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MAX-PLANCK-GESELLSCHAFT

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

Quickfinder

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3ary Structure

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HHblits

HHpred

HHsenser

HMMER3

PatternSearch

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ProtBLAST+

PSI-BLAST

PSI-BLAST+

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New job

Resubmit

Resubmit\_HMM

Resubmit/HHsenser

Realign

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HHpred - Results

Job-ID: seh1\_new

Date: 23:25 on Mar 04 2016

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Reduced alignment

Representative alignment

Full alignment

Create model

Merge Q/T alignments

Forward to PCoils

Forward MSA

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Export

Color alignments

☐ color only SS

☒ color alignments

☐ color alignments

View Alignment

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Resubmit section

3f3f\_A

4u1e\_I

5a9q\_7

1vvh\_C

1got\_B

2pn7\_B

3bg1\_A

4j73\_A

4j87\_A

4l9o\_A

3jrp\_A

3ow8\_A

3w15\_A

4lg8\_A

4wju\_A

2pb1\_B

3fn0\_A

1erj\_A

3jb9\_L

3frx\_A

3jan\_g

4lg8\_A

4j0w\_A

4j87\_A

4wjs\_A

4bh6\_A

4d6v\_A

4a11\_B

5cxb\_B

4jsn\_D

5gan\_H

4j73\_A

3ei3\_B

3w15\_A

4erq\_A

4yvd\_A

5ans\_A

4ggc\_A

4lg9\_A

4j0x\_A

1k8k\_C

4zoy\_A

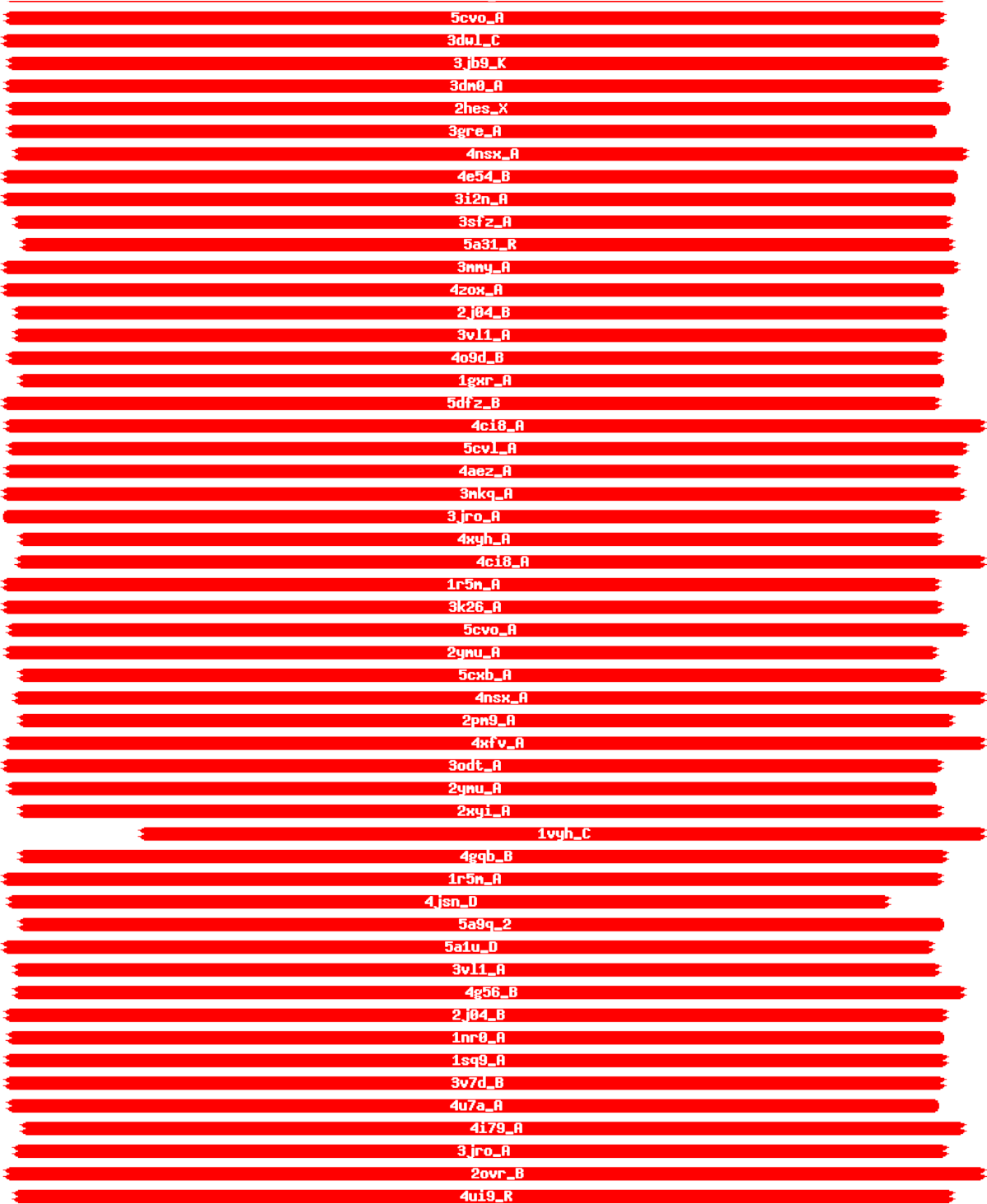
5ans\_A

5cv1\_A

4psw\_B

4gga\_A

3sfz\_A



Query Fri\_Mar\_04\_23:25:19\_+0100\_2016 (seq=MQPFDSGHDD...KCMSVITAQQ Len=349 Neff=10.6 Nseqs=136)  
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 3f3f_A Nucleoporin SEH1; struc	100.0	4.8E-52	1.3E-56	370.4	41.2	349	1-349	3-351 (351)
<input type="checkbox"/>	2 4ule_I Eukaryotic translation	100.0	1.1E-42	3E-47	309.6	34.1	307	1-334	1-323 (347)
<input type="checkbox"/>	3 5a9q_7 Nucleoporin SEH1; trans	100.0	2.5E-40	6.8E-45	295.9	40.4	307	1-349	4-323 (360)
<input type="checkbox"/>	4 1vyh_C Platelet-activating fac	100.0	6.9E-41	1.9E-45	304.7	34.0	286	2-333	101-409 (410)
<input type="checkbox"/>	5 1got_B GT-beta; complex (GTP-b	100.0	2.7E-40	7.5E-45	293.4	36.1	288	2-332	48-340 (340)
<input type="checkbox"/>	6 2pm7_B Protein transport prote	100.0	7.6E-40	2.1E-44	285.0	38.2	275	1-345	1-295 (297)
<input type="checkbox"/>	7 3bg1_A Protein SEC13 homolog;	100.0	7.5E-41	2.1E-45	294.0	31.7	285	1-349	5-307 (316)
<input type="checkbox"/>	8 4j73_A Coatomer subunit beta';	100.0	8.7E-39	2.4E-43	278.9	34.8	263	1-348	5-269 (301)
<input type="checkbox"/>	9 4j87_A Coatomer subunit alpha;	100.0	1.5E-38	4.1E-43	280.5	36.0	265	1-349	3-298 (327)
<input type="checkbox"/>	10 4l9o_A Protein transport prote	100.0	2.5E-37	6.8E-42	275.3	38.9	278	3-347	63-349 (349)
<input type="checkbox"/>	11 3jrp_A Fusion protein of prote	100.0	2.2E-37	6E-42	278.7	37.2	276	1-349	3-301 (379)
<input type="checkbox"/>	12 3ow8_A WD repeat-containing pr	100.0	7.7E-37	2.1E-41	269.0	35.8	289	1-333	24-319 (321)
<input type="checkbox"/>	13 3w15_A Peroxisomal targeting s	100.0	6E-37	1.6E-41	274.8	35.2	249	8-334	61-367 (368)

