_A	Protein WEB1, protein t	100.0	4.5E-35	1.2E-39	254.1	22.8	253	7-284	65-336 (416)
<input type="checkbox"/>	98	3odt_A	Protein DOA1; ubiquitin	100.0	1.8E-33	5.1E-38	235.3	31.5	253	2-297	52-307 (313)
<input type="checkbox"/>	99	4ery_A	WD repeat-containing pr	100.0	1E-32	2.8E-37	229.9	35.9	250	2-282	16-265 (312)
<input type="checkbox"/>	100	4ggc_A	P55CDC, cell division c	100.0	3.3E-33	9E-38	234.2	33.0	243	8-282	24-270 (318)

No 1


☐ >2pm7_B Protein transport protein SEC13, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A

{Saccharomyces cerevisiae} PDB: 2pm9_B 4bzK_F 2pm6_B 3iko_A 3mzk_A 3mzl_A 4bzK_B 4xmm_A 4xmm_A 4bzj_F
Probab=100.00 E-value=2.3e-51 Score=341.24 Aligned_cols=297 Identities=98% Similarity=1.534 Sum_probs=0.0

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Q ss_pred      CceEecCCcCeeEEEECCCCEEEEeCCcEEEEccCccceEEecCCCCEEEEecCCcCCEEEEEcCCcEEF
Q Fri_Mar_04_23: 1 MVIANAHNELIHDAVLDDYGRKRLATCSSDKTIKIFEVGEETHKLIDTLTGHEGPVWRVDWAHPKFGTLLASCSDYDGKVL 80 (297)
Q Consensus    1 ~~~~~h~~~v~~~g~~~l~t~s~d~v~lwd~~~~h~~~v~~~l~~~s~s~d~i~ 80 (297)
               |+.+++.+|...|++++|+|++|+|+.|++|+|+|+...+.+++|++++|+.++|+
T Consensus    1 ~~~~~h~~~v~~~g~~~l~s~s~d~i~iwd~~~~l~gh~~~v~~~v~~~g~~~l~s~s~d~v~ 80 (297)
T 2pm7_B       1 MVIANAHNELIHDAVLDDYGRKRLATCSSDKTIKIFEVGEETHKLIDTLTGHEGPVWRVDWAHPKFGTLLASCSDYDGKVL 80 (297)
T ss_dssp      -CECCSSSSCEEEEEETTSSEEEEETTSCEEEEBCSSCCEEECCSSCEEEEECCGGGCSCEEEEETTTTEE
T ss_pred      CcEEecccccceEEEECCCCEEEEeCCcEEEEccCchEEecCCCCEEEEecCCcCCEEEEEcCCcEEF
```

```
Q ss_pred      EEEccCCEEEEEEEccCccEEEEEEcCCcCCcEEEEEECCCEEEEEecCCcCchhhhhhccceEEEECCcccc
Q Fri_Mar_04_23: 81 IWKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASSDGKVSVEFKENGTTSPILIDAHAGVNSASWAPATIEE 160 (297)
Q Consensus    81 iwd~~~~h~~~v~~~v~~~p~~~g~~~l~s~s~d~i~iwd~~~~h~~~v~~~p~~~ 160 (297)
               +|+++++...+.+.+|...|+++|+|+.+.+++++.|+.+++|+.....+.+|...+.+++|+|+....
T Consensus    81 iwd~~~~h~~~v~~~v~~~p~~~g~~~l~s~s~d~i~iwd~~~~h~~~v~~~p~~~ 160 (297)
T 2pm7_B       81 IWKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASSDGKVSVEFKENGTTSPILIDAHAGVNSASWAPATIEE 160 (297)
T ss_dssp      EEEBSSBCCEEECCSSCEEEEECCGGGCSCEEEEEETTSCEEEEBCSSCCEEECCSSCEEEEECCSSCCEEE
T ss_pred      EEEccCCEEEEEEEccCccEEEEEEcCCcCCcEEEEEECCCEEEEEecCCCCceeecccccCEEEEEcCCCCc
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```
Q ss_pred      cccccCccceEEEEEEcCCeEEEEEEcCCcceeEEEEEEccCCcEeEEEECCCCCCCCEEEEEEcCCeEEEEccCCC
Q Fri_Mar_04_23: 161 DGEHNGTKESRKFTVGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ 240 (297)
Q Consensus    161 ~~~~~l~tg~d~i~wd~~~~h~~~v~~~l~~~s~~~las~s~Dg~i~iw 240 (297)
               +....+.+++|++|+.|+.|++|+|+.+.+.+.+.+.|...|+++|+|+++.+|+|++|+|++|+
T Consensus    161 ~~~~~l~sgs~d~i~iwd~~~~l~gh~~~v~~~v~~~sp~~~las~s~D~v~iwd 240 (297)
T 2pm7_B       161 DGEHNGTKESRKFTVGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ 240 (297)
T ss_dssp      -----CCEEEEEETTSCEEEEETTSCEEEEEECCSSCEEEEECCSSCCEEECCSSCEEEEEESSTT
T ss_pred      cccccCccceEEEEEEcCCcEEEEEEcCCcCCcEEEEEEcCCcCceEEEEEECCCCCCCCeEEEEcCCeEEEEEEccCCC
```

```
Q ss_pred      CceeEEEEccccCCeEEEEEECCCCEEEEeCCCCEEEEEECCCCeEEEEEccC
Q Fri_Mar_04_23: 241 GPWKKTLLKEEFDPDLWRASWSLSGNVLALSGGDNKVTLWKENLEKWEPAQEVHQ 297 (297)
Q Consensus    241 ~~~~~i~~~l~~~d~i~iw 297 (297)
               .+....+.+++|++|+|++|++++.|++|+|+.+.+++|+++++|
T Consensus    241 ~~~~~v~~~s~g~~~las~d~v~W~~~g~w 297 (297)
T 2pm7_B       241 GPWKKTLLKEEFDPDLWRASWSLSGNVLALSGGDNKVTLWKENLEKWEPAQEVHQ 297 (297)
T ss_dssp      SCCEEESSSSCCSSCEEEEECCSSCCCEEEETTSCEEEEETTSCEEEC-----
T ss_pred      CceeeEEccccCCcEEEEEEcCCcEEEEEEcCCcCceEEEEEEcCCcEEEEEEccC
```

No 2



☐ >3jrp_A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic vesicle, endoplasmic reticulum; 2.60Å {Saccharomyces cerevisiae}
Probab=100.00 E-value=2.9e-48 Score=333.24 Aligned_cols=297 Identities=100% Similarity=1.542 Sum_probs=0.0

```
Q ss_pred      CceEecCCcCeeEEEECCCCEEEEeCCcEEEEccCccceEEecCCCCEEEEecCCcCCEEEEEcCCcEEF
Q Fri_Mar_04_23: 1 MVIANAHNELIHDAVLDDYGRKRLATCSSDKTIKIFEVGEETHKLIDTLTGHEGPVWRVDWAHPKFGTLLASCSDYDGKVL 80 (297)
Q Consensus    1 ~~~~~h~~~v~~~g~~~l~t~s~d~v~lwd~~~~h~~~v~~~l~~~s~s~d~i~ 80 (297)
               ++.+++.+|...|++++|+|++|+|+.|++|+|+|+...+.+++|++++|+.++|+
T Consensus    3 ~~~~~H~~~V~~~v~~~s~dg~~~lasg~s~D~v~iwd~~~~l~gh~~~v~~~v~~~g~~~lasg~s~D~v~ 82 (379)
T 3jrp_A       3 MVIANAHNELIHDAVLDDYGRKRLATCSSDKTIKIFEVGEETHKLIDTLTGHEGPVWRVDWAHPKFGTLLASCSDYDGKVL 82 (379)
T ss_dssp      --CEEECCCCCEEEEECCSSCEEEEEETTSCEEEEETTSCEEEEEECCSSCEEEEECCGGGCSCEEEEETTTCEE
T ss_pred      ceEEccccceEEEECCCCEEEEeCCcEEEEccCccceEEecCCCCEEEEecCCCCCEEEEEcCCcEEF
```

```
Q ss_pred      EEEccCCEEEEEEEccCccEEEEEEcCCcCCcEEEEEECCCEEEEEecCCcCchhhhhhccceEEEECCcccc
Q Fri_Mar_04_23: 81 IWKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASSDGKVSVEFKENGTTSPILIDAHAGVNSASWAPATIEE 160 (297)
Q Consensus    81 iwd~~~~h~~~v~~~v~~~p~~~g~~~l~s~s~d~v~vwd~~~~h~~~v~~~p~~~ 160 (297)
               +|+++++...+.+.+|...|+++|+|+.+.+++++.|+.+++|+.....+.+|...+.+++|+|+....
T Consensus    83 iwd~~~~h~~~v~~~v~~~sp~~~g~~~l~s~s~d~v~vwd~~~~h~~~v~~~p~~~ 162 (379)
T 3jrp_A       83 IWKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASSDGKVSVEFKENGTTSPILIDAHAGVNSASWAPATIEE 162 (379)
T ss_dssp      EEEEETTEEEEEECCSSCEEEEECCGGGCSCEEEEEETTSCEEEEETTSCEEECCTTSCCEEEECCTTCEEEEECCCC---
T ss_pred      EEecCCcEEEEEEEEccCccEEEEEEcCCcCCcEEEEEEcCCcEeEEEEcCCcCcehhccccceEEEEccccccc
```

```
Q ss_pred      cccccCccceEEEEEEcCCeEEEEEEcCCcceeEEEEEEccCCcEeEEEECCCCCCCCEEEEEEcCCeEEEEccCCC
Q Fri_Mar_04_23: 161 DGEHNGTKESRKFTVGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ 240 (297)
Q Consensus    161 ~~~~~l~tg~d~i~wd~~~~h~~~v~~~l~~~s~~~las~s~Dg~i~iw 240 (297)
               +..+.+.+++|++|+.|+.|++|+|+.+.+.+.+.+.|...|+++|+|+++.+|+|++|+|++|+
T Consensus    163 ~~~~~l~sgs~D~i~iwd~~~~l~gh~~~v~~~v~~~sp~~~las~s~D~v~iwd 242 (379)
T 3jrp_A       163 DGEHNGTKESRKFTVGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIIWTQDNEQ 242 (379)
T ss_dssp      -----CTTCEEEEEETTSCEEEEETTSCEEEEEECCSSCEEEEECCSSCCEEEETTSCEEEEESSTT
T ss_pred      cccccCccceEEEEEEcCCcEEEEEEcCCcCCcEEEEEEcCCcCceEEecCCCCCEEEEEcCCcEeEEEEcCCCC
```

```
Q ss_pred      CceeEEEEccccCCeEEEEEECCCCEEEEeCCCCEEEEEECCCCeEEEEEccC
Q Fri_Mar_04_23: 241 GPWKKTLLKEEFDPDLWRASWSLSGNVLALSGGDNKVTLWKENLEKWEPAQEVHQ 297 (297)
Q Consensus    241 ~~~~~i~~~l~~~d~i~iw 297 (297)
               .+....+.+++|++|+|++|++++.|++|+|+.+.+++|+++++|
T Consensus    243 ~~~~~v~~~s~dg~~~las~~~dg~v~iw 299 (379)
T 3jrp_A       243 GPWKKTLLKEEFDPDLWRASWSLSGNVLALSGGDNKVTLWKENLEKWEPAQEVHQ 299 (379)
T ss_dssp      SCCEEESSSSCCSSCEEEEECCSSCCCEEEESSSSCEEEEEETTSCEEEEEEcC
T ss_pred      CceeecccccccccCCcEEEEEECCCCEEEEeCCcCceEEEEEEcCCcCceEEEEEe
```

No 3



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T ss_pred EEECCcC--EEEEcCCCCcEEEEEECCC--CCEEEEcCCcEEEECCCC--eEEEcCCCCcEEEEcCccch

Q ss_pred -----ccccccccCccceEEEEcCCcEEEEEEcCCcCeEEEEcCCCCcBeEEEECCCCCCCC

Q Fri_Mar_04_23: 157 -----TIEEDGHNSTKESRKFTGGARNLVKIKVYNSDAQTYVLESTLEGHSWVRDVAWSPTVLLRS 220 (297)

Q Consensus 157 -----l-tg--d--i-wd-----h--v--l--s----- 220 (297)

T Consensus 292 -----g-----l-sgs-D--i-lwd-----h--v--v--g----- 351 (410)

T lvyh_C 292 SISEATGSETKKSGKPG-----PFLSGSRDKTKMWDVSTG---MCLMTLVGHNDNVRGVLFHSGG---K 351 (410)

T ss_dssp GGGGCCSCC-----C-----CCEEEETTSEEEEEETTTT---EEEEEECCSSCEEEEECCSS---S

T ss_pred hhhhhccccccccCCCC-----CCEEEcCCcEEEECCCC--cEEEECCCCcEEEEcCCC--C

Q ss_pred EEEEEcCCcEEEEcCCCCcEEEEEccccCCcEEEEEECCCCEEEEcCCCCEEEE

Q Fri_Mar_04_23: 221 YLASVSDRTCIITWTDNEQGPWKTKLKEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)

Q Consensus 221 --las-s-Dg-i-iw-----i-----l-----d--i-w- 282 (297)

T Consensus 352 --l-sgs-D--i-vwd-----l-----h--V--l-----l-sgs-Dg-i-vwd 408 (410)

T lvyh_C 352 FILSCADDKTLRVWDYKNKR---CMKTLNA--HEHFVTSLDPHKTAPYVVTGSDVQTVKVVW 408 (410)

T ss_dssp CEEETTTTSEEEECCTTSC---CCEEEc--CSCCEEEECSSSSCEEEETTSEEEEC

T ss_pred EEEEEcCCcEEEEcCCcE---EEEECC--CCCCEEEEEcCCCCEEEEcCCcEEEEE

No 9      

☐ >3f3f_A Nucleoporin SEH1; structural protein, protein complex, nucleopori complex, nuclear pore complex, macromolecular assembly, MEM coat; 2.90A {Saccharomyces cerevisiae} PDB: 3f3g_A 3f3p_A 3ewe_A 4xmm_C Probab=100.00 E-value=4e-40 Score=279.78 Aligned_cols=277 Identities=28% Similarity=0.587 Sum_probs=0.0

Q ss_pred CceEecCCcCeeEEEEcCCCCEEEEcCCcEEEEcCCcC--ceEEecCCCCEEEEcCCcCCEEEEcCCcC

Q Fri_Mar_04_23: 1 MVVIANAHNELIHDAVLDDYGRKLTCSDDTKIFFEVEGETH--KLIDLTLGHEGPVWRVDWAHPKFTILASCSYDVK 78 (297)

Q Consensus 1 -----h--v--g--l-t-s-d--v-lwd-----h--v--l--s--D-- 78 (297)

T Consensus 3 -----gh--V--v--s-dg--las-s-D--v-iwd-----h--V--v--s--g--las-s-D-- 82 (351)

T 3f3f_A 3 MQPFDSDGDDLVHDVVDYDFYGRHVATCSDDQHIKVFPLDKDTSNWEISDSWRAHDSSVAIDWASPEYGRITASASYDKT 82 (351)

T ss_dssp CCCECCSSCEEEECSSSEEEETTSEEEEEECSSSCCEEEECSSCEEEECSSCGGGSCEEEETTSC

T ss_pred cccccCCcCCEEEEECCCCEEEEcCCcEEEEECCCCCcEEEEEcccccEEEEEECCCCCEEEEEcCCc

Q ss_pred EEEEEc-----CCeEEEEEEccccCccEEEEcCCcCCcEEEEEECCCCEEEEcCCcCchhhhh-----

Q Fri_Mar_04_23: 79 VLINKEE-----NGRWSQIAVHAVHSASVNSVQWAPHEYGPPLLVAASDGKVSVEFKENGTTSPIIID----- 142 (297)

Q Consensus 79 i-iwd-----v-----l-----d--i-i----- 142 (297)

T Consensus 83 v-iwd-----h--v--sp--g--l-s--d--v-lwd-----h--V--v--s--g--las-s-D-- 162 (351)

T 3f3f_A 83 VKLWEDPDQEECSGRWNKLCFLNDSKGLSYKFAHPLGLKLALGNDGILRLYDALPESDLRSWTLTSEMKVLSIP 162 (351)

T ss_dssp EEEEECTTSCCTTSSCEEEEECCCCSSCEEEECSSCGGGSCEEEETTCEEEECSSSTTCTTCCCEEEECSSC

T ss_pred EEEEEcCCCCccccceEEEEECCCCcEEEEECCCCCcEEEEECCCCcEEEEcCCCCccccccccceEEec

Q ss_pred --hccccceEEEECCCCccccccccCccceEEEEcCCcEEEEEEcCCCCeEEEEcCCCCcBeEEEECCC----C

Q Fri_Mar_04_23: 143 --AHAIGVNSASWAPATIEEDGHNSTKESRKFTGGARNLVKIKVYNSDAQTYVLESTLEGHSWVRDVAWSPT----V 216 (297)

Q Consensus 143 -----l-tg--d--i-wd-----h--v--l--s----- 216 (297)

T Consensus 163 -----l-----l-----h--v--v--sp----- 230 (351)

T 3f3f_A 163 PANHLQSDFLSWCPSR-----FSPKALVSALEQ--AIYQGRKD--GKLHVAALKPGHKSILRSISWAPSIGRWY 230 (351)

T ss_dssp CSSSCCCCEEEECSS-----SSCCEEEETT--EEEEECTT--SCEEEEECSSCCSCEEEECSSSCSS

T ss_pred CCCCCCcEEEECCCC-----CCCEeEEecccc--eEEEEcCC--CcEEEEEECCCCcEEEEECCCCCCCC

Q ss_pred CCCCEEEEEcCCcEEEEcCC-----CCCCCEEEEcCCcC-----CCCCCEEEEc

Q Fri_Mar_04_23: 217 LLRSYLASVSDRTCIITWTDNE-----QGPKTKLLKE 250 (297)

Q Consensus 217 -----las-s-Dg-i-iw-----s----- 250 (297)

T Consensus 231 -----lasgs-D--v-iwd-----s----- 304 (351)

T 3f3f_A 231 --QLIATGCKDGRIRIFKITEKLSPLAESLNSNMFNSADVMDAQGRSDSNTEEKAELOSLQVE---LLSEHDD 304 (351)

T ss_dssp ---EEEEETTSCEEEEEECC-----CCSEEE---EEEECT

T ss_pred ---ceEEEECCCCcEEEEcCccccccccccccccccccccccccccccccccccccceE---Eeeccc

Q ss_pred ccCCcEEEEEECCCCEEEEcCCCCEEEECCCCcEEEEEccc

Q Fri_Mar_04_23: 251 EKFPDVLWRASWSLSGNVLALSGGDNKVTLWKENLGKWEPAVEVHQ 297 (297)

Q Consensus 251 -----i-----l-----d--i-w- 297 (297)

T Consensus 305 --h--V--v--spdg--las-s-D--v-lw----- 349 (351)

T 3f3f_A 305 --HNGEVWSVSNLTGTLLSSAGDDGKVRWLKATYSNFKCMSVITA 349 (351)

T ss_dssp --TSSCEEEECSSSCCEEEETTSEEEEEECTTSCEEEEEEEC--

T ss_pred --CCcEEEEEECCCCEEEEcCCcEEehhccCCcEEEEEEcc

No 10       

☐ >lvyh_C Platelet-activating factor acetylhydrolase IB alpha subunit; lissencephaly, platelet activating factor, regulator of cytoplasmic dynein; 3.4A {Mus musculus} SCOP: b.69.4.1 Probab=100.00 E-value=6.4e-41 Score=290.63 Aligned_cols=246 Identities=22% Similarity=0.342 Sum_probs=0.0

Q ss_pred ceEecCCcCeeEEEECCCCEEEEcCCcEEEEcCCcCccceEEecCCCCEEEEcCCcCCEEEECcCCcEEEE

Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDDYGRKLTCSDDTKIFFEVEGETHKLIDLTLGHEGPVWRVDWAHPKFTILASCSYDGVLI 81 (297)

Q Consensus 2 -----h--v--g--l-t-s-d--v-lwd-----h--v--l--s--D--i-i 81 (297)

T Consensus 101 --l-gH--V--v--p--l-s--Dg-i-vwd-----l--h--V--l-----g--l-s--D--i-l 176 (410)

T lvyh_C 101 KYALSGHRSPVTRVIFHPVFSVMVSASDATIKVWDY---ETGDFERTLKGHDSVQDISFDHS---GKLLASCSADMTIKL 176 (410)

No 11

Q ss_pred		CCcEEEEEec	
Q Fri_Mar_04_23:	286	EGKWEPAgev	295 (297)
Q Consensus	286		295 (297)
		+. + + .	
T Consensus	310		1 319 (360)
T 5a9q_7	310	MDNWKCTGIL	319 (360)
T ss_dssp		SSCEEEEEEE	
T ss_pred		CCCEEEEEEE	

☐ >1got_B GT-beta; complex (GTP-binding/transducer), G protein, heterotrimer signal transduction; HET: GDP; 2.00A {Bos taurus} SCOP: b.69.4.1 PDB: 1b9y_A 1b9x_A* 2trc_B 3v5w_B* 1gg2_B* 1omw_B 1gp2_B 1xhm_A 3ah8_B* 3cik 3krw_B* 3krx_B* 3psc_B 3pvu_B* 3pvw_B* 3uzs_B 1tbg_A* 4kfm_B* 4pnk_B* 1a0r_B* ... Probab=100.00 E-value=7.6e-40 Score=277.03 Aligned_cols=249 Identities=20% Similarity=0.268 Sum_probs=0.0