<input type="checkbox"/>	14	41g9_A	F-box-like/WD repeat-co	100.0	1.7E-36	4.6E-41	275.0	38.0	296	4-343	50-367 (400)
<input type="checkbox"/>	15	4wju_A	Ribosome assembly prote	100.0	1.5E-37	4.2E-42	290.8	31.3	288	2-332	136-514 (515)
<input type="checkbox"/>	16	2pbi_B	Guanine nucleotide-bind	100.0	1.3E-36	3.6E-41	271.2	35.7	293	2-332	57-354 (354)
<input type="checkbox"/>	17	3fm0_A	Protein CIA01; WDR39,SG	100.0	2.6E-36	7.3E-41	268.1	36.5	308	1-345	7-345 (345)
<input type="checkbox"/>	18	1erj_A	Transcriptional repress	100.0	1.3E-36	3.7E-41	274.9	33.8	281	7-334	62-388 (393)
<input type="checkbox"/>	19	3jb9_L	PRE-mRNA-splicing facto	100.0	2.3E-37	6.4E-42	274.5	28.0	287	2-334	43-340 (340)
<input type="checkbox"/>	20	3frx_A	Guanine nucleotide-bind	100.0	5.1E-36	1.4E-40	263.4	35.6	295	2-337	10-319 (319)
<input type="checkbox"/>	21	3jam_g	RACK1; eukaryotic trans	100.0	5.9E-36	1.6E-40	263.7	35.5	298	1-337	10-326 (326)
<input type="checkbox"/>	22	41g8_A	PRE-mRNA-processing fac	100.0	3.2E-36	8.9E-41	268.7	33.6	280	8-333	67-354 (354)
<input type="checkbox"/>	23	4j0w_A	U3 small nucleolar RNA-	100.0	6.4E-36	1.8E-40	265.6	34.0	303	2-349	7-336 (343)
<input type="checkbox"/>	24	4j87_A	Coatomer subunit alpha;	100.0	1.6E-35	4.4E-40	261.1	35.6	260	3-334	47-327 (327)
<input type="checkbox"/>	25	4wjs_A	RSA4; ribosome assembly	100.0	7.2E-36	2E-40	277.5	34.8	287	3-332	108-484 (485)
<input type="checkbox"/>	26	4bh6_A	APC/C activator protein	100.0	2.2E-35	6E-40	258.3	35.4	243	8-337	61-308 (308)
<input type="checkbox"/>	27	4d6v_A	GIB2, G protein beta su	100.0	5.3E-35	1.5E-39	256.2	37.4	289	5-333	11-312 (314)
<input type="checkbox"/>	28	4a11_B	DNA excision repair pro	100.0	2.4E-35	6.6E-40	268.1	35.6	296	2-336	36-366 (408)
<input type="checkbox"/>	29	5cxb_B	Ribosome biogenesis pro	100.0	1.2E-35	3.3E-40	266.5	30.0	294	3-332	15-369 (369)
<input type="checkbox"/>	30	4jsn_D	Target of rapamycin com	100.0	2.2E-34	6.1E-39	253.8	34.2	291	12-349	3-312 (326)
<input type="checkbox"/>	31	5gan_H	U4/U6 small nuclear rib	100.0	2.4E-35	6.7E-40	272.5	28.7	285	7-332	173-465 (465)
<input type="checkbox"/>	32	4j73_A	Coatomer subunit beta';	100.0	4E-34	1.1E-38	249.4	34.1	247	3-330	49-298 (301)
<input type="checkbox"/>	33	3ei3_B	DNA damage-binding prot	100.0	1.9E-34	5.3E-39	259.8	32.8	290	3-335	67-382 (383)
<input type="checkbox"/>	34	3w15_A	Peroxisomal targeting s	100.0	5.3E-34	1.5E-38	255.6	35.0	271	1-349	3-335 (368)
<input type="checkbox"/>	35	4ery_A	WD repeat-containing pr	100.0	1.7E-33	4.6E-38	246.1	37.2	295	1-335	15-312 (312)
<input type="checkbox"/>	36	4yvd_A	Pleiotropic regulator 1	100.0	1.8E-33	5E-38	252.1	37.4	294	3-344	58-362 (374)
<input type="checkbox"/>	37	5ams_A	SQT1, ribosome assembly	100.0	3.5E-34	9.6E-39	262.1	33.3	285	5-335	105-431 (431)
<input type="checkbox"/>	38	4ggc_A	P55CDC, cell division c	100.0	1.9E-33	5.2E-38	247.0	36.5	246	5-337	63-317 (318)
<input type="checkbox"/>	39	41g9_A	F-box-like/WD repeat-co	100.0	1.3E-33	3.5E-38	256.0	35.8	279	7-334	109-399 (400)
<input type="checkbox"/>	40	4j0x_A	Ribosomal RNA-processi	100.0	2.4E-34	6.7E-39	264.2	31.2	304	2-349	25-450 (451)
<input type="checkbox"/>	41	1k8k_C	P40, ARP2/3 complex 41	100.0	5.6E-34	1.5E-38	254.8	31.6	296	3-334	2-360 (372)
<input type="checkbox"/>	42	4zoy_A	SQT1; chaperone, riboso	100.0	1.5E-33	4.2E-38	261.0	35.2	311	1-338	7-488 (491)
<input type="checkbox"/>	43	5ams_A	SQT1, ribosome assembly	100.0	1.2E-33	3.4E-38	258.5	33.8	301	1-349	57-392 (431)
<input type="checkbox"/>	44	5cvl_A	WD repeat-containing pr	100.0	4.9E-34	1.4E-38	271.5	32.0	300	2-335	38-343 (598)
<input type="checkbox"/>	45	4psw_B	Histone acetyltransfera	100.0	9.6E-34	2.6E-38	257.0	32.4	245	7-336	116-385 (401)
<input type="checkbox"/>	46	4gga_A	P55CDC, cell division c	100.0	4.4E-33	1.2E-37	254.2	36.8	247	5-338	143-398 (420)
<input type="checkbox"/>	47	3sfz_A	APAF-1, apoptotic pepti	100.0	1.4E-33	3.9E-38	289.6	35.9	294	2-336	608-1035 (1249)
<input type="checkbox"/>	48	5cvo_A	WD repeat-containing pr	100.0	8.1E-34	2.2E-38	272.3	31.9	300	2-335	23-328 (677)
<input type="checkbox"/>	49	3dwl_C	Actin-related protein 2	100.0	8.4E-35	2.3E-39	261.0	23.2	293	1-333	3-377 (377)
<input type="checkbox"/>	50	3jb9_K	PRE-mRNA-splicing facto	100.0	1.9E-34	5.2E-39	267.1	26.1	286	3-336	157-453 (473)
<input type="checkbox"/>	51	3dm0_A	Maltose-binding peripla	100.0	6.3E-33	1.7E-37	268.7	37.7	295	2-334	375-692 (694)
<input type="checkbox"/>	52	2hes_X	YDR267CP; beta-propelle	100.0	1.5E-32	4.2E-37	241.0	35.6	301	3-337	8-330 (330)
<input type="checkbox"/>	53	3gre_A	Serine/threonine-protei	100.0	5.9E-34	1.6E-38	260.9	27.7	288	3-332	56-437 (437)
<input type="checkbox"/>	54	4nsx_A	U3 small nucleolar RNA-	100.0	1.1E-32	3.1E-37	266.4	38.0	315	5-343	244-624 (684)
<input type="checkbox"/>	55	4e54_B	DNA damage-binding prot	100.0	2.4E-34	6.7E-39	263.4	23.6	297	1-340	111-435 (435)
<input type="checkbox"/>	56	3i2n_A	WD repeat-containing pr	100.0	3.9E-33	1.1E-37	249.1	30.7	298	1-339	10-357 (357)
<input type="checkbox"/>	57	3sfz_A	APAF-1, apoptotic pepti	100.0	3.1E-33	8.6E-38	287.1	34.4	303	5-337	653-1160 (1249)
<input type="checkbox"/>	58	5a31_R	The anaphase-promoting	100.0	2.2E-32	6.1E-37	246.8	35.5	244	8-338	130-378 (386)
<input type="checkbox"/>	59	3mmy_A	mRNA export factor; mRN	100.0	3.6E-33	1E-37	250.2	30.0	273	1-340	31-354 (368)
<input type="checkbox"/>	60	4zox_A	Ribosome assembly prote	100.0	1.8E-32	5E-37	245.7	34.1	305	1-335	7-381 (381)
<input type="checkbox"/>	61	2j04_B	YDR362CP, TAU91; beta p	100.0	8.9E-34	2.4E-38	266.0	26.4	281	5-336	203-518 (524)
<input type="checkbox"/>	62	3v11_A	26S proteasome regulato	100.0	1.5E-32	4.2E-37	250.2	32.3	294	5-336	92-420 (420)
<input type="checkbox"/>	63	4o9d_B	RIK1-associated factor	100.0	4E-32	1.1E-36	247.4	34.4	289	3-334	24-409 (428)
<input type="checkbox"/>	64	1gxr_A	ESG1, transducin-like e	100.0	4.7E-32	1.3E-36	239.1	33.7	285	7-335	49-337 (337)
<input type="checkbox"/>	65	5dfz_B	Serine/threonine-protei	100.0	8.8E-35	2.4E-39	297.2	17.8	291	1-333	1062-1445 (1460)
<input type="checkbox"/>	66	4ci8_A	Echinoderm microtubule-	100.0	5.2E-32	1.4E-36	260.6	36.1	320	2-349	104-512 (655)
<input type="checkbox"/>	67	5cvl_A	WD repeat-containing pr	100.0	4E-32	1.1E-36	258.4	34.6	306	3-343	84-414 (598)
<input type="checkbox"/>	68	4aez_A	CDC20, WD repeat-contai	100.0	6.5E-32	1.8E-36	244.9	34.4	254	2-340	127-385 (401)
<input type="checkbox"/>	69	3mkq_A	Coatomer beta'-subunit;	100.0	1.6E-32	4.3E-37	270.6	32.7	257	1-342	5-266 (814)
<input type="checkbox"/>	70	3jro_A	Fusion protein of prote	100.0	1.5E-32	4.1E-37	268.3	32.2	299	1-333	1-327 (753)
<input type="checkbox"/>	71	4xyh_A	Kinetochore protein MIS	100.0	1.2E-32	3.2E-37	252.1	28.3	251	7-334	129-413 (430)
<input type="checkbox"/>	72	4ci8_A	Echinoderm microtubule-	100.0	7.7E-32	2.1E-36	259.4	35.3	295	6-349	255-624 (655)
<input type="checkbox"/>	73	1r5m_A	SIR4-interacting protei	100.0	2.1E-32	5.8E-37	249.0	29.7	301	1-333	35-359 (425)
<input type="checkbox"/>	74	3k26_A	Polycomb protein EED; W	100.0	4.9E-32	1.3E-36	241.4	30.9	289	1-334	10-365 (366)
<input type="checkbox"/>	75	5cvo_A	WD repeat-containing pr	100.0	7.7E-32	2.1E-36	258.7	34.0	306	3-343	69-399 (677)
<input type="checkbox"/>	76	2ymu_A	WD-40 repeat protein; u	100.0	9E-32	2.5E-36	254.8	34.1	280	2-332	9-290 (577)
<input type="checkbox"/>	77	5cxb_B	Ribosome biogenesis pro	100.0	1.3E-31	3.6E-36	250.7	34.6	285	7-335	128-508 (514)
<input type="checkbox"/>	78	4nsx_A	U3 small nucleolar RNA-	100.0	3E-31	8.2E-36	256.4	37.7	299	5-349	202-585 (684)
<input type="checkbox"/>	79	2pm9_A	Protein WEB1, protein t	100.0	1E-32	2.9E-37	251.1	25.5	268	7-338	65-340 (416)
<input type="checkbox"/>	80	4xfv_A	Elongator complex prote	100.0	7.7E-32	2.1E-36	264.2	33.4	321	2-349	12-443 (792)
<input type="checkbox"/>	81	3odt_A	Protein DOA1; ubiquitin	100.0	1.7E-31	4.6E-36	234.2	32.1	282	1-334	10-295 (313)
<input type="checkbox"/>	82	2ymu_A	WD-40 repeat protein; u	100.0	2.7E-31	7.4E-36	251.5	35.4	279	3-332	297-577 (577)
<input type="checkbox"/>	83	2xyi_A	Probable histone-bindin	100.0	3.3E-32	9.1E-37	249.1	27.9	272	7-334	126-409 (430)
<input type="checkbox"/>	84	1vyh_C	Platelet-activating fac	100.0	5.5E-32	1.5E-36	246.1	28.7	255	50-349	103-380 (410)
<input type="checkbox"/>	85	4gqb_B	Methylosome protein 50;	100.0	3E-31	8.2E-36	235.1	32.6	250	7-336	80-332 (344)
<input type="checkbox"/>	86	1r5m_A	SIR4-interacting protei	100.0	3.5E-31	9.7E-36	240.9	33.2	277	1-334	100-424 (425)
<input type="checkbox"/>	87	4jsn_D	Target of rapamycin com	100.0	3.4E-31	9.4E-36	233.5	31.5	272	3-315	36-323 (326)
<input type="checkbox"/>	88	5a9q_2	Nucleoporin NUP37; tran	100.0	7.1E-32	2E-36	237.1	27.0	285	7-335	14-326 (326)
<input type="checkbox"/>	89	5alu_D	Coatomer subunit beta';	100.0	6.3E-31	1.7E-35	261.8	35.8	288	1-331	7-298 (905)
<input type="checkbox"/>	90	3v11_A	26S proteasome regulato	100.0	1.4E-31	3.7E-36	243.9	27.9	286	5-333	24-362 (420)
<input type="checkbox"/>	91	4g56_B	MGC81050 protein; prote	100.0	6.2E-31	1.7E-35	234.4	31.2	300	5-342	38-350 (357)
<input type="checkbox"/>	92	2j04_B	YDR362CP, TAU91; beta p	100.0	8.9E-33	2.5E-37	259.2	20.3	255	2-336	126-429 (524)
<input type="checkbox"/>	93	1nr0_A	Actin interacting prote	100.0	3.5E-30	9.6E-35	244.5	38.2	309	3-335	184-611 (611)
<input type="checkbox"/>	94	1sq9_A	Antiviral protein SKI8;	100.0	2.1E-31	5.7E-36	240.5	28.4	295	2-336	9-396 (397)
<input type="checkbox"/>	95	3v7d_B	Cell division control p	100.0	1.7E-30	4.6E-35	240.1	34.8	256	2-335	114-381 (464)
<input type="checkbox"/>	96	4u7a_A	Ribosome biogenesis pro	100.0	4.6E-31	1.3E-35	259.7	31.1	289	3-333	450-826 (826)
<input type="checkbox"/>	97	4i79_A	Nucleoporin NUP43; stru	100.0	1.3E-30	3.6E-35	235.9	31.1	258	8-342	28-319 (399)
<input type="checkbox"/>	98	3jro_A	Fusion protein of prote	100.0	9.9E-32	2.7E-36	262.5	24.0	292	5-336	49-377 (753)
<input type="checkbox"/>	99	2ovr_B	FBW7, F-BOX/WD repeat p	100.0	1.4E-29	3.9E-34	232.7	36.6	290	2-349	111-405 (445)
<input type="checkbox"/>	100	4ui9_R	Fizzy-related protein h	100.0	9.3E-30	2.6E-34	236.7	33.7	248	5-338	225-477 (493)

No 1

☐ >3f3f\_A Nucleoporin SEH1; structural protein, protein complex, nucleopori complex, nuclear pore complex,



Q ss\_pred EEecCcccccccccEEEEcCCCCEEEECcCCCCEEEEeCCCeEEEECCCCCcEEEEcccccEEEEcCC

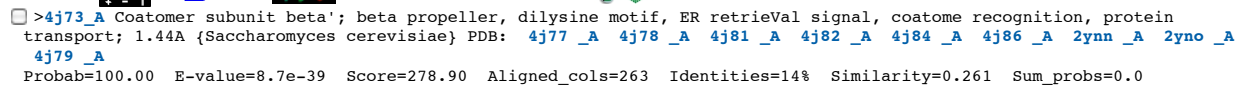
Q Fri Mar 04 23: 82 KLWEDPDQEECSGRRWNKLCITLNDKSGSLYSVKFAPAHGLGLKACLGNIGILRLYDALPESDLRSWTLTSEMKVLSITPP 161 (349)

Q ss_pred		C E E E E c C C C E E E E e	
Q Fri_Mar_04_23:	317	T L T S S A G D D G K V R L W K	332 (349)
Q Consensus	317	--las-s-D--v-iW-	332 (349)
		++      .  + + + +	
T Consensus	325	--l--s-g-D--i-iWd	340 (340)
T lgot_B	325	M A V A T G S W D S F L K I W D	340 (340)

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Q	ss_pred		CCcE	EEEEEE	CCCC	EEEE	cCCc	EEEEE	ccc	CC	EEEEEE	Eccc	C
Q	Fri_Mar_04_23	303	HNGE	VWVS	VN	LTGL	TSAG	DGK	VLW	KATYS	NF	KCMS	VITaTQ
Q	Consensus	303	h	-i	-v	sp	g	-l	a	s	-d	-v	iW
				..		++++		+		++++		+	+
T	Consensus	261	-v	-v	-sp	-g	-l	a	s	-d	-v	iW	-g
T	3bg1_A	261	FND	VVWV	HV	SW	ITAN	LL	AV	SGG	DN	KV	LKES
T	ss_dssp		CS	SS	EEEEEE	CT	TT	CCCC	EEEE	SS	CCCC	EEEE	CT
T	ss_pred		cCCc	EEEEEE	CCCC	EEEE	cCCc	EEEEE	CCCC	EEEEEE	Eccc	C	



Q ss_pred	EEEEcccccccccccccEEEBCCCCCEEEEEECCcCCCEEEEECCCeEEEECCCC-CcEEEEccccEEBec		
Q Pri_Mar_04_23:	VKLWEDPDQEECSGRRWKCLTLDNKSGLSLVSKFPAHLGLKLAACLDGILRLYDALEP-SDLRSWLTSEMKVLIS	159	(349)
Q Consensus	i-vld-----l-----v-----p-----d-----i-vld-----	159	(349)
	++ + ++ +.+..+ ... ++ + + +.++++ ++ + +... ..+		
T Consensus	i-vwd-----l-sg-----h-----v-----p-----d-----v-lwd-----	136	(301)
T 4j73_A	IRVFNNTG-----EKVDFEAPHDYIRSIADVHT--KPYVLSGDSDLTVKLWNWENWALEQTF--	136	(301)
T ss_dssp	EEEEETTT-----CEEEEECCSCSEEEEECS--SSEEEEEETTSCEEEEETTTTEEEE-----		
T ss_pred	EEEEEECCCC-----CEEEEECCCCCEEEEEECc--CEEEEECCCCeEEEECCCCchhh-----		

[illegible]

☐ **>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=1.5e-38 Score=280.50 Aligned cols=265 Identities=15% Similarity=0.262 Sum probs=0.0

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No 10      

☐ **>4190\_A** Protein transport protein SEC13, copii coat assem protein SEC16 fusion protein; beta propeller, vesicle coat budding; HET: EDO; 1.60A {Komagataella pastoris}  
 Probab=100.00 E-value=2.5e-37 Score=275.29 Aligned cols=278 Identities=29% Similarity=0.588 Sum\_probs=0.0








[illegible]



>41g9 A F-box-like/WD repeat-containing protein TBL1XR1; structural genomics consortium, SGC, WD40 repeats,



Q ss pred CCcccCCCcC-eEEEEEECCCCCEEEEeCCCeEEEECCCCCc eeFeeeec-cccc eEEEEEEcCCCCCEEEEeCC








No 18       

>1erj\_A Transcriptional repressor TUP1; beta-propeller, transcription inhibitor; 2.30A {Saccharomyces cerevisiae}  
SCOPE: [b.69.4.1](#) PDB: [Safu\\_3\\*](#)  
Probab=100.00 E-value=1.3e-36 Score=274.94 Aligned cols=281 Identities=16% Similarity=0.281 Sum\_probs=0.0










No 21       

☐ [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-36 Score=263.71 Aligned\_cols=298 Identities=17% Similarity=0.250 Sum\_probs=0.0

[illegible][illegible]

[illegible]