```
Q ss_pred      ceEecCCcCeeEEEECCCCEEEECCCCcEEEEccCcccccEEecCCCCEEEEccCccCEEEEECCCCeEEE
Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDYGGKRLATCSSDKTKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLII 81 (297)
Q Consensus    2 ---h---v---g---l-t-s-d-v-lwd---h---v---l-s-s-D-i-i 81 (297)
                  ...+.||+.|++++|+|++++|++|+.|++|++|. .+.+.+.+.|...|++++|+++ ++|++|+|+.|++
T Consensus    48 ---l-gH---V-----s-d---l-s-s-Dg-v-iWd-----v-----s---g-l-sg-d-i-i 123 (340)
T 1got_B       48 RRTLRGHLAKIYAMHWGTDRLSLSSASQDGKLIWDS---YTNKVHAIPLRSSVWMTCAAYAPS--GNVYACGGLDNICSI 123 (340)
T ss_dssp      EEECCSSCEEEEEECTSSEEEEETTTTEEEET--TTCEEEEECCSSCEEEEECTT--SSEEEEEETTCEEEE
T ss_pred      ceeecCCcCeeEEEECCCCEEEECCCCcEEEECC--CCCCcEEecCCcCEEEEECCC--CEEEEECCcEEEEE
```

```
Q ss_pred      EEccC--CeEEEEEEcccccCccEEEEECcCccCCcEEEEECCEEEEEEEccCccchhhhhhhcccccEEEECCCCcc
Q Fri_Mar_04_23: 82 WKEEN--GRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVEFKNGTTPIIIDAHAIQVNSASWAPATIE 159 (297)
Q Consensus    82 wd-----v-----l-----d-i-i-----v----- 159 (297)
                  ||+. +.....+.|...+.+.|+. +.+++++.|+.|++|+... ..+.+.|...|+++|++
T Consensus    124 w-----h---v-----l-s-s-d-i-lwd---h---v---l----- 196 (340)
T 1got_B       124 YNLKTRGNVRVRSRELAGHTGYLSGCRFLD--DNQIVTSSGDTTCALWDIEITG--QQTTFTHGTGDVMSLSLAPDT-- 196 (340)
T ss_dssp      EETTCBSBCEEEEEECSSCEEEEEEC---TTEEEETTSCEEEETTTT--EEEEECSSCEEEEEECTTS--
T ss_pred      EcccCCCCcccccCccCCEEEEECC--CcEEEEECCEEEEECCCC--cEEEEECcCCcEEEEECcCC--
```

```
Q ss_pred      ccccccCCcccEEEEECcCceEEEEEECCCCcEEEEEEccCCCCcEeEEEECCCCCCCCEEEEECcCceEEEEccCC
Q Fri_Mar_04_23: 160 EDGEHNGTKESRKFTVGGADNLVKIKWYNSDAQTYVLESTLEGHSDWVRDVAWSPVLLRSYLASVSQDRTCIWTQDNE 239 (297)
Q Consensus    160 ---l-tg-d-i-wd-----h---v---l-s---w-----l-s-s-D-i-iw----- 239 (297)
                  .++++|+.|+.|++|+++. +...+.|...|+++|++ +|++|+.|++|++|+++
T Consensus    197 -----l-sgs-d-v-wd-----h---v---p----- 258 (340)
T 1got_B       197 -----RLFVSGACDASAKLWDVREGM---CRQTFTHGESDINAIQFPNG--NAFATGSDDATCRFLDLRAD 258 (340)
T ss_dssp      -----SEEEEEETTSCEEEETTTCS--EEEEECSSCEEEEEECTTS--SEEEEEETTSCEEEETTTT
T ss_pred      -----CEEEEECCEEEEEECCcC--eEEEECCcCCEEEEEEcCC--CEEEEECCcEEEEECcCC
```

```
Q ss_pred      CCcEEEEEcccccCCcEEEEEECCCCEEEECCCCCEEEEE
Q Fri_Mar_04_23: 240 QGPWKTKLLKEEFKPDVLWRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Consensus    240 -----i-----d-i-iw----- 282 (297)
                  . ....+.++++.|.+++|+|++|++++|.+.|++|+
T Consensus    259 -----v-----s-g-l-g-d-i-vwd 298 (340)
T 1got_B       259 Q---ELMTYSHDNIIICGITSVSFSKSGRLLLAGYDDFNCNVWD 298 (340)
T ss_dssp      E---EEEEECCTTCCSCEEEEECTTSSEEEETTSSEEEEE
T ss_pred      C---EEEEccCcccccEEEECCCCEEEECCCCCEEEEE
```

No 13    

☐ >4j87_A Coatomer subunit alpha; beta propeller domain, vesicle trafficking, protein transpor; 1.67A {Schizosaccharomyces pombe} PDB: 4j8b_A 4j8g_A Probab=100.00 E-value=4.6e-39 Score=270.62 Aligned_cols=251 Identities=22% Similarity=0.349 Sum_probs=0.0

```
Q ss_pred      ceEecCCcCeeEEEECCCCEEEECCCCcEEEEccCcccccEEecCCCCEEEEccCccCEEEEECCCCeEEE
Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDYGGKRLATCSSDKTKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLII 81 (297)
Q Consensus    2 ---h---v---g---l-t-s-d-v-lwd---h---v---l-s-s-D-i-i 81 (297)
                  +.+.+.|...|++++|+|++++|++|+.|++|++|. .++++.+.|...|++.|+++ ++|++|+|+.|++
T Consensus    46 ---h---V-----l-sgs-D-v-vwd---h---v---l-s-s-D-i-i 121 (327)
T 4j87_A       46 LDRFDGHDGVRGIAFHTQPIFVSGGDDYKVNVMY--KSRKLLFSLCGHMDYVRVTFHHE--YPWILSCSDDOTIRI 121 (327)
T ss_dssp      EEEEECCSSCEEEEEECSSSSEEEEETTSCEEEET--TTTEEEEECCSSCEEEEECCSS--SSEEEEEETTSCEEE
T ss_pred      EEEEECCCCcEEEEEECCCCEEEECCCCcEEEECC--CCcEEEEECcCCcEEEEEEcCC--CCEEEECCCCcEEE
```

```
Q ss_pred      EEccCCEEEEEEEcccccCccEEEEECcCccCCcEEEEECCEEEEEEEe-----
Q Fri_Mar_04_23: 82 WKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKVSVEF----- 130 (297)
Q Consensus    82 wd-----v-----l-----d-i-i----- 130 (297)
                  ||+++++ .+.+.|...|+++|++ +.+++++.|+.|++|+
T Consensus    122 wd-----h---v-----p-----l-s-s-D-v-iwd----- 197 (327)
T 4j87_A       122 WNWQSRN--CIAITLGHSHYVMCAAFHPS--EDLTVASLDQTVRVWDISGLRMKNAAVPMMSKEDQKAQHNSISNDLF 197 (327)
T ss_dssp      EETTTTE--EEEEECSSCEEEEEECSS--SEEEEEETTSCEEEEECHHHHHHHSCCCCGGGGCTTC-----
T ss_pred      ECCCCC--eEEEEccCccCEEEEEECcC--CEEEEEECcCCcEEEEECcCceccccccCccccccccccccccce
```

```
Q ss_pred      cCCCCchhhhhhhcccccEEEECCCCccccccccCCCCcEEEEECcCceEEEEEEcCCcEEEEEccCCCCeEEE
Q Fri_Mar_04_23: 131 KENGTTSPITIDAHAIQVNSASWAPATIEEDGEHNGTKESRKFTVGGADNLVKIKWYNSDAQTYVLESTLEGHSDWVRDV 210 (297)
Q Consensus    131 -----v-----l-tg-d-i-wd-----h---v---l 210 (297)
                  .....+.|...|.++|+|. .+|++|+.|++|+... ..+.+.|...|++
T Consensus    198 -----h---v-----p-----l-s-D-i-w----- 262 (327)
T 4j87_A       198 GSADAIVKVLVLEGHDRGVNWCAAFHPTL-----PLILSAGDDRLVLRMTASKAW--EVDTCRGRHNNVNSCC 262 (327)
T ss_dssp      --CCEEEEEEECSSCEEEEEECSS-----SEEEEEETTSCEEEEEECSSCEE--EEEEEECCSSCEEE
T ss_pred      cCCCCcEEEEEEcCCCCEEEEEECCCC-----CcEEEEECCEEEEEECcCCcEE--EEEEEEcCccEEEE
```








```
Q ss_pred      ECCCCCCCCEEEEECcCceEEEEECcCCCCcEEEEEcccccCceEEEEEECCCCCEEEEECCCCCEEEEEEE
Q Fri_Mar_04_23: 211 AWSPTVLLRSYLASVSQDRTCIWTQDNEQGPWKTKLLKEEFKPDVLWRASWSLSGNVLALSGGDNKVTLWKEN 284 (297)
Q Consensus    211 ---s---l-las-s-Dg-i-iw-----l-----d-i-iw----- 284 (297)
                  +|+|++ +|++++.||+|++|++... ..+.+. +.++++++|+|++++|++++|+.+.|+.
T Consensus    263 ---p-----l-s-s-Dg-i-vwd-----p-----i-v----- 327 (327)
T 4j87_A       263 LFHPHQ--ELILSASEDKTIRVWDLNRRT--AVQTFRR--ANDRFWFITVHPKLNLFAPAAH--DSGVVMVFKLE 327 (327)
T ss_dssp      EECSSS--SEEEEEETTSCEEEETTTCC--EEEEEECC--SSCEEEEEECSSSSCEEEEE--TTEEEEEEE
T ss_pred      ECCCC--CEEEEEECcCceEEEECCCC--hhhhhh--cCCcEEEEEECCcEEEEEc--CcEEEEECc
```

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```
Q ss_pred      EEcCcCeEEEEEEccCccCCcEIEEEECCEEEEEeCCcChhhhhhccccceEEECCCcccC
Q Fri_Mar_04_23: 82 WKEENGWSQTIAVHAVHSASVSQWAPHEYGPLLLVASDGGKSVVFEEKNGTSPITIDAHAI G VNSASAWPATIEED 161 (297)
Q Consensus    82 wd-----d-i-1-----l-----t-----v-----w-----y-----z----- 161 (297)
                |+++++ . ....+. |...|+++|. +. +.+++++. |+.|++|+|.... ..+++++.++.+.+.+.|. |..
T Consensus    124 Wd-----h-v-n-v-p-----s-g-s-d-v-wld-----v-----w----- 196 (301)
```


[illegible]







T Consensus	121	~~~~v~v~spdg~lasgs~d~i~iwd~-----h~v~l~p~-----l~s~s~D~v~iwd~--	196 (393)
T 1erj_A	121	SSDLYIRSVCFSPDGKFLATGADRLRIWI--ENRKIVMILQGHEQDIYSLDYFPS--GDKLVSGSGDRTVRIWDLRT	196 (393)
T ss_dssp		CCCCBEEEEECTTSSEEEEETTSCEEEET--TTTEEEEECCSSCEEEEEECTT--SSEEEEEETTSEEEEETTT	
T ss_pred		CCcCeEEEEEECCCCCEEEEECCcCEEEEECC--CCcCEEEEECCCCCEEEEECC--CCEEEECCCCCEEEEECC	
Q ss_pred		CeEEEEEEcccccCccCEEEEECC--ccCcCEEEEECCCCCEEEEEccCCcchhhhhh----hccceeeEEEECCcccc	
Q Fri_Mar_04_23:	87	GRWSQIAVHAVHSASVNSVQWAP--HEYGPLLLVASSDGKVSVVEFKENGTSPIIID--AAHAGVNSASWAPATIEE	160 (297)
Q Consensus	87	~~~~v~v~l~p~-----l~s~s~D~v~iwd~--	160 (297)
T Consensus	197	~~~~v~v~l~p~-----l~s~s~D~v~iwd~--	268 (393)
T 1erj_A	197	G---QCSLTLSIEDGVTTAVSPGD--GKYIAAGSLDRAVRVWDSSETGFLVERLDSENESGTGHKDSVYSVVFTRDG--	268 (393)
T ss_dssp		T---EEEEEECCSSCEEEEEECTT--CCEEEEETTSCEEEEEETTCCEEEEECC-----CCSSCEEEEEECTT---	
T ss_pred		C---eEEEEECcCCcCEEEEECC--CCEEEECCcCEEEEECCCCCEEEccccccCCCCCEEEEECCCC--	
Q ss_pred		ccccCCccccEEEEECcCeEEEEEECCc-----eeEEEEECcCCcCeEEEECCCCCCCCCEEEEECCcEE	
Q Fri_Mar_04_23:	161	DGEHNGTKESRKFTVGGADNLVKIKYNSDAQ-----TVVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCI	232 (297)
Q Consensus	161	~~~~l~t~g~d~i~iwd~-----h~v~l~p~-----l~s~s~D~v~iwd~--	232 (297)
T Consensus	269	~~~~l~s~s~D~v~iwd~-----h~v~l~p~-----l~s~s~D~v~iwd~--	335 (393)
T 1erj_A	269	-----QSVVSGSLDRSVKLVNLQANNNKSDSKTPNSGTCEVTYIGHKDFVLSVATQND--EYILSGSKDRGV	335 (393)
T ss_dssp		-----SEEEETTSCEEEEECC-----CEEEEECCSSCEEEEECCGGG--CEEEETTSSEEE	
T ss_pred		-----CEEEEECCcCEEEEECCCCccccccccCCCCCeEEEEECcCCcCEEEEECCCC--CEEEEECCcCEEE	
Q ss_pred		EEECcCCCCceEEEEccccCCcCEEEEEEC-----CCCCEEEECCCCCEEEEE	
Q Fri_Mar_04_23:	233	IWTQDNQGPWKKTLLKEKFPDVLWRASWS-----LSGNVLALSGGDNKVTLWKE	283 (297)
Q Consensus	233	iw-----l~t~g~d~i~iwd~-----h~v~l~p~-----l~s~s~D~v~iwd~--	283 (297)
T Consensus	336	~~~~l~g~H~v~v~p~-----lasgs~Dg~i~iwd~--	387 (393)
T 1erj_A	336	FDWKKSNG--PLMLLQG--HRNSVISAVANGSSLGPEYNVATGSGDKAKRIWKY	387 (393)
T ss_dssp		EEETTTC--EEEEEC--CSCCEEEEEECSSCTTCTTEEEEEETTSCEEEEE	
T ss_pred		EECCCCc--EEEEEC--CCCCEEEEECcCCCCCCCCCEEEEECCCCCEEEcc	
       			