T ss_pred	eeeccCccEEEEccCCCCEEEEcCCcEEeECCCC---CcCeECCCCCCCCEEEECC--CCCEEEEECCcEe		
Q ss_pred	EEecccCcccccccccEEEEECCCCcEEEEECc-----CCCCcEEEEECcCCcEEEECCCCcEEEEccccccEE		
Q Fri_Mar_04_23:	82 KLWEEEDPDQECGRRWNKLTNDKSKGLYSVKFAP-----AHLGLKLACLGNDGLRLYDALPDLRSWTLTSEM	155 (349)	
Q Consensus	82 -lwd-----v-----p-----l-----d-i-ld-----	155 (349)	
T Consensus	182 -iwd-----h-----p-----l-s-s-d-v-iwd-----l-----	244 (485)	
T 4wjs_A	182 RVWDESGKQV-----NQEFRGHAKWVLAALAWQPYHLWRDG--TARLASASKDCTVRVRLVNTGRTEHVL	244 (485)	
T ss_dssp	EEEETTTTTEEC-----SSCBCCSScEEEEECGGGCBTT--BCEEEEETTSCEEEETTTTTEEEEEE		
T ss_pred	EEEECCCCcc-----ccccCCCCcEEEEcCCCCCCCC--CCCEEEEECCcEEEECCCCcEEeEc-----		
Q ss_pred	EecccCccccccEEEEEccCCCCcEEcCCc--eEEEEcCCcEEEE-----		
Q Fri_Mar_04_23:	156 VLSIPPANHLQSDFCCLSWCPFRFSPKLAVALAQ-ATIIYQRGDKGLHVA-----	205 (349)	
Q Consensus	156 -----	205 (349)	
T Consensus	245 -----h-----v-----l-s-s-d-i-vwd-----v-----s-d-----	314 (485)	
T 4wjs_A	245 -----SGHKGSVSCVKWGG-----TDLIYTGSHDRSVRVWDVAVKGTLVHNTAHGHVWNHIALSSDHVLRDAYHDHTKEV	314 (485)	
T ss_dssp	-----CCSScEEEEECT-----TSEEEEEETTSCEEEECHHHHTTSCSEEECCSScEEEEETTSCCTTCC		
T ss_pred	-----cCCCCcEEEEEC--CcEEEEEcCCcEEEECCCCcEEEEccCcEeEEECcCcEeEEECcCcEe		
Q ss_pred	-----EEccCCCCcEEEECCCCCCCCcEEEE		
Q Fri_Mar_04_23:	206 AKLPGHKSLIRSIWAPSIGRWYQLIATG-----	234 (349)	
Q Consensus	206 -----h-----v-----sp-----las-----	234 (349)	
T Consensus	315 -----l-s-s-d-i-wd-----h-----v-----spdg-----las-----	390 (485)	
T 4wjs_A	315 PGTEERRAKAKERFEKAAIKGKVAERLVSASDDFTMYLWDPNTNGSKPVARLLGHQNKVNHVQFSPDG-----TLIASA	390 (485)	
T ss_dssp	CSSHHHHHHHHHHHHHEETTCEEEEEETTSCSEEECHHHHTTSCSEEECCSScEEEEECTTS--SEEEEE		
T ss_pred	cCchhhHHHHHHHHhhccCCCCcEEEEcCCCEEEECcCCCCccceEcCCCCEEEECCCC--CEEEEE		
Q ss_pred	cCCCCEEEEECcC--cc		
Q Fri_Mar_04_23:	235 CKDGRIRIFKITEK--LSPLASSESLTNSNMFNDSADVMDAQGRSDSNTTEKAEQSNLQVELLSEHDDHNGEVSWSV	312 (349)	
Q Consensus	235 s-d-v-vwd-----h-----i-v-----	312 (349)	
T Consensus	391 s-d-i-ld-----l-h-----v-----spdg-----l-s-s-d-----i-vwd-----l-h-----v-----	464 (485)	
T 4wjs_A	391 GWDNSTKLWNARDGKFIKNLRGHVAPVYQCAWSADSLRVVTGSKDCT-----LKVWNVVRTGKMLDLPGEDEVYVADW	464 (485)	
T ss_dssp	ETTSEEEEEETTTCCEEEECSScEEEEECTTSSEEEEEETTSC-----EEEEETTTCCEEEECSScEEEE		
T ss_pred	eCCCcEEEECCCCcEEEEcCCCCcEEEEECcCCCCcEEeEeCCCCcEEeEeCCCCcEEEE		
Q ss_pred	CCCCEEEEECcCCcEEEE		
Q Fri_Mar_04_23:	313 NLGTGLSSAGDDGKVRWLK-----	332 (349)	
Q Consensus	313 spdg--las-s-D--v-iw-----	332 (349)	
T Consensus	465 spdg--l-s--D--v-iw-----	484 (485)	
T 4wjs_A	465 AADGELVASGGKDKAVRTWR-----	484 (485)	
T ss_dssp	CTTSSEEEEEETTTCCEEEEE		
T ss_pred	cCCCCEEEEECcCCcEEcC		
No 26			
<input type="checkbox"/> 4bh6_A APC/C activator protein CDH1; anaphase promoting complex, ACML1, cell cycle, ubiquitination; HET: SEP; 2.90A (Saccharomyces cerevisiae) SCOP: b.69.4.0			
Probab=100.00 E-value=2.2e-35 Score=258.27 Aligned_cols=243 Identities=17% Similarity=0.298 Sum_probs=0.0			
Q ss_pred	CcCeEEEEECcCCCCEEEEECcCCcEEEEECcCCCCcEEeEecccceEEEEECcCCCCcEEEEECcCCcEEeEeccc		
Q Fri_Mar_04_23:	8 HDDLVHDVDFYGRHVAFTCSSDQHKVFKDKDTNWLSDSRAHDSSIVAIDWASPEYGRILIASASYDKTVKLWEE	87 (349)	
Q Consensus	8 h-----v-----s-d--l-t-s-D--v-iw-----h-----v-----v-----las-s-Dg-v-ld-----	87 (349)	
T Consensus	61 -----v-----s-dg--lasg--dg-v-iw-----l-g-h-----v-----l-s-s-D--i-wd-----	132 (308)	
T 4bh6_A	61 TENYTSLSWIGAGSHLAVGQANGLVYDYVMKR-----KCIRTLSGHIDRVACLWN-----NHVLTSGSRDRHLRHLDVR	132 (308)	
T ss_dssp	CSSCEEEEEETTTSSEEEEEETTSCSEEEEETTTT--EEEEECcSScEEEEEC--TTSEEEEESScEEEEETT		
T ss_pred	cCCCcEEEEECcCCCCcEEEEECcCCcEEEEECcCCc--CcEEeEcCCcEEeEEEC--CCEEEEECcCCCCcEEEE		
Q ss_pred	CccccccccccEEEEEcCCCCcEEEEECcCCCCcEEEEECcCCcEEEEECcCCCCcEEeEecccceEEEEECcCCCCc		
Q Fri_Mar_04_23:	88 PDQEECSGRRWNKLTNDKSKGLYSVKFAPAHGLKLACLGNDGLRLYDALPDLRSWTLTSEMVKLSIPPANHLQS	167 (349)	
Q Consensus	88 -----v-----p-----l-----d-i-ld-----	167 (349)	
T Consensus	133 -----h-----v-----v-----las-s-D--v-iw-----h-----	189 (308)	
T 4bh6_A	133 MPDPF-----FTIESHTQEVCGLKWVA--DNKLASGGNDNVVHVYEGTSKSPILTF-----DEHKAA	189 (308)	
T ss_dssp	SSSSC-----SEEECCSScEEEEECSS--SCEEEEEETTSCEEEEETTSCSScEEB-----CCSSC		
T ss_pred	CCcc-----cEEcCCCCcEEEEECc--CCEEEEECcEEeEeECCcCCcEEB-----cCCcc		
Q ss_pred	eeEEEEcccCCCCcEEeEc--CCc--eEEEEECcCCcEEEEECcCCCCcEEeEEEECCCCCCCCcEEEEE--EcCCCCEE		
Q Fri_Mar_04_23:	168 DFCLSWCPFRFSPKLAVALAQ-ATIIYQRGDKGLHVAALKPGLKSLIRSIWAPSIGRWYQLIAT--GCKDGRIRI	242 (349)	
Q Consensus	168 -----i-----h-----v-----sp-----las--s-d--v-v-----	242 (349)	
T Consensus	190 v--v--sp--las--s-D-i-iwd-----v-----s-----g--d--i-l	259 (308)	
T 4bh6_A	190 VKAMAWSPH--KRGVLATGGGTADRLKIKWNVNTSKMDDID--SGSGICNMVWSKNT--NELVTSHGYSKYNLTL	259 (308)	
T ss_dssp	EEEEEECCSS--STTEEEEEETTTCCEEEEEETTTCCEEEEE--CSCCEEEEEECSS--CSEEEEEETTTCCEEE		
T ss_pred	EEEEEECC--CCcEEeECcCCCCcEEEEECcCCCCcEEEEEC--CCcEEEEEECCc--CcEEeEcCCcEEe		
Q ss_pred	EEeCcc		
Q Fri_Mar_04_23:	243 FKITEKLSPLASSESLTNSNMFNDSADVMDAQGRSDSNTTEKAEQSNLQVELLSEHDDHNGEVSWSVWNLGTGLISSA	322 (349)	

Q ss pred EEEeCCCeEEEeccCccccccccccceEEEEcCCCCcEEEEECc---CCCCcEEEEeCCCeEEEECCCCCcccee

> **5cxb\_B** Ribosome biogenesis protein ERB1; ribosome assembly, WD40, beta-propeller, ubiquitin-like DOMA protein binding; 2.10A [Chaetomium thermophilum] PDB: **5cxb\_B** **5cyl\_B**  
 Probab=100.00 E-value=1.2e-35 Score=266.54 Aligned\_cols=294 Identities=16% Similarity=0.196 Sum\_probs=0.0










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Q ss\_pred cccCCcCcEEEEECCCC-CEEEEEcCCCEEEEECCCCCcEeEeecccceEEEEEEcCCCCCEEEEEcCCcE

Q Fri Mar 04 23: 3 PFDGSHDDLVDHVVYDFYG-RHVAETCSSDQHIKVFKLKDTSNWELSDSWRAHSDSIVAIDWASPEYGRITASASYDKTV 81 (349)

No 34       

☐ >3w15\_A Peroxisomal targeting signal 2 receptor; beta-propeller, targeting signal recognition, cytosol; 1.80Å {Saccharomyces cerevisiae}  
Probab=100.00 E-value=5.3e-34 Score=255.64 Aligned\_cols=271 Identities=15% Similarity=0.216 Sum\_probs=0.0

No 36    

>4yvd\_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=1.8e-33 Score=252.09 Aligned\_cols=294 Identities=15% Similarity=0.236 Sum\_probs=0.0

```
Q ss_pred          cccCCCCcEEEEEECCCCCEEEEeCCcEEEECCCCCCEEeEeeeeccccceEEEEEECCCCCCCCEEEECcEE
Q Fri_Mar_04_23:   3 PFDSGHDDLVLHVVDVYDFYGRHVATCSSDQHIKVKFLDKDTSNWELSDSWARHSSIVAIIDWASPEYGRIIASASYDKTKVK      82 (349)
Q Consensus        3 -h-v-h-v-s-d-l-t-s-v-iwd-----h-v-----las-s-Dg-v-----      82 (349)
                   .+.+.|.+.|++++|+|++++|++|.|.+++|+|+... ..+.+.+.|.+++|++ +++|++++|.+.|+
T Consensus        58 -l-h-v-h-v-----l-dq-v-iwd-----v-----l-s--d-i-      131 (374)
```

▢ >5ams\_A SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}  
Probab=100.00 E-value=3.5e-34 Score=262.13 Aligned\_cols=285 Identities=16% Similarity=0.143 Sum\_probs=0.0