<input type="checkbox"/> 2pbi_B Guanine nucleotide-binding protein subunit beta 5; helix WRAP, RGS domain, DEP domain, DHEX domain, GGL domain, propeller, signaling protein; 1.95A {Mus musculus} SCOP: b.69.4.0 Probab=100.00 E-value=2.1e-37 Score=263.43 Aligned_cols=252 Identities=17% Similarity=0.239 Sum_probs=0.0			
Q ss_pred		ceEecCCcCeeEEEECCCCCEEEEECCcCEEEEEccCCc-----	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLDDYQKRLATCSSDKTKIFVEGETHKL	45 (297)
Q Consensus	2	~~~~h~v~v~l~p~-----l~s~s~D~v~iwd~--	45 (297)
T Consensus	57	~~~~l~g~H~v~v~p~-----lasgs~Dg~i~iwd~--	136 (354)
T 2pbi_B	57	RRTLKGHGKVLKMDWCKDKRRIVSSSDGKVIWVDSFTTKEHAVTMPTWVMACAYAPSGCAIACGGLDNKCSVPLT	136 (354)
T ss_dssp		EEEECCSSCEEEEECTTSSEEEEETTSCEEEEEETTCCEEEEECCSSCCCEEEETTSCEEEEEETTSCEEEEECC	
T ss_pred		eeEecCCCCcEEEEEECCCCCEEEEECCcCEEEEECCCCccccceEecCceEEEECCCCCEEEccccCCEEEEECC	
Q ss_pred		-----eEEecCCCCCEEEEECCcCCcCEEEEECCcCEEEEEccCCcCEEEEEEEcccccCccCEEEEECCcCCcE	
Q Fri_Mar_04_23:	46	-----IDTLTGHEGPVWRVDWAPKFGTILASCSYDGKVLWKKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPL	115 (297)
Q Consensus	46	~~~~h~v~v~l~p~-----l~s~s~D~v~iwd~--	115 (297)
T Consensus	137	~~~~h~v~v~l~p~-----l~s~s~D~v~iwd~--	212 (354)
T 2pbi_B	137	FDKNENMAAKKSVAMHTNYLSACSFTNS--DMQILTASDGTALWDVSESGQ--LLQSFPHGADVLCLDLAPSETGNT	212 (354)
T ss_dssp		CCTTCCSGGGCEEEEECCSSCEEEEECCSS--SEEEEEETTSCEEEEEETTC--EEEEEECCSSCEEEEECCSSCCCE	
T ss_pred		ccccccccccceEeeccCceEEEEEECC--CEEEEECCcCEEEEEccCc--EEEEECcCCcCEEEEEccCCCCC	
Q ss_pred		EEEEECCEEEEEEECCcCchhhhhhhcccccEEEEECCccccccccCCcCEEEEECCcCEEEEEEECCcCceE	
Q Fri_Mar_04_23:	116	LLVASSDGKVSVEFKENGTSPIIIDAAHAGVNSASWAPATIEEDGEHNGTKESRKFTVGGADNLVKIKYNSDAQTYV	195 (297)
Q Consensus	116	~~~~l~t~g~d~i~iwd~-----h~v~l~p~-----l~s~s~D~v~iwd~--	195 (297)
T Consensus	213	~~~~l~sg~d~v~iwd~-----h~v~v~p~-----l~s~s~D~v~iwd~--	275 (354)
T 2pbi_B	213	FVSGGCDKKAMVWDMRSGQ--CVQAFETHESDVSVRYYPSPG-----DAFASGSDATCRLYDLRADREV--	275 (354)
T ss_dssp		EEEEETTSCEEEEEETTC--EEEEECSSCEEEEEECTTSS-----SEEEETTSCEEEEEETTTTEE--	
T ss_pred		EEEECCCCCEEEEECCCC--EeEEECcCCcCEEEEECCc-----CEEEEECCcCEEEEECCCCce--	
Q ss_pred		EEEEccCCCCeEEEECCCCCCCCCEEEEECCcCEEEEEccCCCCceEEECccccCCcEEEEEECCCCCEEEEECC	
Q Fri_Mar_04_23:	196	LESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIWTQDNQGPWKKTLLKEKFPDVLWRASWSLSGNVLALSGGD	275 (297)
Q Consensus	196	~~~~h~v~l~p~-----las~s~Dg~i~iwd~-----i~iwd~--	275 (297)
T Consensus	276	~~~~s~g~d~i~iwd~-----h~v~v~p~-----l~s~s~D~v~iwd~--	347 (354)
T 2pbi_B	276	AIYSKESIIFGASSVDVLSG--RLLFAGVNDYTNVWDVLKGS--RVSILFG--HENKVSITLVRSDGTAFCSGSD	347 (354)
T ss_dssp		EEECCTTCCSCEEEEECTTSS--SEEEETTSCEEEEEETTC--EEEEEC--CSCCEEEEEECTTSSCEEEETT	
T ss_pred		eEecCCCCcEEEECCCC--CEEEEECCcCEEEEECCCC--EEEEEC--CCcCeEEEECCCCCEEEEECC	
Q ss_pred		CEEEEE	
Q Fri_Mar_04_23:	276	NKVTLWK	282 (297)
Q Consensus	276	~i~iwd~	282 (297)
T Consensus	348	~i~iwd~	354 (354)
T 2pbi_B	348	HTLRVWA	354 (354)
T ss_dssp		EEEEEC	
T ss_pred		CEEEEE	







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Q Consensus	80	-iwd-----v-----l-----d-i-i-----v----	151 (297)
T Consensus	211	++ +++++ .+ ..+.++++ + + +.+++++. +. +++.+++	
T 4wjs_A	211	-iwd--tg-----l-gh--V--l--p-----l-s-s-Dg-i-iwd-----l-h--V--v	284 (515)
T ss_dssp	211	RLWDPKSGQ--CLGDALRGHSKWTLSLWEPHILVLPKS--KPRLASSSKDGTIKIWIWTSVR--VCQYTMSTGHTNSVSCV	284 (515)
T ss_pred		EEECTTTCC--BCSSCBCSSSEEEEECCGGGSCSTTS--CCCEEEETTSCEEEETTTT--EEEECCCCSSCEEEE	
		EEEECCCC--CccceCCcCeEEEEccccccCCC--CcEEEEcCCCEEEEECCCC--eEEEEcCCCCEEEE	
Q ss_pred		EECCCCccccccccCCcccEEEEeCCcEEEEeCC-----	
Q Fri_Mar_04_23:	152	SWAPATIEEDGEHNGTKESRKFTGGADNLVKIKWYNSD--	190 (297)
Q Consensus	152	l-tg--d-i-wd-----	190 (297)
T Consensus	285	+ +++++ .+++ +. ++ ++ ++..	
T 4wjs_A	285	-l-s-s-D-i-vwd-----v--l--s-d-----	350 (515)
T ss_dssp	285	KWGGQ--LLYSGSHDRTVRVWIDNSQRCINILKSHAHWNHLSLTDYALRIGAFDHTGKKPSTPE	350 (515)
T ss_pred		EECTTS-----EEEEETTSCEEEEGGGTTEEEEEECCSSCEEEEESSHHHHHTTCCTTCCCCSSHH	
		EECCC-----eEEEEcCCeEEEECCCCcEeEccCCcEeEEEEcCCCCEEEEcCCCCcCH	
Q ss_pred		-----CceEEEEcccccEeEEEECCCCCCCCEEEEeCCCEe	
Q Fri_Mar_04_23:	191	-----AQTVLESTLEGHSDVWRDVAWSPTVLLRSYLASVQDRTCI	232 (297)
Q Consensus	191	-----h--v--l--s--D--i--v--p-----las-s-Dg-i-	232 (297)
T Consensus	351	-----l-s-s-d-i-lwd-----h--v--fspd--lasgs-Dg-i-	427 (515)
T 4wjs_A	351	EAQKKALENYKICKKNGNSEEMMYTASDDYTMFLWNPDKSTKPIARMTGHQKLVNHWAFSPDG--RYIVSASFDSIK	427 (515)
T ss_dssp		HHHHHHHHHHHHBSSSBCEEEEEETTSCEEEECTTSCSSCEEECCSSCEEEEECTTS--SEEEEEETTSC	
T ss_pred		HHHHHHhhhhheccccCCcCeEEEEcCCeEEEEccccCCeEEEEcCCcCEEEEECCCC--CEEEEEcCCCEe	
Q ss_pred		EEEcCCCCceEEEcccccCCeEEEEEECCCCEEEEeCCCCEEEE	
Q Fri_Mar_04_23:	233	IWTQDNEQGPWKTKLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK	282 (297)
Q Consensus	233	iw-----i-----l-----d-i-iw-----	282 (297)
T Consensus	428	++.+ +++ + ++++ ++++ .++ ++ +	472 (515)
T 4wjs_A	428	lwd-----h--V--v--spdg--l-s-s-D--v-vwd	472 (515)
T ss_dssp	428	LWDGRDGK--FISTFRG--HVASVYQVAWSSDCRLLVSCSKDTTLKVWD	472 (515)
T ss_pred		EEETTTC--EEEECC--CSSCEEEEECTTSEEEEEETTSEEEEE	
		EECCCC--EEEEcC--CcCeEEEEEECCCCEEEEcCCeEEEE	
<div>No 35</div> <div></div> <div><input type="checkbox"/> 4wjs_A RSA4; ribosome assembly, ribosome biogenesis, biosynthetic protein; 1.80A {Chaetomium thermophilum} Probab=100.00 E-value=1.3e-36 Score=269.07 Aligned_cols=250 Identities=27% Similarity=0.427 Sum_probs=0.0</div>			
Q ss_pred		ceEecCCcCeeEEEEcCCCCEEEEeCCcEEEEccCCcceeEEccCCCCEEEEeC---CccCEEEEEcCCC	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLGYGKRILATCSSDKYIKIFVEGETHKLIDTLTGHEGPVWRVDWAH---PKFGTLLASCSDYG	77 (297)
Q Consensus	2	-----h--v-----g--l-t-s-d--v-lwd-----h--v-----l-s-s-D--	77 (297)
T Consensus	150	+.+.+ ... ++++ + ++ ++++.++ ++ ...+.+.++++ ++ ..+.+ ++++. +	
T 4wjs_A	150	---l-gh--V--v--spdg--las-s-D--i-iwd-----h--v--l--p-----l-s-s-d--	228 (485)
T ss_dssp	150	KFTLKGTGWVLGVSWSPDGKYLATCSMDTTVRVWVPESGK-QVNQEFRGHAKWVLALAWGPYHLWRDGTARLASAKDK	228 (485)
T ss_pred		EEEECCSSCEEEEECTTSSCEEEEEETTSCEEEETTTTT-ECSSCBCSSCEEEEECCGGGCBTBCEEEEETT	
		ceEeCCCCCEEEEECCCCEEEEcCCeEEEECCCCc-ccccccCCcCeEEEEeccccCCCCCEEEEEcCC	
Q ss_pred		eEEEEccCCeEEEEeccccCccEEEEeCCcCCcEEEEECCEEEEEeC-----	
Q Fri_Mar_04_23:	78	KVLWKKEENGWNSQIAVHAVHSASVNSVQWAPHYGPLLLVASSDGVSVVVEFKE-----	132 (297)
Q Consensus	78	-i-iwd-----v-----l-----d-i-i-----	132 (297)
T Consensus	229	+ ++ + +++++ ..+.+++ ++ ..+++++. +. ++v-----v--d--	303 (485)
T 4wjs_A	229	-v-iwd-----l-h--v--v-----l-s-s-d--i-vwd-----s-d--	303 (485)
T ss_dssp	229	TVRIWLVTGR--TEHVLSGHKGSVSVKGG--TDLLYTGSHDRSVRVWDVAVKGLVHNFTHAGHWVNHIALSSDHVL	
T ss_pred		CEEEEETTTT--EEEECCSSCEEEEECT--TSEEEEEETTSCEEEETTTTTSEEEEECCSSCEEEEECTT	
		CEEEEECCCC--eeEecCCCCcEEEECC--CCeEEEEcCCcEEEECCCCeEEEEcCCcEeEEECcCCeE	
Q ss_pred		-----CCcchhhhhhhccccEEEECCCC	
Q Fri_Mar_04_23:	133	-----NGTTSPIITIDAHAGVNSASWAPA	156 (297)
Q Consensus	133	-----v-----	156 (297)
T Consensus	304	-----l-s-s-d--i-wd-----h--v--v--spd	383 (485)
T 4wjs_A	304	RTAYHDHTKEVPGTEERRAKAKERFEKAAIKGKVAERLVSASDDFTMYLWDPNTNGSKPVARLLGHQNKVNHVQFSPD	383 (485)
T ss_dssp		HTTCCCTCCCCSSHHHHHHHHHHHHHEETTFEECEEEEECHHHHTTSCSEEECCSSCEEEEECTT	
T ss_pred		EEEcCCccccCchhhHHHHhhhhhhccCccccEEEEeCCCEEEEEcCCCCCccceEcCCCCEEEECCCC	
Q ss_pred		ccccccccCCcccEEEEeCCcEEEEEECCCCceEEEEeCCCCeEEEECCCCCCCCEEEEeCCcEEEEeC	
Q Fri_Mar_04_23:	157	TIEEDGEHNGTKESRKFTGGADNLVKIKWYNSDAQTYVLESTLEGHSDVWRDVAWSPTVLLRSYLASVQDRTCIWTQ	236 (297)
Q Consensus	157	l-tg--d-i-wd-----h--v--l--s--D--i--w--	236 (297)
T Consensus	384	+ .+ ++ +. +. ++ ...++ ++.+.+ .+. +++ ++ ++ ++++. ++ ++ ++	443 (485)
T 4wjs_A	384	g-----las-s-d--i-lwd-----l-h--v--spdg-----l-s-s-D--i-vwd-----	443 (485)
T ss_dssp	384	G-----TLIASAGWNSDKLWNARDGK--FIKNLRGHVAPVYQCAWSADS--RLVVTGSKDCTLKVVNV	
T ss_pred		S-----SEEEEEETTSCEEEETTTC--EEEECCSSCEEEEECTTS--SEEEEEETTSCEEEE	
		C-----CEEEEECCCCEEEECCCC--EEEECCCCCEEEEECCCC--CEEEEECCCCCEEEEE	
Q ss_pred		cCCCCeEEEEccccCCcEEEEEECCCCEEEEcCCCCEEEE	
Q Fri_Mar_04_23:	237	DNEQGPWKTKLLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK	282 (297)
Q Consensus	237	-----i-----l-----d-i-iw-----	282 (297)
T Consensus	444	+... ..+.+ +++ + ++ ++++. .++ +	484 (485)
T 4wjs_A	444	---l--h--v--v--spdg--l-s--D--i--w--	484 (485)
T ss_dssp	444	RTGK--LAMDLPG--HEDEVYAVDWAADGELVASGGKDAVRTWR	484 (485)
T ss_pred		TTTE--EEEECC--CSSCEEEEECTTSSEEEEETTCEEEEE	
		CCCc--EeEecC--CCcEEEEEECCCCEEEEcCCCCEEcC	

No 37                        

No 44

[illegible]

Q ss_pred	EEccCCEEEEEEcccccCccEEEEEECCccCCcEEEEEECCCEEEEEEccCCC--cchhhhhhhcccccEEEEECCCCcc	
Q Fri_Mar_04_23:	82 WEENGRWSQIAVHAVSHVASVNSQVAPHEYGPLLLVASSDGKVSIVVEFKENG--TTSPITIIDAHAIQVNSASWAPATIE	159 (297)
Q Consensus	82 wd-----v-----d-i-i-----v----- ++. +.+. +++ + +. ++ +. +. ++ +... ..+. +++ + ++.	159 (297)
T Consensus	214 wd-----h-v-1-s-d-----lasgs-d-v-1wd-----h-v-v-p-----	289 (420)
T 4gga_A	214 HDVRVAE--HHVATLSGHSQVCGLRWAPD--GRHLASGGNDNLNVWPSAPGEGGWVPLQTFTQHQAQVAVAWCPWQS--	289 (420)
T ss_dssp	EEFTSSS--EEEEEECCSSCEEEEECTT--SSEEEEFTTSCEEEESSCCSSCCSCSEEECCSSCEEEEECTTCT	
T ss_pred	EECCCCcc-EEEECCCCCCEEEEECCCC--CCEEEEEECCC-EEEEEECCCCCCCCcEEEcCCcEEEEECCCCC-	

Q ss_pred		ccccccCccceEEEEe--CCeEEEEeCCcCeEEEEecccCCcCeEEEECCCCCCCCEEEEe--CCeEEEE		
Q Fri_Mar_04_23:	160	EDGEHNGTKSRKFTGG--ADNLVWKVYNSDAQTVYLESTLEGHGSWDVRVAVSPFTLLRSYLASVS--QDRTCLTWT	235	(297)
Q Consensus	160	l-tg--d-i-wd-y--h-v--s--t--las-s--Q-d-i-iw-	235	(297)
		.++ + . + + +.+ .+++.+ . . ++ ++ . ++++ . + ++		
T Consensus	290	-----lasg-sg--d-i-iwd-----v-l-s-----l-g-d-i-iwd	350	(420)
T 4gga_A	290	-----NVLATGGGTSDRHIRIWNVCSG-----ACLSAVDAHS-QVCSILWSPHY--KELISGHGFAQNQLVIWK	350	(420)
T ss_dssp		-----TEEEEECTTTCEEEETTTT-----EEEEEECCSS-CEEEEEETTT-----TEEEECTTTCEEEEE		
T ss_pred		-----CEEEEECCCCCEEEEECCCC--CEEEeCCCC--CEEEEECCCC--CEEEEEeCCCCCEEEEE		

```

Q ss_pred                ccCCCCcEEEEEccccCCcEEEEEECCCCEEEEcCCCCEEEE
Q Fri_Mar_04_23:       236 QDNQGQGWKTKLKEKFPDVLNRASWSLSGNVLALSGGDNKVTLWK 282 (297)
Q Consensus             236 -----v-----d-i-w----- 282 (297)
                             +....  ....+.. |...|++|+|++|++++|++|++|+
T Consensus             351 -----H-----spdg-l-s-S-D-v-iW 392 (420)
T 4gga_A                 351 YPTMA-----KVAELKG--HTSRVLSLTMSPDGATVASAAADETLRLWR 392 (420)
T ss_dssp                TTTC-----EEEECC--CSSCEEEEEETTSCEEEETTTTEEEEC
T ss_pred                CCCCc-----EEEECC--CcCcEEEEEECCCCEEEEcCCCCEEEE

```

No 45

[illegible][illegible]

Q ss_pred ccccccCccccc-EEEEeCCcEEEEeCCCCeEEEEecccCCcEeEEEECC-CCCCCEEEEEcCCcEEEEEcc
Q Fri_Mar_04_23: 160 EDGEHNGTKESR-KFVTGADNLLVKYIKNSDAQTYVLESTLEHSDVVRDVLAWSP-TVLRSYLASVSDQRTCTIITWDQ 237 (297)
Q Consensus 160 l-tq-d-l-l-wd h-v-l-s-las-s-Dq-i-iw- 237 (297)

			. +++++ +. + +++.+.+.+.+. ++++ + ++ .+ ++++ .+. ++ ++	
T Consensus	217	-----l-s-----i-ibd-----v-----sp-g-----l-s-----d-i-vwd-----		281 (383)
T 3ei3_B	217	-----DWLMTSSVDATVKLWDLRNKDKNSYIAEM-PHEKPVNAAYPNPTDS---TKLLTTDORNEIRVYSSY		281 (383)
T ss_dssp		-----TTEEEEEETTSEEEEEGGGCCCTTCEEEEE-ECSSCEEEEEECTTTS---CEEEEESSSEEEEEETT		
T ss_pred		-----CcEEEEeCCeEEEEeccccCCCCcEEEc-CCCCEEEEeCCCC---CEEEEEcCCCcEEEEEC		
Q ss_pred		CCCCcEEEE-----EccccCCcEEEEEEEC		
Q Fri_Mar_04_23:	238	NEQGPWKKT-----LLKEEFPPDVLWRASWS		263 (297)
Q Consensus	238	-----i-----		263 (297)
			