Q ss_pred		cCcccccccccccccEEEEEcCCCCcEEEEEECCcCCCCcEEEEeCCcCEEEEECCCCCcceeeccccEEFeeCCcCcccc		
Q Fri_Mar_04_23:	87	DPDQEECSGRWRNKLCTLNDSKGLSYLVKFAPAHLLGLKLCAGLNDGTLRLYDALEPSDLRSLTSEMKVLSIPPANHQL	166 (349)	
Q Consensus	87	.-v-.l-d-i-ivd-	166 (349)	
T Consensus	182	.++ +...+.. ...+.++. . + ..++++.  +...+ +....+. + .+.. -h-	236 (400)	
T 4lg9_A	182	HTG-----EAKQQFPFHSAPALVDWQS---NTTFASCSTDCHIVCKLGQDRPIKTF-----QGHTN	236 (400)	
T ss_dssp		TTT-----EEEEECSSSCSSEEEEEESS--SSEEEEETTSCEEEETTSCSSSEEE-----CCCSS		
T ss_pred		CCC-----ccccccCCCCcEEEEEc--CcEEEECCCCcEEEEECcccccee-----CCccc		









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No 43     

☐ >Sams\_A SQT1, ribosome assembly protein SQT1; chaperone, UL16; 3.35A {Saccharomyces cerevisiae}  
Probab=100.00 E-value=1.2e-33 Score=258.47 Aligned cols=301 Identities=15% Similarity=0.115 Sum probs=0.0

Q ss\_pred cccccccceeecccCCcCeEEEEEECCCCCEEEcCCcCeEEEEcccccCEEEEEcccccC  
Q Fri\_Mar\_04\_23: 286 AELQSNLQVELLSEHDDHNGEVWSVNLGTGLTSSAGDDGKVRWVKATYSNEFKCMSVITAQQ 349 (349)  
Q Consensus 286 .....h...i...v...spdg...las-s-D-v-iw... 349 (349)  
T Consensus 335 i-ldw...v...l...dg-i-vwd...h... 392 (431)  
T 5ams\_A 335 ILLYDTSARVRHKF-VLEDSVTKLMFDND--DLFASCI NGKVYQFNARTG---QKFCVCGVN 392 (431)  
T ss\_dssp EEEEETTTTEEEE-ECSSCEEEEEETT--EEEEETTSCEEEETTTC---CEEEECSS  
T ss\_pred EEEEECCcCEEEEE-cCCCCEEEEEECC--EEEEECCEEEEECCCC--cEEEEECC

No 44    

☐ >5cvl\_A WD repeat-containing protein 48; UAF1, USP, deubiquitinase, DUB, protein BI; 3.00A {Homo sapiens} PDB:  
5cvn\_A  
Probab=100.00 E-value=4.9e-34 Score=271.51 Aligned\_cols=300 Identities=15% Similarity=0.167 Sum\_probs=0.0





Q ss\_pred CcccCCcCeEEEEEECCCCCEEEcCCcCeEEEECCCCCceEeecccccEEEEEECCCCCEEEcCCcCe  
Q Fri\_Mar\_04\_23: 2 QPFDGSHDDLVDVVDYFYGRHVATCSSDQHIKVKFKLDKTSNWLSDSWRAHDSSIVADWASPEYGRITIASASYDKTV 81 (349)  
Q Consensus 2 .....h...v...s-d...l-t-s-D-v-iwd...h...v...las-s-Dg-v 81 (349)  
T Consensus 38 .....H...V...l...spdg...latg...dg-I-iwd...h...V...l...s...dg-l-sgs-Dg-I 114 (598)  
T 5cvl\_A 38 DEVEKYNNRGNVNLQDLPALNRLFTAGRDSIRIWSVNQH-KQDPYIASMEHHTDWNIDIVLCC--NGKTLISASSDTTV 114 (598)  
T ss\_dssp CCCCCSBSSCEEEEEETTTEEEETTSSCEEEECSSC-CSCCEEEECSSCEEEEEECCG--GGTTEEEETTSC  
T ss\_pred cccccccCCEEEEECCCCCEEEcCCcCeEEEECCCC-cCceEEcccccCEEEECc--CCCEEEECCEEE

Q ss\_pred EEecccCcccccccccEEEEECCCCCCEEEECcCCCCCEEEECcCCcCEEEEECCCCCceeecccccEEEEcc  
Q Fri\_Mar\_04\_23: 82 KLWEDDPQEECSGRWNKLCITLNDKSGSLYSVKFAPAHGLGKLACLGNDGILRLYDALPSDLRSWLTSEMKVLSTIPP 161 (349)  
Q Consensus 82 -lwd-----v-----p-----l-----d-i-iwd----- 161 (349)  
T Consensus 115 .....H...V...l...s-d...l-s...dg-I-vwd----- 179 (598)  
T 5cvl\_A 115 KVVNAHKG-----FCMSTLRTHKDYVKALAYAKD--KELVASAGLDRIFLWVDNLTALTASNTVTSSSL----- 179 (598)  
T ss\_dssp EEEEETTTT-----EEEEECSSCEEEEEETT--TTEEEETTSCEEEEHHHHHSCSSSCCCCCCEE-----  
T ss\_pred EEECCCC-----ceEEcCCCCcEEEEECcC--CCCEEEECCEEEECcCCcCccccCcccecc-----

Q ss\_pred CccccceEEEEEcccCCCCcEEeCCc-cEEEEcCCCCCEEEECcCCCCCceEEEEECCCCCCcEEEEECCCCCE  
Q Fri\_Mar\_04\_23: 162 ANHLQSDFCLSWCPSPKLAVALAQ-AIYQGRKGDKLHVAAKLPGHKSLIRISWAPSIGRWYLIATGCKDGR 240 (349)  
Q Consensus 162 .....i...v...v...spdg...las-s-d-v 240 (349)  
T Consensus 180 .....v...l...s...g...l-sg-dg-I-vwd...h...v...l...spdg...l-sgs-dg-v 249 (598)  
T 5cvl\_A 180 SGNKDSIYSLAMNQ--LGTITVSGSTKVLRVWDPRCA--KLMKLGHTDNVKAALLNRDG--TQCLSGSSDGTI 249 (598)  
T ss\_dssp CCCCCCEEEEECT--TSSCEEEETTSSSEEECTTCC--EEEEECSSCEEEEECTTS--SEEEETTSEE  
T ss\_pred cCCCCCEEEEECC--CCCEEEECCEEEECcCCCC--eeEEECCEEEECCEEEECcCC--CEEEECCEEE

Q ss\_pred EEEECcC--cc  
Q Fri\_Mar\_04\_23: 241 RIFKITEK--LSPLASESLTNSNMFDSADVMDQGRSDNTEKAELQSNLQVELLSEHDDHNGEVWSVNLGT- 317 (349)  
Q Consensus 241 -vwd-----h...i...v...spdg-- 317 (349)  
T Consensus 250 .....lwd...h...v...l...s-dg-l-sg-dg-vwd...v...vwd...v...l...sp-g 323 (598)  
T 5cvl\_A 250 RLWSLGQRCIATYRVHDEGVVALQVNDAPTHVYSGGRDRK-----IYCTDLRNPDIRVLICEKAPVLKMLDRSADP 323 (598)  
T ss\_dssp EEEETTTTEEEEEECSSCEEEEECTTSCEEEEETTCE-----EEEESSSTTEEEEECSCEEEEEECSSSS  
T ss\_pred EEECCCCcEEEEcCCCCCEEEEECCCCCEEEECCE--EEEECCCCccccccccCCCCCEEEECcCCCC

Q ss\_pred --EEEEcCCcEEEEEccc  
Q Fri\_Mar\_04\_23: 318 --LLSAGDDGKVRWVKATY 335 (349)  
Q Consensus 318 --las-s-D-v-iw... 335 (349)  
T Consensus 324 .....l-s-s-dg-I-iwd... 343 (598)  
T 5cvl\_A 324 PPAIWVATKSTVNKWTLLG 343 (598)  
T ss\_dssp CEEEEEESSSCEEEECTT  
T ss\_pred ccEEEEECcCCcEEEEECC

No 45    

☐ >4psw\_B Histone acetyltransferase type B subunit 2; HAT WD40, histone acetyltransferase, accoa, phosphorylation, cytoplasmatic, transferase; HET: TPO COA; 2.10A {Saccharomyces cerevisiae} PDB: 4psx\_B\*  
Probab=100.00 E-value=9.6e-34 Score=256.97 Aligned\_cols=245 Identities=18% Similarity=0.301 Sum\_probs=0.0

Q ss\_pred CCcCeEEEEEECCc-CEEEECcCCcCEEEEECCCCCceEeecccccEEEEEECCCCCC-EEEEECcCEEE  
Q Fri\_Mar\_04\_23: 7 GHDDLVDVVDYFY-GRHVATCSSDQHIKVKFKLDKTSNWLSDSWRAHDSSIVADWASPEYGR-ITIASASYDKTVKLV 84 (349)  
Q Consensus 7 -h...v...s-d...l-t-s-D-v-iwd...h...v...las-s-Dg-v-lw 84 (349)  
T Consensus 116 -h...v...p...lat...dg-v-iwd...h...v...l...s-s-dg-i-iw 188 (401)  
T 4psw\_B 116 BHEEITRARIYMPQDPNIVATINGQTFLYSRS-E---GLQSTLKFHKDNGYALSFST--LVKGRLLSGSDHPTVALV 188 (401)  
T ss\_dssp EESSCEEEETTTTEEEETTTSCEEEEETT-T---EEEEECSSCCEEEECSS--SSTTEEEETTSCEE  
T ss\_pred CCCCcEEEEEECCCCCEEEcCCCCCEEEECcC--CCCCcCCCCCEEEECc--CCCCcEEEECCCCcEEEE