T Consensus	282	-----p-----s-d-----s-d-----i-ibd-----v-----s		361 (383)
T 3ei3_B	282	DWSKPDQIIITHPRQFQHLTPIKATWHPMYDLIVAGRPDDQLLNDKRTIDYDANSGLVHQLRDPNAAGISLNKFS		361 (383)
T ss_dssp		BTTSCEEEECBCCCTTSCCCCEECSSSEEEECBCCTTCTTCCCEEEEEETTCCEEEEEBTTBCSCCEEEEC		
T ss_pred		CCCcccccEEEEccccccccccEeEEEECCCCcEEEEccCCccccccCCCcEEEECCCCcEEEEeCCCCCCcEEEEEEEC		
Q ss_pred		CCCCEEEEcCCCCEEEEEC		
Q Fri_Mar_04_23:	264	LSGNVLALSGGDNKVTLWKEN	284 (297)	
Q Consensus	264	-----l-----d-----i-iw----	284 (297)	
		+ ++ ++++ +. ++ +..		
T Consensus	362	pdg--l-s-s-d--i-iw----	381 (383)	
T 3ei3_B	362	PTGDVLASGM-GFNILITWNR	381 (383)	
T ss_dssp		TTSSEEEEEE-TTEEEEEEC		
T ss_pred		CCCcEEEEc-CCeEEEEEC		

No 46                               

☐ >4wjs_A_RSA4; ribosome assembly, ribosome biogenesis, biosynthetic protein; 1.80A {Chaetomium thermophilum}
 Probab=100.00 E-value=6.4e-36 Score=264.69 Aligned cols=253 Identities=24% Similarity=0.414 Sum_probs=0.0

[illegible]

```
Q ss_pred      EEEEEcCcCEEEEEEEccCcCcEEEEEECC---ccCcCEEEEECCCEEEEEecCCcChhhhhhhcccceEEEECC
Q Fri_Mar_04_23: 80 LIWKEENGWRGSQIAVHAVHSASVSNVQWAP---HEYGPLLLVASSDGKVSVFKEKNGTTSPIITIDAHAIQVNSASWAP 155 (297)
Q Consensus    80 |wd-----v-----l-d-i-i-----v-----|
                  ++|+|++++...+...+|...|++|+|...+.+++++|+|++|+|...+...+|...+...+|++
T Consensus    182 |wd-----h-v-l-p-----l-s-d-v-wd-----l-h-v-----| 258 (485)
T 4ws_A        182 RVWDPEESGK-QVNQEFRGHAKWVLALAWQYHLHLDGTARLASASKDCTVRIWLVTG--RTEHVLSGHKGSVCVKWGG 258 (485)
T ss_dssp      EEEEETTTT--ECSSCBCCSSCEEEEEECGGCBTTBCEEEETTCCEEEETTTT---EEEEEECCSSSCEEEEBCT
T ss_pred      EEEEECCCCc-----CCCCCCCCCEEEEECCCCCCCCCCCCCEEEEECCCC---EEEECCCCCEEEEECC
```

	Q	ss_pred	CcccccccccCccceEEEEeCCcEEEEEKCCCeeE-----	
	Q	Fri_Mar_04_23:	A TIEEDGEHNGTKESRKFTGGADNLVKIKYNSDAQTYVL-	196 (297)
	Q	Consensus	156 -----l-tg--d-~----wd----- . ..+++ +. .++ ...+....+	196 (297)
	T	Consensus	259 ~~~~~l-s-s-d-.i-vvd-----v-----s-d-----	324 (485)
	T	4ws_A	259 T-----DLITGSHDRSVRVWDAVKGTLVNHFNTAHGHWNHIALSSDHVLRATAYHDHTKEVPGTBEERRAK	324 (485)
	T	ss_dssp	T-----SEEEEETTCSEEEEETTTEEEEECSSCSSEEETTTHHHHHHTTCTCTCCCCSHHHHHHH	
	T	ss_pred	C-----CEEEEECCCCCEEEEECCCCCeEEEEEECcCEECEEEEEECcCcccccchhhhhhHH	

```
Q ss_pred -----EEFccCCcEeEEEECCCCCCCfEEEEEcCCcEEEEEc
Q Fri_Mar_04_23: 197 -----ESTLGHSDDWYDVAWSPTVLLRSYLASVSQDRCTCIWTQ      236 (297)
Q Consensus 197 ~~~~~h~v~l~s~~~~las-s-Dg-i-!w~      236 (297)
                                     ...+ + |...|+ ++|+ ++ .+ ||++|. |+ ++|+.
T Consensus 325 ~~~~~l-s-s-d~-i-wd~~~~h-v-v-spdg~~~~las-s-d~-i-lwd~~~~      401 (485)
T 4ws_A 325 AKERFEKAAIKIGKVAERLVSADDFTMYLWDPTNNGSKPVARLLGHQNKVNHVFSPDG---TLIASAGWDNSTKLWNA      401 (485)
T ss_dssp HHHHHHHHHEETTECECEEEEEETTSECEEECHHHHTTSCEECECCSSCEEEEEECTT---SEEEETTSCEEEET
T ss_pred HHHhhhhhcccCccccCECEEEEECECEEEEEcCCCCCcceeEeCCCCCEEEEECCCS-----EEEEECcCCCEEEEC
```

```





Q ss_pred      cCCCCcEEEEcccccCCcEEEEECCCCEEEEEcCCCCEEEEE
Q Fri_Mar_04_23: 237 DNEQGPKWTKLLKEKFPDVLWRASWSLGSNVLALSGGDINKVTLWK 282 (297)
Q Consensus    237 .....-i-iw-.....-l-s-S-D-i-vwd 282 (297)
                ....+...|...|++++|++++|++++|++++|+
T Consensus    402 .....-l-h-v-spdl-l-s-S-D-i-vwd 442 (485)
T 4wjs_A       402 RDGK--FIKNLRG--HVAVPVYQCAWSADSRLLVVTGSKDCTLKVWN 442 (485)
T ss_dssp      TTCC--EEEEEC--CSSCEEEETCTSSEEEEETTCSEEEEE
T ss pred      CCCc--CCCCEEc--CCCCEEEEECCCCEEEEEcCCcEEEEE





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No 47                               

☐ **>xyh_A** Kinetochore protein MIS16; centromere, CENP-A, MIS18 complex, histone; 2.30A {Schizosaccharomyces japonicus}
 Probab=100.00 E-value=1.9e-36 Score=264.20 Aligned cols=257 Identities=23% Similarity=0.340 Sum probs=0.0

Q ss_pred ceEecCCCcEEEECC-CCCEEEEeCCCCEEEEccCC-----cccEEeeCcCCCCEEEEeCCcCC-EEEE
Q Fri_Mar_04_23: 2 VVIANAHNELHLDVLDY-YGKRRLATCSDSKTKIFVEGE-----THKILDTLGTGHGPVWRVDWAHPKFGT-ILASC 73 (297)
Q Consensus 2 -v--v---l-t-s-d-v-l-wd-----wv-----l-s- 73 (297)














T Consensus	124	+...+ ... ++++ + ++++ + +++ + ++ ++...+ ... ++++ +++ +. + ++	
T 4xyh_A	124	IVQKIHHGEGDVNKARFMPQNPDIATLGLNGGYIFDLNLYREQPIVQTGHQACLRHHTSEGFGLGNWNT--QSGTTLATG	201 (430)
T ss_dssp		EEEEEESSCCCEEEETTEEEEEEECGGCGEEEEEggcgsscsEETTCCSEEECCSSCCCEEEECSS--STTEEEFE	201 (430)
T ss_pred		EEEECCCCeEEEEcCCCCEEEECCCCeEEEECCCCccccccccCCCCEEeCCCCEEEEECcCC--CCCEEEE	
Q ss_pred		cCCcEEEEEEccCCE-----EEEEecccCccEEEEECcCccCCcEEEEECCEEEEEEEcCCcCc--hhhhhhc	
Q Fri_Mar_04_23:	74	SYDGKVLWKEENGW-----SQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKGVSVVEFKENGT--SPIITIDAH	144 (297)
Q Consensus	74	s-D-i-ibd-----h-v-----l-----d-i-i-----	144 (297)
T Consensus	202	+. ++ ++ + .++.. ..+...+ ... +++ + ++ ..+++++. + ++ + +... ..+..	
T 4xyh_A	202	TEDTSCVWDIKGKSLSEKSIDVAPSVVYHRTAVVNDLQFHLQH--EALLTSVSDDCQLQIHTRLPSSSSASQCVKAH	280 (430)
T ss_dssp		CTTSCEEEEECTTCCCBTTBCEEECCSEEECCSSCEEEEECTTC--TTEEEETTSTEEEEETTCTTSCSEEEEC	280 (430)
T ss_pred		cCCcEEEEEECCCCccccCCCCccccceeeCCCCcEEeEEECcCC--CEEEEEcCCcEEEEEEcCCCCCCcEEecC	
Q ss_pred		ccceEEEECCCCccccccccCccceE-EEEEcCcEEEEEECcCCcEeEEEEECcCCcEeEEEECCCCCCCCEE	
Q Fri_Mar_04_23:	145	AIGVNSASWAPATIEEDGHNHGTESRK--FVTGGADNLVYKIWNDSDAQTYVLESTLEGHSDWVRVAVASPTVLLRSYLA	223 (297)
Q Consensus	145	...-v-----h-v-----l-s-----la	223 (297)
T Consensus	281	...+...+ ++ .. ++ + .++ + +... ++...+ ... +++ + ++ ..+ +	
T 4xyh_A	281	BQPVNGVAFNPFN-----DYLLATASADHTVALWDLRLNQ--RLHTLEGHDEYVNVQWSPHD--EPILV	342 (430)
T ss_dssp		SSCEEEECSSC-----TTEEEETTSCSEEEETTCTTS--CSEEECCSSCEEEECSSC--TTEEE	342 (430)
T ss_pred		CCcEEEEECcCC-----CcEEEEECcCCcEEEEECcCCcC--CcEEeCCCCEEEEECcCC--CEEE	
Q ss_pred		EEcCCcEEEEECcC-----CCcEeEEeccccCCcEeEEEECCCCC-EEEECCCCCEEEEEEC	
Q Fri_Mar_04_23:	224	SVSQDRTCNLTWQDN-----EGGPWKTLLEKEKFPDVLWRASWSLSGN--VLALSGGDNKVTLWKEN	284 (297)
Q Consensus	224	s-s-Dg-i-ibd-----l-----i-i-ibd-----	284 (297)
T Consensus	343	+++ + .++ +..+... ... +++ + +++ + +++ + .++ +..	
T 4xyh_A	343	TSSSTRRVCVWDLISKIEEQTVEDSEDGAP--LMFMGG--HTNRVSDLSWNPNNKWWLASLADDNLQIWSPS	413 (430)
T ss_dssp		EEETTSCSEEEEGGGTCCCHHHHTSCCTT--EEEEEC--CSCSEEEECSSSTTCSEEEETTSEEEEEEC	413 (430)
T ss_pred		EEcCCcEEEEECcCccccccccccCcE---eEEeCC--cCCcEEEEECcCCcEEEEEEcCCcEEEEEC	
   			
<input type="checkbox"/> >4j0w_A U3 small nucleolar RNA-interacting protein 2; beta-propeller, WD domain, RNA binding protein, preribosome; 1.70A {Homo sapiens} PDB: 4jxm_A Probab=100.00 E-value=5.6e-36 Score=253.65 Aligned_cols=259 Identities=17% Similarity=0.196 Sum_probs=0.0			
Q ss_pred		ecCCcCeeEEEEcCCCCEEEEECcCCcEEEEECcCccceEEecCCCEEEEEcCCcCCEEEEECcCCcEEEEEC	
Q Fri_Mar_04_23:	5	ANAHNELIHDAVLDYGRKRLATCSSDKTIKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVLWKE	84 (297)
Q Consensus	5	~-h~-v~-l~-t~-s~-d~-v~-lwd~-h~-v~-l~-s~-d~-i~-ibd~-	84 (297)
T Consensus	63	+...+ ... ++++ + ++ ++++ ++ + + +.+++..+...+ ... +++ +++ ++.++++ ++ ++ +	
T 4j0w_A	63	~gh~-v~-s~-dg~-lasgs~-i~-ibd~-h~-v~-l~-s~-d~-v~-lwd~-	138 (343)
T ss_dssp		PPGHSSHVLCMAISSDGKYLASGDRSKLLIWEA--QSQHLYTFTGHRDAVSGLAFFRRG--THQLYSTSVKVVNV	138 (343)
T ss_pred		CSCSSCEEEECTTSCSEEEETTSCSEEEET--TTTEEEEECCSSCEEEECTT--SSEEEETTSTEEEEEEG	
		CCCCCcEEEEECcCCcCCCCccccccCcE---eEEeCC--cCCcEEEEECcCCcEEEEEEcCCcEEEEEC	
Q ss_pred		cCCcEEEEEEcCccCccEEEEECcCCcCCcEEEEECCEEEEEECcCCcchhhhhhhccccceEEEECCCCcccccc	
Q Fri_Mar_04_23:	85	ENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLLVASSDGKGVSVVEFKENGTTSPIITIDAHATGVNSASWAPATIEEDGEH	164 (297)
Q Consensus	85	++++ .+...+ ...+...+ + +.+++++ + ++ +++... ..+...+ ...+...+ +.	164 (297)
T Consensus	139	-----h~-v~-l~-sg~-d~-i~-wd~-h~-v~-l~-s~-d~-i~-ibd~-	203 (343)
T 4j0w_A	139	AENS--YVETLFGHQDAVAALDALSR--ECVATAGGRDGTVRVWKIPPE--SQLVFYGHGQSIDCIHLINE--	203 (343)
T ss_dssp		GGTE--EEEEECSSCCCEEEECSS--SEEEECBTTCEEEETT--EEEEECSSCEEEEEETT-----	
T ss_pred		CCcC--ceEEeCCCCcEEEEcCC--CEEEEEECcCCcEEEEECcCC--ccEEeCCCCcEEEEECcCC-----	
Q ss_pred		cCCcccEEEEEEcCCcEEEEEEcCCcEeEEEEECcCCcC-----EeEEEECCCCCCCCEEEEEEcCCcEEF	
Q Fri_Mar_04_23:	165	NGTKESRKVFTGGADNLVYKIWNDSDAQTYVLESTLEGHSDW-----VRDVAVASPTVLLRSYLASVSDRTCI	233 (297)
Q Consensus	165	~-l~-tg~-d~-i~-wd~-h~-v-----v~-l~-s-----las~-s~-Dg~-i~-i	233 (297)
T Consensus	204	..+++ + .++ + +... +...+... .. +++ + ++ ..+ +++ ++ +	
T 4j0w_A	204	~-l~-s~-s~-d~-v~-lwd~-v-----v-----lasgs~-d~-v~-l	270 (343)
T ss_dssp		-----EHMVSGADGVALWGLSKKR--PLALQREAHGLRGEPLGEPFVWISSVAALLNT--DLVATGSHSSCVRL	270 (343)
T ss_pred		-----TEEEETTSCSEEEECSSC--CSEETTTCESSTTCCECCCCCEEEECTS--SEEEECSSSEEE	
		-----CEEEECcCCcEEEEECcCCc--cEEehhhhhCCCCccccccccEEeEEcCC--CEEEECcCCcEEF	
Q ss_pred		EEcCCCCcEEEEcCccCccEEEEECcCCcEEEEECcCCcC-----CCCEEEEECCCCcEEeEEccC	
Q Fri_Mar_04_23:	234	WTQDNEQGPWKTLLEKEKFPDVLWRASWSLSGNVLALSG--GDNKVTLWKENLEGKWEPAFVHQ	297 (297)
Q Consensus	234	w-----i-----d~-i~-ibd~-	297 (297)
T Consensus	271	+...+...+... +... +++ + ++ ++++ .+.+++ +...+...+..	
T 4j0w_A	271	W--v--vafspdg~l~-w-----w-----	334 (343)
T ss_dssp		WQCGEGFRQLDLLCDIP--LVGFINSKLFSSSGDFLVAGVGQEHRLGRWWRKEARNSVCIIPLRR	334 (343)
T ss_pred		EEECGGGCCEEEEEE--CCSEEEEEECSSSEEEEEESSTTCSSCCCTTSCSEEEEC--	
		EECCcCchhhhhcCC--CEEEEEEEcCCCEEEEEECcCCcEEeEEccccccccEEEEEC	









   			
<input type="checkbox"/> >3jam_g RACK1; eukaryotic translation initiation, small ribosome subun 43S, translation; 3.46A {Kluyveromyces lactis} PDB: 3j81_g 3j80_g Probab=100.00 E-value=5.9e-35 Score=245.37 Aligned_cols=247 Identities=21% Similarity=0.290 Sum_probs=0.0			
Q ss_pred		ceEEcCCcCeeEEEECCCCEEEEECcCCcEEEEECcCccceEEecCCCCEEEEECcCCcCEEEEECCCCeEEF	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLDYGRKRLATCSSDKTIKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGKVL	81 (297)

☐ >4j5n_D Target of rapamycin complex subunit LST8; helical repeat, kinase, WD40 repeat, protein kinase, raptor, transferase; 3.20A [Homo sapiens] PDB: 4j5p_D* 4j5v_D* 4j5x_D* 4j5t_D* 4j5b_D*
 Probab=100.0 E-value=8.5e-36 Score=250.70 Aligned cols=243 Identities=14% Similarity=0.255 Sum probs=0.0

No 52     

>4j0x_A Ribosomal RNA-processing protein 9; beta-propeller, WD domain, RNA binding protein, preribosome; 2.50A {Saccharomyces cerevisiae}
Probab=100.00 E-value=1.5e-35 Score=259.30 Aligned_cols=266 Identities=15% Similarity=0.131 Sum_probs=0.0

T ss_dssp	TTTCBC-----	-----CCCBCCCC	EEEECTTBS	EEEEECSSS	EEEEEECTSS	EEEEEE	
T ss_pred	cCcccccCccce	EEEC	CCCC	EEEEEE	CCCCccccCCC	ceEEEEe	CCCC
No 53							
<input type="checkbox"/> >5gan_H U4/U6 small nuclear ribonucleoprotein PRP4; snRNP, GTPase, U5 snRNA, PRP8, spliceosom snRNP, BRR2, transcription; HET: GTP; 3.60A {Saccharomyces cerevisiae} PDB: 5gap_H Probab=100.00 E-value=3.3e-36 Score=265.19 Aligned_cols=246 Identities=20% Similarity=0.361 Sum_probs=0.0							
Q ss_pred	cCccCeeEEEEc	CC-CEEEEE	CCCC	EEEE	ccCcc-	-ceEEcc	CCCC
Q Fri_Mar_04_23:	6	NAHNELI	HDVLDY	GKRLAT	CS	DKIKIF	VEGETH
Q Consensus	6	h	v	g	l	t	s
T Consensus	215	h	v	g	l	t	s
T 5gan_H	215	DSHVGK	IGAI	DWHP	SNQMS	CAEDG	LKIN
T ss_dssp							
T ss_pred							
Q ss_pred	E	ccC	Cee	EEEE	c	CC-CEEEEE	CCCC
Q Fri_Mar_04_23:	83	KEENG	RWSQ	IAVHA	VHSAS	VNSVQ	WAPHE
Q Consensus	83	d	i	v	g	l	t
T Consensus	293	d	i	v	g	l	t
T 5gan_H	293	DASTHQ	-ELL	LEQ	HDK	GVS	LSFQ
T ss_dssp							
T ss_pred							
Q ss_pred	c	ccC	Cee	EEEE	c	CC-CEEEEE	CCCC
Q Fri_Mar_04_23:	163	EHNGT	KESRK	FVTGG	ADNL	VKIWK	YNSDA
Q Consensus	163	h	v	g	l	t	s
T Consensus	362	h	v	g	l	t	s
T 5gan_H	362	YQVAT	GGG	DGI	NVD	IRK	DEG
T ss_dssp							
T ss_pred							
Q ss_pred	C	cee	EE	cccc	C	Cee	EEEE
Q Fri_Mar_04_23:	241	GPWKT	LLK	EEK	FPD	VLRAS	WSLS
Q Consensus	241	g	p	w	k	t	l
T Consensus	429	g	p	w	k	t	l
T 5gan_H	429	KMGSL	AG--	HTD	KIIS	LDIS	NNSH
T ss_dssp							
T ss_pred							
No 54							
<input type="checkbox"/> >lgxr_A ESG1, transducin-like enhancer protein 1; transcriptional CO-repressor, WD40, transcription repressor, WD repeat; 1.65A {Homo sapiens} SCOP: b.69.4.1 PDB: 2ce8_A 2ce9_A Probab=100.00 E-value=8.3e-35 Score=244.76 Aligned_cols=241 Identities=16% Similarity=0.251 Sum_probs=0.0							
Q ss_pred	C	Cc	Cee	EEEE	c	CCCC	EEEE
Q Fri_Mar_04_23:	7	AHNEL	IHDV	LDYDG	KRLAT	CS	DKIKIF
Q Consensus	7	h	v	g	l	t	s
T Consensus	95	h	v	g	l	t	s
T lgxr_A	95	NRDNY	IRSK	CLPD	GCTL	IVGGE	ASTL
T ss_dssp							
T ss_pred							
Q ss_pred	C	EE	EEEE	c	CCCC	EEEE	c
Q Fri_Mar_04_23:	87	GRWSQ	IAVHA	VHSAS	VNSVQ	WAPHE	YG
Q Consensus	87	h	v	g	l	t	s
T Consensus	173	h	v	g	l	t	s
T lgxr_A	173	QT--	LVR	QFG	HTD	GAS	CIDIS
T ss_dssp							
T ss_pred							
Q ss_pred	C	cc	Cee	EEEE	c	CCCC	EEEE
Q Fri_Mar_04_23:	167	TKESR	KFVT	GGA	ADNL	VKIWK	YNSDA
Q Consensus	167	h	v	g	l	t	s
T Consensus	237	h	v	g	l	t	s
T lgxr_A	237	EWLAV	GMESS	NV	VLH	VNKP	----
T ss_dssp							
T ss_pred							
Q ss_pred	E	cccc	C	Cee	EEEE	c	CCCC
Q Fri_Mar_04_23:	247	LLKEE	KFPD	VLRAS	WSLS	SGN	VNL
Q Consensus	247	g	p	w	k	t	l
T Consensus	299	g	p	w	k	t	l

Q Consensus	236	-----i-----l-----d-i-iw--	283 (297)
T Consensus	265	-----v-----s-dg--l-sg--dg-i-vw--	315 (319)
T 3frx_A	265	LDPOY---LVDDLRFEPAGYSKAAEPHAYSLAWSADGQTLFAGYTDNVIRVWQV	315 (319)
T ss_dssp		ETTEE---EEEECCCCCTCCGGGCCCEEEECTTSSEEEETTSCEEEEEE	
T ss_pred		cccc---ccccCCCCccccCCCCeEEEECCCCeEEEECCCCeEEEE	
<div> <div>No 57</div> <div>     </div> </div> <div> <input type="checkbox"/> >4d6v_A GIB2, G protein beta subunit GIB2; signaling protein, scaffold protein, ribosome binding; 2.20A {Cryptococcus neoformans var) PDB: 4aow_A 5flx_g 4d61_g 4d51_g 4kzx_g 4kzz_g 4kzy_g 5a2q_g Probab=100.00 E-value=1.3e-34 Score=242.03 Aligned_cols=250 Identities=21% Similarity=0.344 Sum_probs=0.0 </div>			
Q ss_pred		ceEecCCcCeeEEEECCCCEEEEeCCcCEEEecCCcCeeEecCCCCEEEEeCCcCCEEEeCCcCEEE	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLGYGKRLATCSSDKTKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGVKVI	81 (297)
Q Consensus	2	-----h-v-----g-l-t-s-d-v-lwd-----h-v-----l-s-s-D--i-i	81 (297)
T Consensus	56	-----h-v-----s-----l-s-s-d--i-vwd-----h-v-----l-s-s-d--i-i	131 (314)
T 4d6v_A	56	KKILHGHNFVSDVAISSDGFALSSSDHTRLRLWDL--NTGLTTKKFVGHTGDVLSVSFSAD--NRQIVSASRDRSIKL	131 (314)
T ss_dssp		EEEECCCCSCEEEECTTSSEEEETTSCEEEET--TTTEEEECSSCEEEECTT--SSCEEEETTSCEEE	
T ss_pred		cccccccCEEEEECCCCEEEEeCCcCEEEEC--CCCEeEEEECCCCEEEECCC--CCEEEEeCCcEE	
Q ss_pred		EEccCCeEEEEEEcccccCEEEeCCcCCeEEEECCCCEEEEeCCcchhhhhhhcccccEEEECCCCcccc	
Q Fri_Mar_04_23:	82	WKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVASSDGVKSVVVEFKENGTTSPITIDAHAIQVNSASWAPATIEED	161 (297)
Q Consensus	82	wd-----v-----l-----d-i-i-----v-----v-----	161 (297)
T Consensus	132	wd-----v-----l-s--d--i--wd-----v-----s--g----	204 (314)
T 4d6v_A	132	WNTLGEC-KFDIVEDGHTVEVWSCVRFSPNPAIPVTSAGWDKTVKVVWELSN--KLKTHHGHGTGYLNTLAVSPDG--	204 (314)
T ss_dssp		ECTTSC-E-EEECTTCCSSCEEEECSSSSCEEEETTSCEEEETTTT--EEEEECSSCEEEECTTS----	
T ss_pred		ecCCCCc-eEeeecCCcCEEEECccccceEEEEeCCcCEEEECcccc--ceEEeCCcCEEEEECCCC--	
Q ss_pred		ccccCCcccEEEEEeCCcCEEEEEECCCCeEEEEEccCCcCEEEECSSSSCEEEEECCCCCEEEECCEEEccCCCC	
Q Fri_Mar_04_23:	162	GEHNGTKESRKQVGTGGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPVLLRSYLASVSQDRCTCIWTQDNEQG	241 (297)
Q Consensus	162	-----l-tg--d--i--wd-----h--v--l--s-----las-s-Dg-i-iw-----	241 (297)
T Consensus	205	-----l-s--dg-v-iwd-----i-----i-iwd-----	265 (314)
T 4d6v_A	205	-----SLAASGGKDGITMLWDNLNGKHLVSLD-----AGDVINALVFSFN-----RYWLCAATASSIKIFDLESKS-	265 (314)
T ss_dssp		-----SEEEEESSSEEEESSSSSEEEEEE--SSCEEEEEECSS--SSSEEEETTSCEEEETTTTE-	
T ss_pred		-----CEEEECCEEEEECCCCeEEEEc-----CCCEEEEEcCC--ceEEEEcCCcEEEEEccccCc-	
Q ss_pred		ceEEEEcc-----ccCCeEEEEEECCCCEEEEeCCCCEEEE	
Q Fri_Mar_04_23:	242	PWKKTLLKE-----KFPDVLWRASWSLGSNLALSGGDNKVLWK	283 (297)
Q Consensus	242	-----i-----l-----d-i-iw--	283 (297)
T Consensus	266	-----v--l--s--dg--l-sg--dg-v-vw--	312 (314)
T 4d6v_A	266	--LVDDLQPDFGLSDKARKPECTSLAWSADGQTLFAGFSDNLVRVWAV	312 (314)
T ss_dssp		--EEEECCCCSSCCSSCCCCCEEEECTTSSEEEETTSCEEEEEE	
T ss_pred		--eehhccCCCCccccCCeEEEECCCCEEEEeCCcCEEEEEE	
<div> <div>No 58</div> <div>     </div> </div> <div> <input type="checkbox"/> >4yvud_A Pleiotropic regulator 1; WD40 repeat, mRNA processing, mRNA splicing, structural GENO structural genomics consortium, SGC, RNA binding protein; 1.70A {Homo sapiens} Probab=100.00 E-value=1.6e-34 Score=246.87 Aligned_cols=244 Identities=23% Similarity=0.317 Sum_probs=0.0 </div>			
Q ss_pred		ceEecCCcCeeEEEECCCCEEEEeCCcCEEEecCCcCeeEecCCCCEEEEeCCcCCEEEeCCcCEEE	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLGYGKRLATCSSDKTKIFVEGETHKLIDTLTGHEGPVWRVDWAHPKFGTILASCSYDGVKVI	81 (297)
Q Consensus	2	-----h-v-----g--l-t-s-d-v-lwd-----h-v-----l-s--d--i-i	81 (297)
T Consensus	57	-----h-v-----l--dg-v-iwd-----v-----l-s--d--i-i	132 (374)
T 4yvud_A	57	YRVISGHLGWRCIAVEPGNQWFTGSADRTIKIWL--ASKLLSLTGHISTVRGVIVSTR--SPYLFSGEDKQVKC	132 (374)
T ss_dssp		EEEECCCCSCEEEECTTSSEEEETTSCEEEET--TTCEEEECSSCEEEEECCSS--SSEEEETTSCEEE	
T ss_pred		eEEECccccCEEEEECCCCEEEEeCCcCEEEEC--CCCEeEEEEcCCcCEEEEECCC--CCEEEECCCCeEE	
Q ss_pred		EEccCCeEEEEEEcccccCEEEeCCcCCeEEEECCCCEEEEeCCcchhhhhhhcccccEEEECCCCcccc	
Q Fri_Mar_04_23:	82	WKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVASSDGVKSVVVEFKENGTTSPITIDAHAIQVNSASWAPATIEED	161 (297)
Q Consensus	82	wd-----v-----l-----d-i-i-----v-----v-----	161 (297)
T Consensus	133	wd-----v-----l--dg-v-iwd-----i-----i-iwd-----	202 (374)
T 4yvud_A	133	WDLEYNK--VIRHYHGLHSAVYGLDLHPT--IDVLVTCRSDTARIWDVTKA--SVHLSGHTNAVAVRVCQAAE----	202 (374)
T ss_dssp		EETTTTE--EEEECCCCSSCEEEEECCSS--SSEEEETTSCEEEETTTCC--EEEEECSSCEEEEECCSS--	
T ss_pred		EECCCCc--eEEEEccccCEEEEECCC--CEEEEEcCCcCEEEEECCCC--eEEEECCCCeEEEEECCCC--	
Q ss_pred		ccccCCcccEEEEEeCCcCEEEEEECCCCeEEEEEccCCcCEEEECSSSSCEEEEECCCCCEEEECCEEEccCCCC	
Q Fri_Mar_04_23:	162	GEHNGTKESRKQVGTGGADNLVGIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPVLLRSYLASVSQDRCTCIWTQDNEQG	241 (297)
Q Consensus	162	-----l-tg--d--i--wd-----h--v--l--s-----las-s-Dg-i-iw-----	241 (297)
T Consensus	203	-----l--dg-i-i-d-----i-----l--s--d--i--d-----	264 (374)
T 4yvud_A	203	-----PQITGSHDTTIRLWDLVAG--KTRVTLTNHKKSVRAVLHPRH--YTFASGSPDN--IKQWKFDPDS--	264 (374)
T ss_dssp		-----SCEEEETTSCEEEETTTT--EEEEECSSSCCEEEECTTS--EEEEECSSCEEEETTTTE-	
T ss_pred		-----CEEEEECCCEEEEECCCC--eEEEEcCCCCCEEEEECCCC--CEEEeCCcCEEEEECCCC--	
Q ss_pred		ceEEEEccccCCcCEEEEEECCCCEEEEeCCCCEEEE	

Q ss_pred		cceEEEECCcccccccccCccce--EEEEEEcCcEIEEEECcCCcceeEEEEEEccCCCcReEEEECCCCCCCCEEEE		
Q Fri_Mar_04_23:	147	GvNSASWAPATIEEDGEHNGTKESR-KFVTGGADNLVKIKWYNSDAQTYVLESTLGHSDVVRVDVAWSPTVLRLSYLASV	225	(297)
Q Consensus	147	v-----l-tg-d-i-wd-----h-v-v-l-s-p-----las-	225	(297)
		.+.+++ ++ . ++ + . ++ ++.... ++..+ +++ ++ . + +++		
T Consensus	279	-v-l- -p-----latg-dg-i-wd-----h-v-v-l-sp-----l-s	340	(430)
T 2xy_i_A	279	EVNCLSFNPYS-----EFILATGSADKTVALDLRLNKL--KLHSFESHKDEIFQVQWSPHN--ETILLASS	340	(430)
T ss_dssp		CEEEEEECSSC-----TTHEEEETTTEEEEEETTCTTS--CSEEEECCCCCEEEEEECSSC--TTEEEEE		
T ss_pred		CeeEEEECCCC-----CCEEEEECcCcEIEEECCCCCCC--CcEeEECCCCCEEEEEcCCC--CEEEEE		

Q ss_pred eCCcEEEEccCCCCc-----EEEcCCcCCcEEEEEECCCC-EEEEcCCCCEEEEEC
Q Fri_Mar_04_23: 226 SQDRTCIWTQDNEQGPWK-----KTLLEKFKFPDVLWRASWSLGSN-VLALSGGDNKVLWKEN 284 (297)
Q Consensus 226 s-Dg-i-iw-----i-----l-----d-i-iw----- 284 (297)
+|||.++|+..... ..+....|...|.+++|+|+++ .|++++|||.++|+..
T Consensus 341 ~Dg-v-iwd-----h~v-----l-s-s-dg-v-iw----- 409 (430)
T 2xyi_A 341 GTDRRLHVWDLKIGIEQSTEDADGPPPELLFIHGHTAKISDFSWNPNEPWIICSVSEDNIMQVWQMA 409 (430)
T ss_dssp ETTSCCEEEGGTTCCCHHHHHCCCTTEEECCCCSSCEEEECSSSTTEEEETTEEEEEEC
T ss_pred ECCCCEEECCCCCCCCCCCCCCEEEECcCCcCCcEEEECCCCCEEEECcCCCCEEEC

No 61      PubMed
☐ >5ams_A SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}
Probab=100.00 E-value=9.2e-35 Score=253.41 Aligned_cols=247 Identities=13% Similarity=0.132 Sum_probs=0.0

Q ss_pred ceEecCCcCeeEEEEcCCCCEEEEcCCcEEEEcCCc-----
Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDDYQKRLATCSSDKTIKIFVEGET----- 42 (297)
Q Consensus 2 ~-h~v-----g~l-t-s-d~v-lwd----- 42 (297)
+..+|...|++++|+|+|++++|..+|+|+....
T Consensus 102 ~-h~v~s~g~l~s~dg~i~vwd-----v~p~l~dg~i~i 181 (431)
T 5ams_A 102 AGTLTGYGESVISCSFTSGGFLVTADMSGKVLVHMQKGAQWKLASQMQVEVEIVWLKTHPTIARTAFGATDGSVWC 181 (431)
T ss_dssp EEECCCCSCEEEECCTTSEEEETTSCEEEEGGGTEEEECSSCEEEECSSSTTEEEETTTCCCEE
T ss_pred eEEcCCcCCCEEEECcCCCCEEEEcCCcEEEECCCCcEEEEcCCcCCcEEEEcCCCCEEEEcCCcEEEE

Q ss_pred -----ccEEec-----CCCCEEEEc-----CcCcCEEEECcCCcEEEEcCCcEEEEEc-----ccCccEE
Q Fri_Mar_04_23: 43 ~-h~v-----h~v-----l-s-D-i-iwd----- 103 (297)
Q Consensus 43 ~-h~v-----l-s-D-i-iwd----- 103 (297)
..+..+|...|++++|+ ++ +++|++++|++|++|+++++ ..+..+ .|...|..
T Consensus 182 wd~-h~v-----l-s~dg~i~wd-----i 257 (431)
T 5ams_A 182 YQINEQDGSLEQLMSGFVHQDCSMGEFINDKGEN--TLELVTCSLDSTIVAWNCFPTGQ--QLFKITQAEIKGLEAPWI 257 (431)
T ss_dssp EEECTTCCCEEEECcCCSSCEEEECSSSS--CEEEETTSCEEEETTTCC--EEEECGGGTTTCCCEE
T ss_pred EEecCCCCcEEEEcCCcCCcEEEEcCCcCCc--CEEEECcCCcEEEECCCCc--EEEEcCccCCcCCCEE

Q ss_pred EEEcCC-----ccCCcEEEEECCEEEEEcC-Ccchhhhh-----hccccEEEEECcCCCCCCCCcCC
Q Fri_Mar_04_23: 104 SVQWAP-----HEYGPLLVASSDGKVSVEFKF--NGTSPITID-----AHATGVSASWAPATIEEDGHNHT 167 (297)
Q Consensus 104 ~-l~d~i~i-----v----- 167 (297)
+++|+| + ++++++.|+|++++ .|...+.+++|+|++
T Consensus 258 ~-p~l~dg~i~iwd-----v~s----- 323 (431)
T 5ams_A 258 SLSLAPEITLTKGN--SGVACGSNGLAVINCNGG--AILHLSTVIELKPEQDELDAISISISWSKF----- 323 (431)
T ss_dssp EEEECTTTTSC--TTEEEETTSCEEEEGGGTS--EEEEECSSCCSSCGGGCEEEETTT-----
T ss_pred EEEECcCCcCCc--CEEEECcCCcEEEECCCCc--CEEEECcCCcEEEECCCCc--EEEEcCCC-----

Q ss_pred cccEEEEcCCcEEEEECcCCcEEEEcCCcCCcEEEECCCCCCCCEEEEcCCcEEEEcCCcCCcEEEE
Q Fri_Mar_04_23: 168 KESRKFTVGADNLVKIKYNSDAQTYVLESTLEGHSDGVRDVAWSPTVLLRSYLASVSQDRTCIWTQDNEQGPWKTL 247 (297)
Q Consensus 168 ~-l~t~g~d~i~wd-----h~v~l~s-----las-s-Dg-i-iw----- 247 (297)
..+|++|+|+|++|+|... ..+...+|...|+++|+| ..+|++++|...|++|+|+... ..
T Consensus 324 ~-l~g~dg~i~iwd-----v-----l~dg~i~vwd----- 387 (431)
T 5ams_A 324 ~-SLMAIGLVCGEILLYDTSAW--RVRHKF-VLEDVSTKLMPDN--DDLFAFCINGKVQFNARTGQ--EKFFV 387 (431)
T ss_dssp ---TEEEETTSCEEEETTTT-----EEEEE-ECSSCEEEET-----TEEEETTSCEEEETTTCC--EEEE
T ss_pred ---CEEEECcCCcEEEECCCCc--eEEEEE-cCCCCEEEEECc-----CEEEECcCCcEEEECCCCc--EEEE

Q ss_pred eCCCCCCEEEEEEC-----CCCCEEEEcCCCCEEEEEC
Q Fri_Mar_04_23: 248 LKEKFKFPDVLWRASWS-----LSGNVLALSGGDNKVLWKEN 284 (297)
Q Consensus 248 ~-i-----l-----d~i~iw----- 284 (297)
+.. |...|.+++|+ |++++|++++|..|++|+..
T Consensus 388 ~-h~v-----l-s~dg~i~vw----- 430 (431)
T 5ams_A 388 CVG--HMGVLDFFILLHPVANTGTQKRVITAGDEGVSLVFEVP 430 (431)
T ss_dssp ECC--CSSCEEEECcCCSSCCCEEEETTSCEEEEC
T ss_pred EEC--CCcCEEEECcCCCCCCEEEECcCCcEEEEEC

No 62      PubMed
☐ >3w15_A Peroxisomal targeting signal 2 receptor; beta-propeller, targeting signal recognition, cytosol; 1.80A {Saccharomyces cerevisiae}
Probab=100.00 E-value=5e-35 Score=250.12 Aligned_cols=254 Identities=12% Similarity=0.155 Sum_probs=0.0

Q ss_pred CceEecCCcCeeEEEEcC--CCCCEEEEcC-----CcEEEEcCCcCCcEEEEcCCcCCCEEEECcCCcCEEEEC
Q Fri_Mar_04_23: 1 MVVIANAHNELIHDAVLDDY--YKRLATCSS-----DKTIKIFVEGETHKLIDLTGHEGVPWRVDNAHPKFTILAS 72 (297)
Q Consensus 1 ~-h~v-----g~l-t-s-----d~v~lwd-----h~v-----l-s 72 (297)
+|...+...+.+++|+| ++++++. |++|++|+.....|...|++++|+++ ++|++
T Consensus 2 ~-v~sp~i~v~v~sp-----l~dg~i~vwd-----las 80 (368)
T 3w15_A 2 SMLRYHMQFGSGYGVQYSPFFDNRLAVAAGSNFGLVGNKLPILRIDRSGRIVVNSPLTQDCLFDLANWESH--ENQVLV 80 (368)
T ss_dssp -EEEECTTEEEEEECSSCTTEEEEEEGGGTSSCEEEETTSCEEEEEECSSCEEEETTC--TTEEE
T ss_pred cccEEcCCcCCcEEEECCCCCCEEEECcCCCCCEEEECcCCcEEEEcCCcCEEEECcCCcCEEEEC

Q ss_pred EcCCCCEEEEcCCc-eEEEEEcCCcCCcEEEEcC--ccCCcEEEEECCEEEEEcCCcChhhhhhhc-----
Q Fri_Mar_04_23: 73 CSYDGKVLVWKEENG-RWSQIAVHAVHSASVNSVQWAP-HEYGPLLVASSDGKVSVEFKNGTSPITIDAH----- 144 (297)
Q Consensus 73 ~-s-D~i~iwd-----l~d~i~i----- 144 (297)
++|++|+|+|++++ . ..+..+|...|+++|+| + +|++++|++|++|+.... ..+..+|
T Consensus 81 ~-s-D~i~lwd-----l~gh~v~v~sp-----l~s~s-D~i~lwd-----l~h----- 154 (368)
T 3w15_A 81 AQGDGTLRLFDTTTFKEF--PIAIFKEHREVFSCNWLNVN--RQNFSSWDGSIKINSPLRKQ--SLMTLTPRPLEITK 154 (368)
T ss_dssp EETTSEEEETTSCTSS--CEEEECSSCEEEECSSS--SSCEEEETTSCEEEETTCSS--CEEECCCCHHHHH
T ss_pred ECCCCEEEECCCCC--CceehhccCcEEEEcCCCC--CEEEECcCCcEEEECCCCc--ceEEcCCCCcEE