Q ss\_pred ecccC-----ccccccccceEEEEcC-CCCCCEEEECc-CCCCCEEEECcCCcCEEEEECCCCCceeecccccEEEE  
Q Fri\_Mar\_04\_23: 85 EEDPD-----QECCSGRRWNKLCITLND-SKGLYSVKFAP-AHLGLKACLGNDGILRLYDALPSDLRSWLTSEMKVLS 158 (349)  
Q Consensus 85 d-----v-----p-----l-----d-i-iwd----- 158 (349)  
T Consensus 189 d-----v-----h...v...l...s-dg-i-iwd----- 248 (401)  
T 4psw\_B 189 EVGSGGDPKTP-----VRTWNLHSDIINDKNKWHNFN--KDLFGTVSEDSLLKINDVRANNITIDTV 248 (401)  
T ss\_dssp ECSSSCSSSC-----SEESSSSCCEEEECSSC--TTEEEETTSCEEEEETTSCSCEEE-----  
T ss\_pred ECCCCCcccc-----ceEEcCCCCcEEEEECCc--CCCEEEECcCCcEEEECCCCcEEEE-----

```
Q ss_pred cCCCCccccceEEEEcccccCCCCc-eEEecCCc-eEEEEcCCcEEEEEEccCCCCceEEEECCCCCCCcEEEEEEcc
Q Fri_Mar_04_23: 159 IPPANHLQSDFLSWCPSPFSPK-LAYSALEQ-ATLYQRGKDGKLVAAKLPGHKSLIRISWAPSGIRWYQLIATGCK 236 (349)
Q Consensus 159 -----h-v-v-sp-----i-----las-s-
      .+...+.+++|+|  ++. +++++.++ +.+|+..... .+...+.|...|.+++|+|++ .+|++++.
T Consensus 249 -----v-----l-tg-dg-i-iwd-----h-v-v-p-----l-s-
T 4psw_B 249 -----KCPQPFNTLAFSH-----HSSNLLAAGHDSYVLYDLRNMKE--PLHHMSGHEDAVNNLEFSTHVD---GVVVSSTS 316 (401)
T ss_dssp ----ECSSCEEEEEECSS--SCSSEEEEEETTSCEEEEEETTTTS--CSSEECSSSCSEEEEEECSSST---TEEEEEET
T ss_pred ----cCCCCcEEEEcC--CCCCEEEEcCCcEEEECCCCC--CcEEECCECCCEEEEECCCCC--CEEEEEEC
```

```
Q ss_pred CCEEEEEEEcC-----cccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
Q Fri_Mar_04_23: 237 DGRIRIFKITE-----KLSPPLASEESLTNSNMFNDSADVMDAQGRSDSNTTEKAEQLQSNLQVELLSEHDD 302 (349)
Q Consensus 237 d-v-vwd-----|+.|++|+|. . +.+.+.+. 302 (349)
      |+.|++|+|. . +.+.+.+.
T Consensus 317 dg-v-iwd-----
T 4psw_B 317 DNRLMMWDLKQIGAEQTPDDAEDGVP-----ELIMVHAG 350 (401)
T ss_dssp TSCEEEEEGGGTTCCTCHHHHTTCCT-----TEEEEECC
T ss_pred CCcEEEEECCCCccccCccccccCc-----ceEEEEcC
```

```
Q ss_pred CCcEEEEEECCCC-EEEEcCCcEEEEEccccc
Q Fri_Mar_04_23: 303 HNGEVSVSWNLGT-ILSSAGDDGKVLWKATYS 336 (349)
Q Consensus 303 h--i-v--spdg--las-s-D-v-iw----- 336 (349)
      |...|+++|+|+++ +|++++.|+.|+|+....
T Consensus 351 h--v--s--g--l-sg-i-iwd----- 385 (401)
T 4psw_B 351 HRSSVNDFDLNPQIPWLVASAEENILQVWKCSHS 385 (401)
T ss_dssp CSSCEEEEEECSSSTTEEEEEETTSCEEEEEETTT
T ss_pred cCCCCeEEEECCCCCEEEEECCCEEEEEEEccccc
```

No 46       

☐ >4gga\_A P55CDC, cell division cycle protein 20 homolog; cell cycle, mitosis, securin, ubiquitination, WD40; 2.04A {Homo sapiens} SCOP: b.69.4.0 PDB: 4ggd\_A  
Probab=100.00 E-value=4.4e-33 Score=254.16 Aligned\_cols=247 Identities=19% Similarity=0.381 Sum\_probs=0.0

```
Q ss_pred cCCCCcEEEEEECCCCCEEEEECCCEEEEECCCCCceEEeecccccEEEEEECCCCCEEEEECCCEEEEE
Q Fri_Mar_04_23: 5 DSGHDDLVDVDFYGRHVATCSSDQHIKVKFLDKDTSNWLSDSWRAHDSSIVADWASPEYGRITIASASYDKTVKLV 84 (349)
Q Consensus 5 h--h--v--s-d--l-t-s-D-v-iw-----h--v--v--las-s-Dg-v-lw 84 (349)
      .+|.|...|.+++|+|++++|++|.|++|++|+|+... ..+.+.|...|.+++|+ +.|+++|+|.|++|
T Consensus 143 h--v--s--g--l-sg-i-iwd-----h--v--l--l-sgs-dg-i-iw 214 (420)
T 4gga_A 143 MEQPGEYISSVAWIKENGYLAVGTSSAEVQLWDVQQQ---KRLNMTSHSARVGLSWN---SYILSSGSRGSHHHH 214 (420)
T ss_dssp CCSTTCCEEEEEECTTSCEEEEEETTSCEEEEEETTT---EEEEECSSSCSEEEEE---TTSEEEEEETTSCEEEEE
T ss_pred cCCCCcEEEEEECCCCCEEEEECCCEEEEECCCC---EEeEEcCCCCcEEEEEC---CCEEEECCCCcEEEE
```

```
Q ss_pred ecccCccccccccceEEEEcCCCCcEEEEEEcCCCCcEEEEEEcCCCCcEEEEEEcCCCC---ccccccccceEEecC
Q Fri_Mar_04_23: 85 EEDPDQEECSGRRWNKCLTNDSKGSLSYVKFAPAHLGLKLACLGNDGILRLYDALEPS---DLRSWLTSEMKVLSIP 160 (349)
Q Consensus 85 d-----v-----p-----l-----d-i-iwd----- 160 (349)
      |+..... .+...+.|...|.+++|+|+ +.|++++.|+.|++|+|+... .+...+
T Consensus 215 d--h--v--l--s-d--lasgs-d--v-iwd----- 272 (420)
T 4gga_A 215 DVVRVAEH-----HVATLSGHSQVCGLRWAPD--GRHLASGGNDLVNVWVPSAPGEGGWVPLQTF-- 272 (420)
T ss_dssp ETTSSSC-----EEEEEECCSSCEEEEEETTT--SSEEEEEETTSCEEEEESSCCSSCCSCEE
T ss_pred ECCCCc-----cEEEEcCCCCcEEEEEECC--CEEEEECCCEEEEECCCCCCcEEEEE
```








```
Q ss_pred CCCCCcEEEEEcccccCCCCcEEec--CCc-eEEEEcCCCCEEEEEEccCCCCceEEEECCCCCCCcEEEEEC--
Q Fri_Mar_04_23: 161 PANHLQSDFLSWCPSPFSPKLAWSA--LQ-ATLYQRGKDGKLVAAKLPGHKSLIRISWAPSGIRWYQLIATGCG-- 235 (349)
Q Consensus 161 -----h-v-v-sp-----i-----las-s-
      ..|...+.+++|+|. ....++++. .++ +.+|+.... .+...+.|. .|.+++|+|++ ..|++++
T Consensus 273 --h--v--v--p-----lasg-gs-d-i-iwd-----v--l--s-----l--g- 341 (420)
T 4gga_A 273 --TQHQAQVAVAWCPW--QSNVLATGGTSDRHRIWNVCSG--ACLSAVDAHS-QVCSILWSPHY--KELISGHGF 341 (420)
T ss_dssp -CCSSCEEEEEECTT--CTEEEEEECTTCEEEEEETTTT---EEEEEECCSS-CEEEEEETTT---TEEEEEECT
T ss_pred -CCCCcEEEEECC--CCEEEEcCCCCCEEEEECCCC--CcEEEEcCCc-ceEEEECCCC--CEEEEEcC
```

```
Q ss_pred CCEEEEEEEcCcccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccccc
Q Fri_Mar_04_23: 236 KDGRIRIFKITEKLSPPLASEESLTNSNMFNDSADVMDAQGRSDSNTTEKAEQLQSNLQVELLSEHDDHNGEVSVSWNL 315 (349)
Q Consensus 236 -d-v-vwd-----h--i-v--spd----- 315 (349)
      .|+.|++|+|. . +.+.+.+.|...|.+++|+|
T Consensus 342 -d-i-iwd-----h--v--spd----- 375 (420)
T 4gga_A 342 AQNLVIWKYPTM-----AKVAELKGHTSRVLSLTMSPD 375 (420)
T ss_dssp TTCCEEEEEETTC-----CEEEEECCSSCEEEEEECTT
T ss_pred CCCeEEEECCCC-----CEEEEEcCcCcEEEEEECCC
```

```
Q ss_pred CCEEEEEcCCcEEEEEcccccC
Q Fri_Mar_04_23: 316 GTILSSAGDDGKVLWKATYSNE 338 (349)
Q Consensus 316 g--las-s-D-v-iw----- 338 (349)
      |++|++|+.|++|+|++|+|+....
T Consensus 376 g--l-s-s-D-v-iw----- 398 (420)
T 4gga_A 376 GATVASAAADETLRLWRCFELDP 398 (420)
T ss_dssp SSCCEEEEEETTTTEEEEECCSCSSC
T ss_pred CCEEEEECCCCCEEEEECCCCC
```

No 47       

☐ >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\*

No 48       

>5cvo\_A WD repeat-containing protein 48; WDR48, WD repeat, beta propeller, USP46, covalent DUB, deubiquitinase, hydrolase-protein binding complex; 3.89A {Homo sapiens}

Probab=100.00 E-value=8.1e-34 Score=272.31 Aligned cols=300 Identities=15% Similarity=0.166 Sum probs=0.0