```

Q ss_pred      EcccCCeEEEEEEcccccCccEEEEECcCccCCeEEEEEECCCEEEEEccCCCcchhhhhhhcccccEEEEECCcccc
Q Fri_Mar_04_23: 82 WKEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASDGKVSVEFKENGTTSPITIDAHAIQVNSASWAPATIEED 161 (297)
Q Consensus    82 wd-----v-----l-----d-i-i-----v----- 161 (297)
                ||++++. ....+..|...|.+++|++ +.+++++.|+|.++|+|+... ....+..|...+.+++|++
T Consensus    198 wd-----h-----v-l-s-----l-sg-dg-v-iwd-----h-----v-l-sp----- 268 (386)
T 5a31_R       198 RDVRMPD-PFFETIESHTQEVCGLKWNVA--DNKLASGGNDNVVHYEGTSKS--PILTFDEHKAQVKAWSAPHK--- 268 (386)
T ss_dssp      EETTSSS-SCSEEECCSSCEEEEEESS--SEEEEEETTSCEEEEETTCS--CSEEECCSSSEEEEECCSS--
T ss_pred      EEECCc-cEEEEcCccCEEEEECCC--CEEEEEcCEEEEEEECCcC--EeEEcccccEEEEECCC--

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Q ss_pred      ccccCCccc-EEEEe--CCeEEEEEEcCCcEEEEEcccccEeEEEECCCCCCCCEEEE--EeCCCEEEEEc
Q Fri_Mar_04_23: 162 GEHNGTKESR-KFVTGG--ADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLAS--VSQDRTCIWTQ 236 (297)
Q Consensus    162 -----l-tg-----d-i-wd-----h-v-l-s-----las--s-Dg-i-iw- 236 (297)
                . ++++|+ .|+|.++|+++. +...+. +...|.+++|++ .++++ |+|.++|++
T Consensus    269 -----l-sg-g-d-i-iwd-----v-d-s-i-iwd----- 331 (386)
T 5a31_R       269 -----RGVLATGGGTADRLKIKWVNTS--IKMSDID-SGSQICNMVWSKNT--NLVTSHGYSKYNLTLDWC 331 (386)
T ss_dssp      -----TTEEEEECTTCEEEEEETTTT--EEEEEE-CSSCEEEEEECSS--SCEEEEECTTCEEEEECS
T ss_pred      -----CEEEEECCCCCEEEEECCC--CEEEc-CCCCEEEEEEcCC--CEEEEEcccccEEEEE

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Q ss_pred      cCCCCcEEEEEcccccCCeEEEEEECCCCCEEEEECCCCCEEEEE
Q Fri_Mar_04_23: 237 DNEQGPWKTLTKKEKFPDVLWRASWSLGNVLALSGGDNKVTWK 282 (297)
Q Consensus    237 -----i-----l-----d-i-iw- 282 (297)
                .... ....+..|...|.+++|++|++|++++.|++|++|+
T Consensus    332 -----h-v-l-spdg-l-s--d-i-iw- 372 (386)
T 5a31_R       332 NSMD---PAILKG--HSFRVLHLTLSDGTTVVSGAGDETLRYWK 372 (386)
T ss_dssp      SSSC---EEEEEC--CSSCEEEEEECTTSSEEEEEETTTSEEEEE
T ss_pred      CCCC---EEEEEC--CCCCEEEEEECCCCCEEEEECCCCCEEEEE

```

No 65               

☐ >5cyl_A WD repeat-containing protein 48; UAF1, USP, deubiquitinase, DUB, protein BI; 3.00A {Homo sapiens} PDB:
5cyl_A
Probab=100.00 E-value=3.6e-35 Score=266.00 Aligned_cols=248 Identities=18% Similarity=0.243 Sum_probs=0.0

```

Q ss_pred      EcccCCcEEEEECCCCCEEEEEcCCcEEEEEccCcc-cceEEccCCCCCEEEEEcCCcCCCEEEEEcCCCEEEEE
Q Fri_Mar_04_23: 4 IANAHNELIHDAVLDYGYKRLATCSSDKTIKIFVEGET-HKLIIDLTLGHEGPVWRVDWAHPKFGTLLASCSYDGKVLIV 82 (297)
Q Consensus    4 h-v-v-----g-l-t-s-d-v-lwd-----h-v-v-----i-iw 82 (297)
                ++.+.|...|++++|+|++|++|+|.+.|++|+|+... ....+.+|...|.+++|++ +.++++.|++|++|
T Consensus    40 H-V-V-l-spdg-latg-dg-I-iwd-----h-v-v-l-s-d-g-l-sgs-dg-I-vw 117 (598)
T 5cyl_A       40 VEKYNRNGVNALQLDPALNRLFTAGRDSIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCN--GKTLISASSDTTVKVV 117 (598)
T ss_dssp      CCCSBSSCEEEEEETTTTTEEEETTSCEEEEECSSCCCEEEEECCCCSSCEEEEEEGG--GTTEEEETTSCEEEE
T ss_pred      cccccCCeEEEECCCCCEEEEEcCCeEEEECCCCCcEEecccCCcCEEEEEEC--CEEEEEcCCCEEEEE

```

```

Q ss_pred      EcccCCeEEEEEEcccccCccEEEEECcCccCCeEEEEEECCCEEEEEcCCcC-----hhhhhhhcccccEEEEECC
Q Fri_Mar_04_23: 83 KEENGWRSQIAVHAVHSASVNSVQWAPHEYGPLLVAASDGKVSVEFKENGTT-----SPITIDAHAIQVNSASWAP 155 (297)
Q Consensus    83 d-----v-----l-----d-i-i-----v----- 155 (297)
                |++++. ....+..|...|.+++|++ +.+++++.|+|.++|+|+... ....+..|...+.+++|++
T Consensus    118 d-----h-v-l-s-d-----l-s-dg-I-vwd-----h-v-l-s-sp-----v-l-s- 193 (598)
T 5cyl_A       118 NAKHGF--CMSTLRTHKDYKALAYAKD--KELVASAGLDROIFLWVNTLTALTASNNTVTSSLSGNKDSIYSLAMNQ 193 (598)
T ss_dssp      ETTTTE--EEEECCCCSSCEEEEEETT--TTEEEETTSCEEEEHHHHSSSSCCCCCEEECCCCCEEEEEECT
T ss_pred      ECCCC--eEEEcCCCCcEEEEECC--CEEEEEcCCeEEEECCCCccccccCccceccccCCCCCEEEEECC

```

```
















Q ss_pred      CccccccccCCcccEEEEEcCCeEEEEEEcCCcEEEEEccCccEeEEEECCCCCCCCCEEEEEcCCCEEEEE
Q Fri_Mar_04_23: 156 ATIEEDGEHNGTKESRKFPVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVSQDRTCIWT 235 (297)
Q Consensus    156 -----l-tg-----d-i-wd-----h-v-l-s-----las-s-Dg-i-iw- 235 (297)
                ++ .++++|+|.++|++|+|+... ....+.+|...|.+++|++ .+|++++.|||.++|+
T Consensus    194 -g-----l-sg-dg-I-vwd-----h-v-l-s-spdg-----l-sgs-dg-v-lwd 253 (598)
T 5cyl_A       194 LG-----TIIVSGSTEKVLRLVPRDCA--KLMKLGKHTDNVKALLNRDG--TQCLSGSSDGTIRLWS 253 (598)
T ss_dssp      TS-----SCEEEETTSSEEECTTTC--EEEECCCCSSCEEEEEECTTS--SEEEETTSEEEEE
T ss_pred      CC-----CEEEEECCCCCEEEcCCCC--eEEEcCCCCCEEEEEECcC--CEEEEEcCCCEEEEE

```

```

Q ss_pred      cCCCCcEEEEEcccccCCeEEEEEECCCCCEEEEECCCCCEEEEE
Q Fri_Mar_04_23: 236 QDNEQGPWKTLTKKEKFPDVLWRASWSLGNVLALSGGDNKVTWK 282 (297)
Q Consensus    236 -----i-----l-----d-i-iw- 282 (297)
                +... ....+.. +...|++++|+|++++|++++.|||.++|+
T Consensus    254 -----h-v-l-s-dg-l-sg-dg-v-vwd 295 (598)
T 5cyl_A       254 LGQOR---CIATYRV--HDEGVWALQVNDAFTHVSGGRDRKIYCTD 295 (598)
T ss_dssp      TTTTE--EEEEEC--CSSCEEEEEECTTSCEEEEETTCEEEEE
T ss_pred      CCCC--eEEEEc--CCCCEEEEEECCCCCEEEEECCCCCEEEEE

```

No 66               

☐ >4qgb_B Methylosome protein 50; TIM barrel, beta-propeller, methyltransferase, methylation, transferase-protein binding complex; HET: 0XU; 2.06A {Homo sapiens} PDB: 4x60_B* 4x61_B* 4x63_B*
Probab=100.00 E-value=8.1e-35 Score=246.00 Aligned_cols=253 Identities=21% Similarity=0.259 Sum_probs=0.0

```

Q ss_pred      ceEecCCcEEEEECCCCCEEEEEcCCcEEEEEccCccceEEe--ccCCCCCEEEEEcCCcCCCEEEEEcCCCEEE
Q Fri_Mar_04_23: 2 VVIANAHNELIHDAVLDYGYKRLATCSSDKTIKIFVEGETHKLIIDLTL--TGEHGPVWRVDWAHPKFGTLLASCSYDGKV 79 (297)
Q Consensus    2 -----h-v-v-----g-l-t-s-d-v-lwd-----h-v-v-----l-s-s-D-i 79 (297)
                ....+|...|++++|+|+++++ ++.|.++|+|+.....+ .+|...|.+++|++ ++|++++.|.
T Consensus    75 -----l-i-iw-----v-----dg-i 151 (344)
T 4qgb_B       75 CSAGVQTEAGVADLTWVGEGILV-ASDSGAVELWELDENETLIVSKFYEHDDIVSTVSVLSS--GTQAVSGSKDICI 151 (344)
T ss_dssp      CSEEEESSCEEEEEETTTTTEE--EETTSEEEEEECTTSSCEEEEEEECCSSCEEEEEECTT--SEEEEEETTSCIE
T ss_pred      ccccccccCEEEEEcCCcEEe-eCCCCEEEEEECCCCcEEEEEEcccccCCcCEEEEEEC--CEEEEECCCCCE

```


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```
Q ss_pred C-----CCcchhhhhhhcccccEEEEECCCCccccccccCCcccEEFE-EEcCCcEE
Q Fri_Mar_04_23: 132 E-----NGTTSPTITDAHAIGVNSASWAPATIEEDGHEHNGKESRKFFV-TGGADNLV 182 (297)
Q Consensus 132 ~~~~~v~~~~~1~tg~d~i 182 (297)
T Consensus 275 ~~~~~h~~~~~v~v~sp~~~~~1~s~s~d~i 341 (514)
T 5cxb_A 275 KASAPEDASLLPGAHVSKRRKATSSVSTAQRGLGLWSIHTAPATAAIFDPRD-----RTVAYSASQDHTV 341 (514)
T ss_dssp TTTCCCCGGGTTCCCC-----CEEECCSEEECCSSCEEEEECCSSC-----TTEEEETTSEE
T ss_pred CCCCCCCCCCCCCCCCCCCCCCCCCCCCCcCceEEEEccCCcEEEEECCCC-----CcEEEEECCCEE
```

```
Q ss_pred EEEEEcCCcEEEEEccCCcEEEEECC-----CCCCCEEEEEEcCCcEEEEEccCCCCcEEEEEcccccCCcEE
Q Fri_Mar_04_23: 183 KIWKYNDAQTYVLESTLEGHSDWVRDVAWSP-----TVLLRSYLASVSQDRTCIWTQDNEQGPWKTLLEKEKFPDVLW 258 (297)
Q Consensus 183 ~wd~v~l~s~h~~~~~las~s~Dg~i~iw~ 258 (297)
T Consensus 342 ~iwd~v~~~~~la~g~dg~i~lwd~h~~~~~v~ 411 (514)
T 5cxb_A 342 RTLDLTGQ-----VVSILT-LTHPLLSLSALTAGTTS-----PLLAAGTSARHITMVDPRASSATTSVMTLRG--HANKVV 411 (514)
T ss_dssp EEEETTTC-----EEEEEE-CSSCEEEEEECCTTCSS--CEEEETTSCSEEECSSSSSCC-CEEECC--CSSCEE
T ss_pred EEECCCCc-----EEEEEE-cCCcEEEEEccCCCCc-----CEEECCCCcEEEEECCCCcEEEEEcc--CCcEE
```

```
Q ss_pred EEECCCCCE-EEEEcCCCCEEEEE
Q Fri_Mar_04_23: 259 RASWSLSGNV-LALSGGDNKVTWLK 282 (297)
Q Consensus 259 ~~~~~l~~~~~d~i~iw~ 282 (297)
T Consensus 412 ~l~sp~~~~~ll~s~s~Dg~v~iwd 436 (514)
T 5cxb_A 412 SLSPSPENEYSLVSGSHDGTCTRVWD 436 (514)
T ss_dssp EEECCSSCSSEEEETTSCSEEEE
T ss_pred EEEcCCCCcEEEEEcCCcEEEEE
```

No 78      

☐ >1r5m_A SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A {Saccharomyces cerevisiae}
Probab=100.00 E-value=2.4e-34 Score=249.39 Aligned_cols=254 Identities=17% Similarity=0.225 Sum_probs=0.0

```
Q ss_pred CceEEcCCcCeeEEEEEcCCCCEEEEECCcEEEEEccCccceEEcCCcCCCEEEEEcCCcCCCEEEEEcCCcEE
Q Fri_Mar_04_23: 1 MVTIANAHNELIHDVLDYGRKRLATCSSDRTIKIFEVEGETHKLIDLTGHEGPPVWRVDWAHPKFGTILASCSYDGLV 80 (297)
Q Consensus 1 ~~~~~h~~~~~g~l~t~s~d~v~lwd~h~~~~~v~ 80 (297)
T Consensus 100 ~~~~~h~~~~~s~l~dg~v~vw~ 174 (425)
T 1r5m_A 100 LSASSGKTNQVTCIAWSHDSNGSIVTGVENGLRLWKNK--TGALLNVLNFRAPIVSVKWKND--GTHIISIMVENVVTI 174 (425)
T ss_dssp CC-----CBCEEEEEECTTSSEEEETTSCSEEEET--TSCEEEECCEEECTT--SSEEEETTCTEE
T ss_pred hhhhhhccCCcEEEEEcCCCCEEEEECCcEEEEECC--CCcEEEEcCCCCCEEEEEcCC--CCEEEEEcCCcEE
```

```
Q ss_pred EEEccCCcEEEEE-----ecccCccEEEEE
Q Fri_Mar_04_23: 81 IWKEENGWRSQIAV-----HAVHSASVNSVQ 106 (297)
Q Consensus 81 iwd~v~~~~~v~~~~~ 106 (297)
T Consensus 175 ~~~~~g~i~d~ 254 (425)
T 1r5m_A 175 LWNVISGTVMQHFEIKETGGSSINAENSHGDSLGVDVWDDKFIPIPGKGAIFVYQITEKTPTGKLIHGHGPISVLE 254 (425)
T ss_dssp EEEETTTEEEEEECC-----CCBSCEEEETTTEEEECGGGCEEEETTSCSSCEEECCSSCEEEEEE
T ss_pred EEECCCCcEEEEEEccCccceEEcccccEEcEEEEECCcEEEEEcCCcEEEEEcCCcEEEEEcCCcEEEEEcCCcEEEEE
```





```
Q ss_pred eCCcCCcCEEEEEECCCEEEEEEcCCcchhhhhhhcccccEEEEECCccccccccCCcccEEEEEcCCcEEEEE
Q Fri_Mar_04_23: 107 WAPHEYGPLLVASSDGVSVVFEKNGTTSPTITDAHAIGVNSASWAPATIEEDGHEHNGKESRKFFVTGGADNLVLIWK 186 (297)
Q Consensus 107 ~~~~~l~~~~~d~i~i~v~~~~~1~tg~d~i~wd 186 (297)
T Consensus 255 ~~~~~l~~~~~dg~i~i~d~v~~~~~1~d~i~i~d 316 (425)
T 1r5m_A 255 FNDT--NKLILLSASDGLTRLIWHGGNGN--SQNCYFGHSQSIVSASVWGD-----KVISCSMDGSVRLWS 316 (425)
T ss_dssp EETT--TTEEEETTSCSEEEECSSSB--CSEEECCSSCEEEETT--EEEEEETTSEEEEEE
T ss_pred ECCC--CCEEEEEECCCEEEEEECCcC--cccchcccccEEEEECCC-----eEEEEECCcEEEEE
```

```
Q ss_pred EcCCCCcEEEEEcCCcCCcEEEEECCCCCCCCCEEEEEECCcEEEEEccCCCC-----cEEEEEc
Q Fri_Mar_04_23: 187 YNSDAQTYVLESTLEGHSDWVRDVAWSP-----TVLLRSYLASVSQDRTCIWTQDNEQGP-----PWKKTLLK 249 (297)
Q Consensus 187 ~~~~~h~~~~~v~l~s~~~~~las~s~Dg~i~iw~ 249 (297)
T Consensus 317 ~~~~~i~~~~~s~~~~~dg~v~iwd~ 389 (425)
T 1r5m_A 317 LKQN-----TLLALSIVDGVPIFAGRISDQ--OKYAVAFMDGQVNVYDLKKLNSKRSRLYGNRDGILNPLPIPLIASYQ 389 (425)
T ss_dssp TTTT-----EEEEEECTTCSEEEETTS--SEEEETTSCSEEECHHHHC-----CEECCEEEEC
T ss_pred CCCC-----CeeEEEcCCCCCEEEEEECCcC-----CEEEECcCCcEEEEECCcCcccccEEcCCccccccccccceee
```

```
Q ss_pred cccCCcEEEEECCCCCEEEEcCCCCEEEEEc
Q Fri_Mar_04_23: 250 EEKFPDVLWRASWSLSGNVLAALSGGDNKVTWLKEN 284 (297)
Q Consensus 250 ~~~~~i~~~~~l~~~~~d~i~iw~ 284 (297)
T Consensus 390 ~~~~~v~~~~~s~dg~l~dg~v~i~ 424 (425)
T 1r5m_A 390 SSQNDYIFDLSWNCAGNKISVAYSLOEGSVVAIP 424 (425)
T ss_dssp CTTCCEEEEECTTSSEEEETSSSEEEEC
T ss_pred ccccCCcEEEEEcCCCCCEEEEEEccCCCEEEEc
```

No 79      

☐ >4zoy_A SQT1; chaperone, ribosome biogenesis, WD40-repeat; 1.50A {Chaetomium thermophilum} PDB: 4zn4_A 4zoz_A
Probab=100.00 E-value=7.7e-34 Score=250.40 Aligned_cols=253 Identities=18% Similarity=0.278 Sum_probs=0.0

Q ss_pred	CceEecCCcCeeEEEECC--CCEEEECcCC-----cEEEEccCCcc-----ceEE			
Q Fri_Mar_04_23:	1 MVVIANAHNELIHDVLDYY--KRLATCSSDK-----TKIFVEGETH-----KLIDT	48 (297)		
Q Consensus	1 ~~~~~h~v~~~~~g~l~t~s~d~~~~~v~lwd~~~~~l~s~D~i~iwd~~~~~	48 (297)		
T Consensus	7 ~~~~l~H~v~~~~~s~~~~~l~s~dg~~~~~i~vw~~~~~	84 (491)		
T 4zoy_A	7 SIAYFDGHKDSVFIAQHPYLPNIVATGGSGDADDPAGKGYVLDI--SAAAGRPVLPSPSYNDPSSAPQQTSLNPIFE	84 (491)		
T ss_dssp	CSEEECCSSSEEEEECCSCTTEEEEEECSSSTTCCSEEEEEEG--GGC-----CBCCSE			
T ss_pred	eeeeeecccccEEEECCCCcEEEEccCCccccCceEEEEc--CCcccccccccccccCccccccccccccceE			
Q ss_pred	eccCCCCEEEEEc--CccCCEEEECcCCcEEEEECcCCe-----			
Q Fri_Mar_04_23:	49 LTGHEGVPWRVDWA--HPKFGTILASCSDGKVLWKKEENGR-----	88 (297)		
Q Consensus	49 ~~~~h~v~~~~~l~s~s~D~i~iwd~~~~~	88 (297)		
T Consensus	85 ~~~~h~v~~~~~l~s~dg~v~iwd~~~~~i~~~~~l~~~~~	162 (491)		
T 4zoy_A	85 IDGHTDSINALTFTLPR--GDFLVSGMGDGRMRVYAVSPQNGALAQKFLEASQETEEINWFAPCPSPDHNTIALGAS	162 (491)		
T ss_dssp	ECCSSSEEEEECTTT--CCEEEETTCCEEEEEECCTTTTCCSEEEEEECSSSEEEEECCCTTSTTEEEEEET			
T ss_pred	EccCCcEEEEEEcCC--CCEEEECcCCcEEEEcccccCCcceeEeecccccCccccccccCCCCCCCCEEEEEc			
Q ss_pred	-----EEEEEEcccccCceEEEEECcCCcCCcEEEEECCEEEEEEE-----cCCcChhhh			
Q Fri_Mar_04_23:	89 -----WSQIAVHAVHSASVNSVQWAPHEYGPLLVASSDGKVSVEF-----KENGTTSPIT	140 (297)		
Q Consensus	89 ~~~~~~l~d~i~i~~~~~	140 (297)		
T Consensus	163 dg~v~i~d~~~~~v~~~~~l~s~dg~i~iwd~~~~~	240 (491)		
T 4zoy_A	163 DGSVWVFTLDASDPSPVQIVQSYFLHTGPGTAGAWSPD--GLLLATVSEDESLHVDVFGVAASKSLVTDNGQTVVSLT	240 (491)		
T ss_dssp	TSCEEEEEEC--CCEEEECSSSEEEECTT--SSEEEETTSCEEEETTHHHHTTCCCTTSSSEEEEC			
T ss_pred	CCEEEEEECcCCcCccEeeEeccccCccceEEEEcCC--CCEEEECcCCcEEEEECcCCccccceccCccCceEEEEe			
Q ss_pred	hhh-----ccccEEEECCCCccccccccCccceEEEEECcCEEEEE-----			
Q Fri_Mar_04_23:	141 IDA-----HAIGVNSASWAPATIEEDGHEHNGKESRKFTVGGADNLVKIWKY-----	187 (297)		
Q Consensus	141 ~~~~~v~~~~~l~tg~d~i~wd~~~~~	187 (297)		
T Consensus	241 ~~~~~v~~~~~l~dg~i~d~~~~~	307 (491)		
T 4zoy_A	241 NVQDQFAVEGGLFSVAVSPTG-----AVVAVGGAGGQIKIVGLPRLSQPQQPSQSQRRTGKAPAGRGRPS	307 (491)		
T ss_dssp	TTCTTCTTCEEEECTTS-----SSEEEEGGGCEEEECCTT-----			
T ss_pred	ccccccccCceEEEEcCCC-----CCEEEECCEEEEEECcCCccccccccccccccccccccCCCC			
Q ss_pred	-----cCCcceeEEEEECcCCcCEEEEECCCCCCCCEEEEECcCEEEEEccCCCCceEEEEcccccCCc--eEE			
Q Fri_Mar_04_23:	188 -----NSDAQTYVLESTLEGHSDWVRDVAWSPVTLLRSYLASVSQDRCTCIWTQDNEQGPWKTLKKEKFPD-VLW	258 (297)		
Q Consensus	188 ~~~~~h~v~~~~~l~s~s~Dg~i~iw~~~~~l~s~Dg~i~iw~~~~~i~~~~~	258 (297)		
T Consensus	308 ~~~~~v~~~~~l~s~dg~i~iwd~~~~~h~~~~~v~~~~~	377 (491)		
T 4zoy_A	308 QQQQTTSHQAGT---ILASLQIQSDNIESLAFSPSA--PILAAAGTDSIAVFDTSRSF--ALRRHLRGAHAEDPVV	377 (491)		
T ss_dssp	-----CTTC-----EEEEECSSSEEEECSSS-----SSEEEETTSCEEEETTTT-----EEEEETTTTTTSCFE			
T ss_pred	ccccccccccce--EeeccCCCCcEEEEECCTT--CeEEEEcCCcEEEEECcCCc--eEEEEcCccCceE			
Q ss_pred	EEEECC-----CCCEEEECcCCCEEEEE			
Q Fri_Mar_04_23:	259 RASWSL-----SGNVLASGGDNKVTLWK	282 (297)		
Q Consensus	259 ~~~~~l~d~i~iw~~~~~	282 (297)		
T Consensus	378 ~~~~~l~s~dg~i~iwd~~~~~	408 (491)		
T 4zoy_A	378 KVEFVKSPPNAMAGWLLTSCGMDGVVRRWD	408 (491)		
T ss_dssp	EEEECCSSSSGGGTTTEEEETTSCEEEEE			
T ss_pred	EEEEccccccccCCCCEEEEECcCCcEEEE			
No 80				
<input type="checkbox"/> >3k26_A Polycomb protein EED; WD40, structural genomics, NPPSFA, national project on prote structural and functional analysis, structural genomics CON SGC; HET: M3L; 1.58A {Homo sapiens} PDB: 3jzn_A* 3k27_A* 3jpx_A* 3jzh_A* 3iiw_A* 4x3e_A* 3ijc_A* 3iiv_A* 3ij0_A* 3ijl_A* 2qyv_A				
Probab=100.00 E-value=2.1e-34 Score=244.71 Aligned_cols=248 Identities=18% Similarity=0.232 Sum_probs=0.0				
Q ss_pred	CCcCeeEEEEcCCC---CEEEEECcCCcEEEEccCccceEEccCCCCEEEEECc--CccCCEEEECcCCcEEEE			
Q Fri_Mar_04_23:	7 AHNELIHDVLDYDG---KRLATCSSDKTIKIFVEGETHKLIDTLTGHEGVPWRVDWAH--PKFGTILASCSDYDGKVL	81 (297)		
Q Consensus	7 ~~~~h~v~~~~~g~l~t~s~d~v~lwd~~~~~l~s~D~i~i~~~~~	81 (297)		
T Consensus	67 ~~~~~v~~~~~l~s~dg~i~iwd~~~~~v~~~~~l~s~dg~v~v~~~~~	142 (366)		
T 3k26_A	67 DADENFYTCAWTYDSNTSHPLLAVAGSRGIIIRINP--ITMQCIKHVYGHGNAINELKFHPRD--PNLLLSVSKDHALRL	142 (366)		
T ss_dssp	CTTCEEEEEEECTTTCTCEEEEEETTCBEEECT--TTCBEEEEESCCSEEEEECS--TTEEEETTSCEEE			
T ss_pred	ccCCcEEEEEEcCCCCCcEEEEECcCEEEEEEC--CCccceEEecCceEEEEEECCC--CCEEEECcCCcEEEE			
Q ss_pred	EEccCCeEEEEEE---cccCccEEEEECcCCcCCcEEEEECCEEEEEECcCCcChhhhhhh-----			
Q Fri_Mar_04_23:	82 WKKEENGWSQIAVH---AVHSASVNSVQWAPHEYGPLLVASSDGKVSVEFKENGTTSPITIDA-----	143 (297)		
Q Consensus	82 wd~~~~~l~v~~~~~l~d~i~i~~~~~	143 (297)		
T Consensus	143 wd~~~~~v~~~~~l~d~i~iwd~~~~~	216 (366)		
T 3k26_A	143 WNIQTDT--LVAIFGGVGRHDEVLSADYDLL--GEKIMSCGMDHSLKLWRINRSK--RMMNAIKESYDNPKNRPFIS	216 (366)		
T ss_dssp	EETTTTE--EEEEECSTTSCSSCEEEEEECTT--SSEEEETTSCEEEEECSH--HHHHHHHHHTCCGGCCSSCCCC			
T ss_pred	ECCCCC--eEEEEcccccCCcEEEEECcC--CCEEEECcCCcEEEEECcCC--ccccccccccccCccccceeecc			
Q ss_pred	-----ccccEEEEECcCCccccccccCccceEEEEECcCceEEEEECcCCc-----eeEEEEe			
Q Fri_Mar_04_23:	144 -----HAIGVNSASWAPATIEEDGHEHNGKESRKFTVGGADNLVKIWKYNSDAQ-----TVVLESTL	200 (297)		
Q Consensus	144 ~~~~~v~~~~~l~tg~d~i~wd~~~~~	200 (297)		

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      |...+.+++|+.      .+++++.|+.|++|++....      ....+..+
T Consensus      217 -----v-----1-----d-i-wd----- 281 (366)
T 3k26_A          217 QKIHFPDFTSTRIRHRYVDCVRNLG-----DLILSKSCENAIVCWKPGKMDDDIDKIKPSESNVTILGRF 281 (366)
T ss_dssp         EEECCSSEEECSSSCCCEEEEE-----TEEEECSSSEEEEESSSTCCGGGCCCTTCCCEEEEEEE
T ss_pred         eeeccCcccccccccEEEEEecC-----CEEEECCEEEEEEccccccccccccCccccceeecc

Q ss_pred         cCCCCcEeEEEECC--CCCCCEEEEEECCCEEEEEEccCCC-CceeEEEEccccCcEeEEEEEECCCCCEEEEEEcCCCC
Q Fri_Mar_04_23: 201 EGHSDWVRDVAVSPT--VLLRSYLASVQDRCTCIWTQDNEQ-GPWKKTLLKEEFKFPVLRASWSLSGNVLASGGDNK 277 (297)
Q Consensus      201 --h--v--l--s-----las-s-Dg-i-iw-----i-----l-----d-- 277 (297)
      ..|...|.+++|+|+ + .+|++++.||.|++|++.... .....+...+...|.+++|+|++++|++++.||.
T Consensus      282 -----v-----s-----l-----dg-i-vwd-----v-----s-----l-----s-----dg-- 358 (366)
T 3k26_A          282 DYSQCDIWMYRFSMDFWQ---KMLALGNQVGKLYVWDLEVEDPHKAKCTTLTHHKCGAAIRQTSFSRDSILLIACDDAS 358 (366)
T ss_dssp         ECSSCCSSCCCECTTS---SEEEECTTSCEEEECSSSSGGGCEEEECCTTCCSCSEEEECTTSSEEEETTSE
T ss_pred         CCCcCeEEEEECcCCCC---CEEEECcCCCEEEECcCCCCccccceEEEEccccCcEEEEECCEEEEEECCCC

```

Q ss_pred EEEEE

Q Fri_Mar_04_23: 278 VTLWK 282 (297)

Q Consensus 278 i-iw- 282 (297)

|++|+

T Consensus 359 i-iw- 363 (366)

T 3k26_A 359 IWRWD 363 (366)

T ss_dssp EEEEE

T ss_pred EEEec

No 81    

☐ >3sfz_A APAF-1, apoptotic peptidase activating factor 1; apoptosis, caspase activation, cytochrome C, procaspase-9, A nucleotide, cytosol; HET: ADP; 3.00A {Mus musculus} PDB: 3shf_A* 3j2t_A* Probab=100.00 E-value=2.8e-34 Score=280.09 Aligned_cols=249 Identities=20% Similarity=0.376 Sum_probs=0.0