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No 51

**>3dm0\_A** Maltose-binding periplasmic protein fused with RA; MBP RACK1A, receptor for activated protein C-kinase 1, beta propeller WD40 repeat; HET: GLC; 2.40A {Escherichia coli}  
 Probab=100.00 E-value=6.3e-33 Score=268.73 Aligned\_cols=295 Identities=17% Similarity=0.275 Sum\_probs=0.0

```







Q ss_pred          CccccCCCcCeEEEEEECCC-CCEEEEecCCeEEEECCCCCCC-eEeeeeecccccEEEEEECCCCCCEEEEECCC
Q Fri_Mar_04_23:   2 QPFDSGHDDLVHVDVVFYF-YGRHVATCSSDQHILVKFKLDKDTSN-WELSDSWRAHDSSIVAIWDASPEYGRILIASASYDK      79 (349)
Q Consensus        2 -h-v--l-t-s-D--v-iwd-----h-v-v-v-v-v-v-v-v-v-v-las-s-Dg      79 (349)
                   +..+..|+.|++++|+++ ++|+|. |+|++|||+|..... ..+...+|...|++++|++ +++|++|+.|+
T Consensus        375 -h-v--l-t-s-d-i-w-----h-v-v-v-v-v-v-v-v-v-v-l-s-d-      452 (694)
T 3dm0_A           375 KGTRMARHDTMVTATPATPIDNADIVSASRDKSIILWKLTKDKKAYGVAQRRLTGHSHFVEDVVLSS---DGQFALSGSGWG      452 (694)
T ss_dssp          EEEEECCSSCEEEEECTTCSEEEEEETTSEEEEECCCCSTTCSEEEEEECSSCEEEEEECT---YSSEEEEETTTS
T ss_pred          ccccccccEEEEEeCCCCCEEEEeCCeEEEeCCCCccccceeeccCcCcEEEEECC--CCCEEEEeCCC

Q ss_pred          eEEEEeccCcccccccccEEEEECCCCeEEEEECcCCCCcEEEEeCCeEEEEEECCCCCcEEEEcccccEEEEEc
Q Fri_Mar_04_23:   80 TVKLWEEDPDQECSGRRWNKCLTNDSKGSLYSVKFPAPAHLGLKLACLGNDDGITRLYLDALEPSDLRSWTLTSENKVLISL    159 (349)
Q Consensus        80 -v-lwd-----v-lwd-p-----l-l-d-i-ibd-----      159 (349)
                   .|++|||+.+ ..+..+..+|+|.++|++|+|+ +.|-+dd-.|++|++|+|+.....
T Consensus        453 i-ibd-----h-v-v-v-v-v-v-v-v-v-v-l-s-D-v-ibd-----      511 (694)
T 3dm0_A           453 ELRLWLDAAG-----VSTRRVFGHTKDVLVSFAFLD---NRQIVSASRRRTIKLNLTIGE-----CKYTISE    511 (694)
T ss_dssp          EEEEETTTTT-----EEEEEECCSSCEEEEEECTT---SSCEEEETTSCSEEECTTSC-----EEEEECs
T ss_pred          EEEEECCCC-----CEEEEEeCCCCEEEEEECC--CCEEEECCCCeEeeECCCC-----cEEEEc
  
```










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T ss_pred	EEEEccccCEEEEECCCCcEEEECCCEEEEECCCCccccchhhccCCCCEEEEEC--CCCEEEECC	
Q ss_pred	eEEEEcc-----CcccccccccEEEEE--CCCC--cEEEECC--CCCCEEEECCCEEEEECCCC	
Q Fri_Mar_04_23:	80 TVKLWEED-----PDQEECSGRWVKLCTLN--DSKG--SLYSVKFAP--AHLGLKLACLGNDGILRLYDALEP	142 (349)
Q Consensus	80 -v-lwd-----p-----l-----d-i-ibd-----	142 (349)
T Consensus	134 -v-ibd-----v-----l-----dg-i-ibd-----	202 (437)
T 3gre_A	134 QIIVLVKNHYQQESEVKFLN-----CICIKINLKNFGKNEYAVRMRAFNVEE--KSLLVALTNLRSVIFDIRTL	202 (437)
T ss_dssp	EEEEEEEEEEEEETEEEEEE-----EEEEEEGGGGSSCCCEEEEEEECCSS--CEEEEEETTSEEEEEETTC	
T ss_pred	eEEEEcccccccccccc-----cEEEEECCCCCCEEEEECCCC--cEEEECCCCeEEEECCCC	
Q ss_pred	CccccccccEEEEcCCC--ccccceEEEEccCCCCcEEEcCCc-eEEEEcCCCCEEEEEcc-CCCCcEE	
Q Fri_Mar_04_23:	143 SDLRSWTLTSEMVKLSIPPA--NHLQSDFCLSWCPSPFSEKLAVALAQ-AITYQRGKDGKLVAAKLP-GHKSLIRSI	218 (349)
Q Consensus	143 -----i-----h-----v-----	218 (349)
T Consensus	203 -----v-----s-----l-s-----dg-i-ibd-----i-----	263 (437)
T 3gre_A	203 ERLQII-----ENSPRHGAVSSICIDE--ECCVLILGTRGIIDIRFN--VLIRSWSGDHPATHV	263 (437)
T ss_dssp	EEEEEE-----ECGGGCCEEEEECT--TSCEEEEETTSCEEEEEETTT--EEEEEBCTCEEEEE	
T ss_pred	CEEEEE-----cCCCCCCEEEEECC--CCCEEEEECCCEEEEECCCC--CCEEEcCCCCCEEE	
Q ss_pred	EECC--CCCCCCEEEEECCCCEEEEcCcccccc-----cccccccccc-----c	
Q Fri_Mar_04_23:	219 SWAP---SIGRWQLIATGCKDGRIRIFKITEKLSPLAS-----EESLTNSNMFN-----S	267 (349)
Q Consensus	219 ~sp-----las-s-d~v-vwd-----	267 (349)
T Consensus	264 ~p~-----l-----d-i-vwd-----v-----i-----	339 (437)
T 3gre_A	264 EVCFYKNS---VIVVGGSSKFTLWNVKGCQYAFINSDEQPSMEHFLPIKGLLELNFCGIRSLNALSTISVSN	339 (437)
T ss_dssp	EECTTCTTE---EEEEESTTEEEEEETTTTEEEEESSSSCCGGGGSCBCSSGGGGCCCCCGGGGGCEEEET	
T ss_pred	EEEcCCCC---eEEEEcCCCCEEEEECCceeeEeccccCCCCceccccchheeEccccCCCCeEEEEcC	
Q ss_pred	ccccccccccccccccccccccccceeecc-----cccccccccc-----CCCCeEEEE	
Q Fri_Mar_04_23:	268 ADVDMDAQGRSDSNTTEKAEQLQSNLQVELLESHD-----DHNGEVWSV	310 (349)
Q Consensus	268 -----h~i~v-----	310 (349)
T Consensus	340 ~l-s~dg~i-ibd-----fs-----v-----l-----	413 (437)
T 3gre_A	340 DKILLTDEATSS---IVMFLNELSSSKAVISPSRFSDVFIPQVTANLTMLLRMKRSTHVSDDSLYHHDIIINSI	413 (437)
T ss_dssp	TEEEEEGGGT-----EEETTCGGGGCEEECC--CCCEEEEEETTEEEEEEC-----CCCEEE	
T ss_pred	CEEEEECCCC---EEEECCcCceEecCCcCceeeccccCCCCeEEEEcCchhhccccchCcCEEEEE	
Q ss_pred	EECC--CCCEEEcCCCCEEEEE	
Q Fri_Mar_04_23:	311 SWNL--TGTILSSAGDGVRLWK 332 (349)	
Q Consensus	311 ~sp~dg~las-s-D~v-iW~	332 (349)
T Consensus	414 ~s~-----l-s~dg~v-iW~	437 (437)
T 3gre_A	414 STCEVDETPLLVAACNSGLIGIFQ 437 (437)	
T ss_dssp	EEEESSSEEEEEETTSCEEEEC	
T ss_pred	EEEcCCCCEEEECCCCCEEEc	
<b>No 54</b>      		
<input type="checkbox"/> >4nsx_A U3 small nucleolar RNA-associated protein 21; ribosome biogenesis, UTPB complex, 90S preribosome, small SU processome, protein binding; HET: FLC; 2.10A {Saccharomyces cerevisiae} Probab=100.00 E-value=1.1e-32 Score=266.36 Aligned_cols=315 Identities=13% Similarity=0.140 Sum_probs=0.0		
Q ss_pred	cCCCcCEEEEECCCC-EEEEECCCEEEEECCCCCceEeecc-c---ceEEEEcCCCCCEEEEECC	
Q Fri_Mar_04_23:	5 DSGHDDLVDVDFYGR-HVATCSSDQHIKVKFKDTSNVELSDSWRA-H--DSSIVADWASPEYGRILIASASYDK	79 (349)
Q Consensus	5 ~h~v~s~d~l~t~s~D~v~iW~	79 (349)
T Consensus	244 ~v~dg~l~dg~i~vwd~h~v~l~s~d~	317 (684)
T 4nsx_A	244 IKIPQSRISLSFRTDGSSHLVGTSSGDLIFYDLRR--SRHVLKNIHRESYGGVQTATFLN--GQPIIVTSGGD	317 (684)
T ss_dssp	EECTTCEEEEECCSSCEEEEEETTSCEEEETTTT---EEEEETTSCEGGGTSCSEEEECT--TSSEEEECCSS	
T ss_pred	EEcCCcCEEEEECCCCCEEEEECCCCCEEEEECCCC--cEEEEcccccCCCCCEEEEECC--CCCEEEcCCC	
Q ss_pred	eEEEEccCcccccccd---ceEEEECCCCCEEEEECCcCCcCEEEEECCCEEEEEC-----	
Q Fri_Mar_04_23:	80 TVKLWEEDPDQEECSGR--WNKLCTLNDKSGSLYSVKFAPAHGLKLACLGNDGILRLYDA-----	139 (349)
Q Consensus	80 -v-lwd-----v-----p-----l-----d-i-ibd-----	139 (349)
T Consensus	318 -i-w~d~l~s~d~i~w~	396 (684)
T 4nsx_A	318 SLKEYVFPDPSLQSGSDVVVQPPRYLRSRGHSQPPSYIAFADSQ-SHFMLSASKDRSLWSFLRKDAQSQMSQRLHKK	396 (684)
T ss_dssp	EEEEEECC---CCCEEEEECCSSCEEEEECTTSCEEEEETTSCEEEEECCSSCEEEECT--TSC	
T ss_pred	cEEEECCCCccccccccCcceEEcCCCCCEEEEECC-CCEEEEECCcEEcEccccccccchccccchc	
Q ss_pred	-----CCCCceeecccccEEEEcCCcCcccccEEEEEccCcccc	
Q Fri_Mar_04_23:	140 -----LEPSDLRSWTLTSEMVKLSIPPAHLQSDFCLSWCPSPFSE	181 (349)
Q Consensus	140 -----	181 (349)
T Consensus	397 ~g~-----v~-----g~-----d~v~wd~v~s~g~	473 (684)
T 4nsx_A	397 QDGRVGGSTIKSKFPEIVALALENARIGEWENIKTAHDKFARTWDMNRKRVGRWTFDITDDGVKSVAMSQ--CGN	473 (684)
T ss_dssp	-----CCCCEEEEECSTTTTSCEEEEETTSCEEEEECCSSCEEEECT--TSC	
T ss_pred	ccccccccccccCCCCeEEecCccCccccEEEcCCCEEEEECCccccceEecCCCCCEEEEECC--CCC	
Q ss_pred	ceEEcCCc-eEEEEcCCCCEEEEEcCCCCceEEEECCCCCceEEEECCCCCEEEEEcCc-----cccccccc	
Q Fri_Mar_04_23:	182 KLAVALAQ-AITYQRGKDGKLVAAKLPGHKSLIRSIWAPSIGRWQLIATGCKDGRIRIFKITEK--LSPLASAESL	258 (349)