```

Q ss_pred         CceEecCCcCeeEEEECCCCCEEEEEECCCEEEEEEccCCcCceEEecCCCCCEEEEcCCcCcEEEEEcCCCEEE
Q Fri_Mar_04_23: 1 MVTIANAHNELTHDAVLDDYQKRLATCSSDKTIKIFVEGETHKLIDTLTGHEGPPVWRVDWAHPKFGTILASCSYDGKVL 80 (297)
Q Consensus      1 -----h--v--l--s-----g--l-t-s-d--v-lwd-----h--v-----l--s--d--i- 80 (297)
      +...+.+|...|++++|+| |++|++|+ .+|++|++|+ .+.+.+.+++|.+.|.+++|+++ +++|++++.|++|+
T Consensus      607 -----h--v--fs-dg--las-s-d--i-lwd-----l--h--V--v-fspd--g--las-s-d--v- 682 (1249)
T 3sfz_A          607 SRLVVRPHTDVYHACFSQDQRIASCGADKTLQVFKA--ETGEKLLDIKAHEDEVLCASFSSD--DSYIATCSADKVKV 682 (1249)
T ss_dssp         CSEEECCSSCEEEECTTSSEEEETTSCSEEEET--TTCEEEECSSCEEEECTT--SSEEEETTSEEE
T ss_pred         ceeEecCCCCeEEEECCCCCEEEEEECCCEEEEEEc--CCCCEEEEEcCCCCEEEEEecC--CCEEEEECCEEE

```

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Q ss_pred         EEEccCCeEEEEEEccCcCceEEEEECcCCcCCeEEEEEECCCEEEEEEcCCcCchhhhhhhcccccEEEECCcccc
Q Fri_Mar_04_23: 81 IWKEENGRRWSQIAVHAVHSASVNSQVWAPHYEGPFLLVASSDGKVSVVFKEGNTTSPILIDAHAFGVNSASWAPATIEE 160 (297)
Q Consensus      81 iwd-----v-----l-----d--i-i-----v----- 160 (297)
      +|+.+++ .+.+.+|...|.+++|+|+.+.+.+++++.|+.|++|+|+.+... ..+.+.+|...|.+++|++
T Consensus      683 vWd--g--h--v-----s-----l--sgs-d--i--wd-----h--v-----spdg-- 755 (1249)
T 3sfz_A          683 IWDSATG--LVHTYHSEQVNCCHFNKSNHLLLATGSNDFLKLWDLNQKE--CRNTMFGHTNSVNHCRFSPDD-- 755 (1249)
T ss_dssp         EEEETTCC--EEEEECSSCEEEEEECCSSSSCEEEETTSCSEEEETTSS--EEEECCSSCEEEEEECSST--
T ss_pred         EEECCCE--EEEECCCCCCEEEEEECCCEEEEEEcCCCEEEEEEcCCc--eEEEEcCCCEEEEEECCCC--

```

```

Q ss_pred         cccccCCCCcEEEEEECCcEeEEEEECcCCcceeEEEEe-----
Q Fri_Mar_04_23: 161 DGEHNGTKESRKFTVGADNLVKIWKYNSDAQTYVLESTL----- 200 (297)
Q Consensus      161 -----l-tg--d--i--wd----- 200 (297)
      .++++|+.|++|++|++|++ .+.+.
T Consensus      756 -----l-s-s-dg-v-vwd-----v-----s-dg--l-----i 821 (1249)
T 3sfz_A          756 -----ELLASCSADGTLRLWDVRS--NERKSINVKRFFLSSDPEDVVEIVKCCSWSADGDKLIVAAKNKV 821 (1249)
T ss_dssp         -----TEEEESSSEEEEGGGT-----EEEEEECCCC-----CCCCCBBCCBCTTSSEEEETTTEE
T ss_pred         -----CEEEEEECCCEEEEEECCCC-----ccccccccccccCCCCccccceEEEEEcCCCCCEEEEEECCCE

```

```

Q ss_pred         -----cCCCCcEeEEEECCCCCCCCCEEEEEECCCEEEEEEccCCCCcEeEEEEccccCCcEeEEEEEECCC
Q Fri_Mar_04_23: 201 -----EGHSDWVRDVAVSPTVLLRSYLASVSDRTCLITWTQDNEQGPWKKTLLKEEFKFPDLVLRASWSLS 265 (297)
Q Consensus      201 -----h--v--l--s-----las-s-Dg-i-iw-----i----- 265 (297)
      .+|...|.+++|+|++ .+++++.|+.|++|+.... ..+.+.+ |...|++++|++
T Consensus      822 -----d--l-----s-----l-----d--v-lwd-----h--V--v--spd 893 (1249)
T 3sfz_A          822 LLFDIHTSGLLAEIHTGHSTIQYCDFSPYD--HLAVIALSQYCVELWNIDSRL--KVADCRG--HLSWVHGVMPSPD 893 (1249)
T ss_dssp         EEEETTCCCEEEECSSSSCCCEEEECSSST--TEEEECSSCEEEETTTE--EEEECC--SSCEEEETTCTT
T ss_pred         EEEECCECCcEccccCcCcCEEEEEECCc--CEEEEEECCCEEEEEECCCC--eeEecC--ccccEEEEEECCC

```

```

Q ss_pred         CCEEEECcCCCCEEEEE
Q Fri_Mar_04_23: 266 GNVLALSGGDNKVTLWK 282 (297)
Q Consensus      266 --l-----d--i-iw- 282 (297)
      |++|++++.|++|++|+
T Consensus      894 g--l-s-s-D--i-vWd 910 (1249)
T 3sfz_A          894 GSSFLTASDDQITRVWE 910 (1249)
T ss_dssp         SSEEEETTSCSEEEEEE
T ss_pred         CCEEEEEECCCEEEEEE

```







No 82    

☐ >3gre_A Serine/threonine-protein kinase VPS15; seven-bladed propeller, WD repeat, scaffold protein, ATP-binding, endosome, golgi apparatus; 1.80A {Saccharomyces cerevisiae} Probab=100.00 E-value=2.5e-35 Score=257.24 Aligned_cols=254 Identities=13% Similarity=0.112 Sum_probs=0.0

```

Q ss_pred         ceEecCC-cCeeEEEECCCC-EEEEECcCCCEEEEcCcc--CccceeEEecCCCCCEEEEEEcCCcCcEEEEEcCC
Q Fri_Mar_04_23: 2 VVIANAH-NELIHDVLDYQK-RLATCSSDKTIKIFVEG--ETHKLIIDTLTGHEGPPVWRVDWAHPKFGTILASCSYD 76 (297)

















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No 83      

>3i2n_A WD repeat-containing protein 92; WD40 repeats, structural genomics, structural genomic consortium, SGC, apoptosis, transcription; 1.95A {Homo sapiens}

Probab=100.00 E-value=9e-35 Score=247.57 Aligned cols=251 Identities=14% Similarity=0.184 Sum_probs=0.0

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T Consensus	445	dg-i-v-d-----v-----spdg-----la--d-i-iw-----	509 (655)
T 4ci8_A	445	TGRNFWFDTEKD--LVTHVDGNQLSVMRYSPDG-----NFLAIGSHNLCIYIGVSDNGRKYTRVGKCS	509 (655)
T ss_dssp		SSEEEEEETTTC--EEEEECSSSCSEEEEEECTTS-----SEEEEEETTSCSEEEEEETTTTEEEEEEEEC	
T ss_pred		CCCCCCCCCCCC--EEEEECccccEEEEECCCC-----CEEEEECCCCCCCCCCCCCCCCeEEeEEEC	
Q ss_pred		cCCCCeEEEECCCCCCCCEEEEEECCeEEEEccCCCCeEEEEcccc-----CCc	
Q Fri_Mar_04_23:	202	GHSWVRDVAWSPTVLRSYLASVSQDRTCIWTQDNEGPPKKTLKKEK-----FPD	255 (297)
Q Consensus	202	-h---v-l--s-----las-s-Dg-i-iw-----	255 (297)
T Consensus	510	++++ + + +.++++ .+. + + +.... +.... +..	580 (655)
T 4ci8_A	510	GHSFITHLDWSVNS--QFLVNSGDIYILYVWPSACK-----QVSVETTRDIEWATYCTLGHFVFGVWPGSDGT	580 (655)
T ss_dssp		CCSSCEEEEEBTTS---SCEEEEEETTCCEEEEGGTE-----ECCCHHHHTTCBSCCCSSSTTTTSSCTTCTCT	
T ss_pred		CCCCCCEEEEECCCC--CEEEEECCCCeEEEECCCCe-----eCChhhcccccEEccccCCCCeEEcCCCCC	
Q ss_pred		eEEEEEECCCCEEEECCCCEEEEEECCCCeEEeEEccC	
Q Fri_Mar_04_23:	256	VLWRASWSLSGNVLALSGGDNKVTLWKENLEGGWEPAGEVHQ	297 (297)
Q Consensus	256	-i-----l-----d--i-iw-----	297 (297)
T Consensus	581	-.+++ + ++++ ++++ . .++ +.+.....+. +.	622 (655)
T 4ci8_A	581	DINAVCRAHEKKLLSTGDDFKVHLFSYPCSQFRAPSHIYGG	622 (655)
T ss_dssp		SEEEEEECSSSEEEEEETTSCEEEEESCSSSSCCCEEEEC	
T ss_pred		ceEEEECCCCEEEECCCCeEEEEcCCCCCCCCCceEEcC	
<div>No 90</div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div>			
<div><input type="checkbox"/> >lgxr_A</div> ESG1, transducin-like enhancer protein 1; transcriptional CO-repressor, WD40, transcription repressor, WD repeat; 1.65A {Homo sapiens} SCOP: b.69.4.1 PDB: 2ce8_A 2ce9_A			
Probab=100.00 E-value=3e-33 Score=235.23 Aligned_cols=247 Identities=15% Similarity=0.252 Sum_probs=0.0			
Q ss_pred		ceEecCCcCeeEEEECCCCEEEEEECCcCEEEEEccCC-ccceEEec--cCCCCEEEEECcCCcCEEEEECCCCe	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLDYIGKRLATCSSDKTIKIFVEGE--THKLIDTLT--GHEGPVWRVDWAHPKFGTILASCSDGK	78 (297)
Q Consensus	2	-h---v-----g--l-t-s-d--v-lwd-----h-s-s-D--	78 (297)
T Consensus	44 +++ + ++++ ++++ +. + + +... ..+. ++++ +++ +++ ++++ . +.	120 (337)
T lgxr_A	44	QINTLNHGEVVCVAVTINPTRHVTGG--KGCVKQWIDISHPGNKSPPVSQLDCLNRDNYIRSCKLLPD--GCTLIIVGGEAST	120 (337)
T ss_dssp		EEEEECSSCCCEEEECSSSEEEEC--BSEEEEEETTSCTTSCSEEEECSTTSBEEEEECTT--SSEEEEESSSE	
T ss_pred		eeEecCCCCeEEEEecCCcEEEEcC-CEEEEEccCccCccccccccCCCCeEEEEEECCC--CcEEEECCCCe	
Q ss_pred		EEEEccCCeEEEEEEccCccCEEEEECCcCCeEEEECCCEEEEEECcCCcchhhhhhhcccccEEEEECCcC	
Q Fri_Mar_04_23:	79	VLIWKEENGRWSQIAVHAVHSASVNSVQWAPHEYGPLLVAASSDGKVSVEFKENGTTSPIIIDAHAIQVNSASWAPATI	158 (297)
Q Consensus	79	i-iwd-----v-----l-----d-i-i-----v-----	158 (297)
T Consensus	121	++ + ++++..... ...+.+++ + + +.+++++.+.+++ + +... ..+. ++++ +++ + ++	195 (337)
T lgxr_A	121	LSINDLAAPTPIRIKAEITTSAPACYALAI SPD--SKVCFSCCSDGNIAVWDLHNQ--TLVRQFGHTDGASCIDISNDG--	195 (337)
T ss_dssp		EEEECCCC--EEEEECSSSCSEEEECTT--SSEEEEEETTSCEEEETTTT--EEEEECSSSCSEEEECTTS--	
T ss_pred		EEEECCCCccceeeccccceEEEEEECCC--CEEEEECCCEEEEECCCC--ceEEECcCCCEEEEECCCC--	
Q ss_pred		cccccccCccceEEEEECcCceEEEEECcCCcEEEEEccCCcEeEEEECCCCCCCCEEEEEECCcCEEEEEccC	
Q Fri_Mar_04_23:	159	EEDGEHNGTKESRKFTVGGADNLVLIWYKNSDAQTYVLESTLGHSDWVRDVAWSPTVLRSYLASVSQDRTCIWTQDN	238 (297)
Q Consensus	159	-----l-tg--d-i-wd-----h-v-l-s-----las-s-Dg-i-iw-----	238 (297)
T Consensus	196+. ++ + +... ..+. ++++ +++ + ++ + +.	255 (337)
T lgxr_A	196	-----TKLWTGGLDNTVRSWDLREG-----ROLQHQDFTSQIFSLGYCPTG--EWLAVGMESSNVVILHVNK	255 (337)
T ss_dssp		-----SEEEEEETTSCEEEETTTT-----EEEEECSSCEEEECTTS--SEEEEEETTSCEEEETTTT--	
T ss_pred		-----CEEEEECCCCEEEECCCC-----cccccccCCcCEEEEECCCC--CEEEEECCCEEEEECCCC	
Q ss_pred		CCcCceEEeccccCCeEEEEEECCCCEEEEEECCCCEEEE	
Q Fri_Mar_04_23:	239	EQGPWKTKLKEEKFPDVLWRASWSLSGNVLALSGGDNKVTLWK	282 (297)
Q Consensus	239	-----i-----l-----d-i-iw-----	282 (297)
T Consensus	256+. +.+.+++ + ++++ ++++ . .++ + +.	293 (337)
T lgxr_A	256	PD---KYQLHL--HESCVLSLKFAFCGKFWFSTGKDNLLNAWR	293 (337)
T ss_dssp		SC---EEEEEC--CSSCEEEECTTSSEEEETTTSEEEEE	
T ss_pred		Cc---ceEEec--CCCCEEEEEECCCCEEEECCCCeEEEE	
<div>No 91</div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div> <div></div>			
<div><input type="checkbox"/> >3dwl_C</div> Actin-related protein 2/3 complex subunit 1; propellor, actin-binding, ATP-binding, cytoskeleton, nucleot binding, WD repeat; HET: ATP; 3.78A {Schizosaccharomyces pombe}			
Probab=100.00 E-value=2.9e-35 Score=251.65 Aligned_cols=259 Identities=17% Similarity=0.154 Sum_probs=0.0			
Q ss_pred		ceEecCCcCeeEEEECCCCEEEEEECCcCEEEEEccCC-ccceEEecCCCCEEEEECcCCcCEEEEECCCCeEE	
Q Fri_Mar_04_23:	2	VVIANAHNELIHDAVLDYIGKRLATCSSDKTIKIFVEGET--HKLIDTLTGHEGPVWRVDWAHPKFGTILASCSDGKVL	80 (297)
Q Consensus	2	-h---v-----g--l-t-s-d--v-lwd-----h-s-s-D--	80 (297)
T Consensus	48	+.+.+. ... +++ + ++++ ++++ .+. + + +.... ..+. ++++ +++ +++ ++++ . +.	125 (377)
T 3dwl_C	48	ARTFSDHDKIVTCVDWAPKSNRIVTCSQDRNAYVYKRPDGTWQKTLVLLRLNRAATFVRNSPN--EDKFAVGGSGARVIS	125 (377)
T ss_dssp		CCCBCSSCEEEECTTTTCEEEETTTTSEEEC-----CCCCECCCCSSCEEEECTT--SSCCEEESSSCEE	
T ss_pred		EEeccccCCEEEEECCCCEEEEECcCEEEEEccCccceEEecCCcCEEEEECCC--CEEEEECCCEEE	
Q ss_pred		EEeCCcC-EEEEEEcc-cCceEEEEECcCCcCCeEEEECCCEEEEEEC-----CCcchhhhhh	
Q Fri_Mar_04_23:	81	IWKEENGR-WSQIAVHAV--HSASVNSVQWAPHEYGPLLVAASSDGKVSVEFK-----ENGTSPPIIID	142 (297)

No 92                

☐ >1r5m_A SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A {Saccharomyces cerevisiae}
Probab=100.00 E-value=6.3e-34 Score=246.78 Aligned_cols=249 Identities=15% Similarity=0.259 Sum_probs=0.0

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[illegible]

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```
T 4ggc_A      100 K--RLRNMTSHSARVGSLSWNSY---ILSSGSRSGHIIHHHDVRA-EHHVATLSGHSQEVCGLRWAPDG----- 162 (318)
T ss_dssp     E--EEEEEECCSSCEEEEEETT---EEEEETTSEEEETTSS-SEEEEECCSSCEEEETTS-----
T ss_pred     c--eeeeccccCCeEEEEcCCC---EEEEEcCCCCEEEEcCCC-cccEEEECCCCCEEEEECCCC-----

Q ss_pred     cccEeEEEEcCcEeEEEEEcCCCCeEEEEEcCCCCcEeEEEECCCCCCCCEEEEE--CCeEEEEEcCCCCcEEF
Q Fri_Mar_04_23: 168 KESRKfVTGGADNLVKIWKYNSDAQTYVLESTLEGHSDWVRDVAWSPTVLLRSYLASVS--QDRTCIWTQDNEQGPWKK 245 (297)
Q Consensus   168 ~~~~l~tg~d~i~wd~h~v~l~s~las~s~Dg~i~iw~ 245 (297)
               .+|++|+.|+.|++| |+.+.+.+.+.+.+.|.+++|+|++ ..+++++ .|++|++| |+.+.
T Consensus   163 ~~~~las~s~D~v~vwd~h~v~v~p~l~s~s~D~i~iwd~ 232 (318)
T 4ggc_A      163 ---RHLAGGNDNLVNVWPSAPGEGGWVPLQTFIQHGAVKAVAWCPWQ--SNVLATGGGTSDRHIRIWNVCSGA----- 232 (318)
T ss_dssp     ---SEEEEEETTSEEEEESSCBTTBSCSEEECCCSCEEEETTS--TTEEEECTTCEEEETTCC-----
T ss_pred     ---CEEEECcCcEeEEcCCCCcCCCCeEEcCCcEeEEEcCC--CEEEFcCCCCcEEEECCCCc-----

Q ss_pred     EEEccccCcEeEEEEECCCCEEEEc--CCCCEEEEE
Q Fri_Mar_04_23: 246 TLLKEEKFPDVLWRASWSLSGNVLALSG--GDNKVTLWK 282 (297)
Q Consensus   246 ~~~~i~l~d~i~iw~ 282 (297)
               .+.+.+.+.+++|+|+++|++++ .|+.|++|+
T Consensus   233 ~~~~V~sp~l~d~i~iwd~ 270 (318)
T 4ggc_A      233 -CLSAVDAHsQVCSILWSPHYKELISGHGFAQNQLVIWK 270 (318)
T ss_dssp     -EEEEECSSCEEEEEETTTEEEECTTTCCEEEEE
T ss_pred     -EeEEcCCcEeEEECcCCCCeEEEEcCCCCEEEEE
```

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.