No 57       

☐ >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=3.1e-33 Score=287.08 Aligned\_cols=303 Identities=21% Similarity=0.338 Sum\_probs=0.0

No 59



[illegible]

No 61









☐ >j04\_B YDR362CP, TAU91; beta propeller, type 2 promoters, transcription, hypotheticala protein, preinitiation complex, yeast RNA polymerase III; 3.2A {Saccharomyces cerevisiae}  
 Probab=100.0 E-value=8.9e-34 Score=265.99 Aligned cols=281 Identities=13% Similarity=0.107 Sum\_probs=0.0

[illegible]

```
Q ss_pred CEEEEECcCCeEEEEEccCcccccccceeeEEBCECCCCcEeeeeCcCCC-CcEEEEECcCCeEEEECCCCCccee  
Q Fri_Mar_04_23: 70 RITASASyDKTKVLKEEDPDQECSGRRRNKLCTLNDSKSLGYSVKFAPAHL-GLKLACLGNDILRLYDALEPSDLRSW 148 (349)  
Q Consensus 70 -las-s-Dg-v-lwd-----v-p--l-d-i-iwD----- 148 (349)  
. .[+][+].. [+].[+]. [+. +... ..+++[.]... ++[+]+++ +. .... ++++.[+].[+]|++++.....+  
T Consensus 278 -l-s-g--dg-i-wd-----h-v---l-s-s-d-i-iw|---- 349 (524)  
T 2j04_B 278 TTVVCGFKNGFVAEFDLTDPEVP-----SFYDQVHDSYLVSSTAYSDFEDTVSVAVDGYFYFINPKDIATTKTT 349 (524)  
T ss_dssp EEEEEETTS EEEEEETTCBCSS-----SEEBESSSCSEEESBEECTTCCEEFEFTTEEEEEGGGHHHHCCE  
T ss_pred CeEEEEECcCeEEEEECcCCCCCC-----EEBeccccCeeeEEEECCCCCcEEEEEcCCeEEEEECcGCCccee
```

[illegible]

```
Q ss_pred          CCcEEEEECCCCEEEEEeCccccccccc-----cccccccccccccccccccccccccccccccccccc-----c
Q Fri_Mar_04_23:  226 RWYQLIATGCKDGRIRIFKITKSLPLASE-----ESLTNSNMFDNSADVDMDAQRSDSNTEEKAEIQSN-----L    292 (349)
Q Consensus        226   -las-s-d-v-vwd-                      -                    -                    -                    -                    -    292 (349)
                   .+|++|+.|++|++|.|+.....      .....|++++..      .+|+.      .
T Consensus        410   -l-sgs-dg-v-iwd-                      h-                v-            spdg               -v-lw-    471 (524)
T 2j04_B           410   --PMVLGSADGSLITTAARRLLHGINKSSATQKSRLRWKWDSYIKDDK--                        YRIDSSYEVYPLTV    471 (524)
T ss_dssp           ---CBCEEEFTTTTEECBSCSSSTTC---CCCEEECBSCSSSCE---EEECCECCCCCC---
T ss_pred          ---CeEEEEeCCCEEEeechhhhhccccCccccC-----eEEEEEEeCCCCC-eEeccccccccCCC
```

```

Q ss_pred          cceeeccCCCCeEEEEEECC---CCEEEecCCCeEEEEecccC
Q Fri_Mar_04_23:  293 QVLLSEHDDHNGEVWSVSNWLT---GTLSSAGDGGKVRLLWATYS 336 (349)
Q Consensus        293      -h- i v -spd---g--las-S-D-v-iW- 336 (349)
                    .....+.+.+|...|++|+|+|+  |++|+|+.|+|+|++|+...
T Consensus        472      -h-V-v--sp-----g--lasg--dg-vrl- 518 (524)
T 2j04_B           472 NDVSKAKIDAHGINITCTKWNETSAGGKCYAFSNSAGLLTLEYLSLE 518 (524)
T ss_dssp           -----CCSCCCEEECCSTTTTTEEEECTTSEEEEECSCC
T ss_pred          CCcCceecCccceEEEEeCCCCCcCCEEEeCCCCEEEEeCcc

```

No 62      

☐ >3v11\_A 26S proteasome regulatory subunit RPN14; beta-propeller, chaperone, RPT6; 1.60A {Saccharomyces cerevisiae} PDB: 3acp\_AA  
 Probab=100.00 E-value=1.5e-32 Score=250.15 Aligned cols=294 Identities=11% Similarity=0.115 Sum probs=0.0

Q ss pred cCCCCc**eEEEEEE**CCCCC-**EEEEEE**cCC**eEEEE**CCCCCc**eeEeeee**cccc**eEEEEEE**cCCCCC**EEEEEE**cCC**eEEE**



No 63

☐ **>ao9d\_B** RIK1-associated factor 1; propeller, heterochromatin formation, DOS2, transcript regulation; 2.00A  
 {Schizosaccharomyces pombe}  
 Probab=100.00 E-value=4e-32 Score=247.42 Aligned\_cols=289 Identities=13% Similarity=0.142 Sum\_probs=0.0

[illegible]

No 65

PDB  
PROTEIN DATA BANK

SMDP  
NCBI

PubMed

>5dfz\_B Serine/threonine-protein kinase VPS15; autophagy, vacuolar protein SORT yeast, complex II, PI3P, kinase,  
lipid, WD40, BARA; 4.40Å {Saccharomyces cerevisiae}  
Probab=100.00 E-value=8.8e-35 Score=297.19 Aligned\_cols=291 Identities=12% Similarity=0.087 Sum\_probs=0.0






















Q ss_pred	CcCccCCcCcCeEEEECCCCC-E-EEEEcCCCCEEEeeCCceEeeee-eccccceEEEEECcCCCCCCEEEEEdCC		
Q Fri_Mar_04_23:	1 MQPFDSGHDLLVDVVFYGR-KHVATCSDDHQIKVKLKDKDTSNWELSDS-WRAHSSIVAVDWASPEYGRIIASASYD	78 (349)	
Q Consensus	1 -h-v~v-s-d-l-t-S-D-V-Iwd-h~-h~-las-s-D	78 (349)	
T Consensus	++...[+].[+][++++][+] [+][+].[[+]]+[.]++..... ++.[+].[+++]+  + [+] +. 1062 v-l~qh~V-v-a-spdg-laSGS-DgtVrlWd-H~V-svfasp-q~laSGS-D	1139 (1460)	

No 66

☐ [>ac18\\_A](#) Echinoderm microtubule-associated protein-like 1; structural protein, EML1, EML4-ALK, HSP90 inhibitors, tubulin-binding, beta propeller; 2.60Å {Homo sapiens}  
 Probab=100.0 E-value=5.2e-32 Score=260.55 Aligned\_cols=320 Identities=13% Similarity=0.144 Sum\_probs=0.0

[illegible]



No 69                       

No 70                                  







No 71                                  

```

Q ss_pred      EEeeeCcCccc-----cccccccEEEEEEcCCCCcEEEEEEcCCCCcEEEEEEcCCcEEEECCCC---Cccceeee
Q Fri_Mar_04_23: 81 VKLWEDDPQ-----ECSGRRWNKLTCTINDSKGSLYSVFKFAPAHGLKGLACLGDGITRLRYDALEP---SDLRSWT
Q Consensus    81 v-lwd-----v-p-----l-d-1-ldw-----
























```



No 72       PubMed

☐ >4ci8\_A Echinoderm microtubule-associated protein-like 1; structural protein, EML1, EML4-ALK, HSP90 inhibitors, tubulin-binding, beta propeller; 2.60A {Homo sapiens}  
Probab=100.00 E-value=7.7e-32 Score=259.39 Aligned\_cols=295 Identities=15% Similarity=0.217 Sum\_probs=0.0

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No 75                       

☐ >5cvo\_A WD repeat-containing protein 48; WDR48, WD repeat, beta propeller, USP46, covalent DUB, deubiquitinase, hydrolase-protein binding complex; 3.89A {Homo sapiens}  
Probab=100.00 E-value=7.7e-32 Score=258.66 Aligned\_cols=306 Identities=17% Similarity=0.211 Sum\_probs=0.0

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No 78     

☐ **>4nsx\_A** U3 small nucleolar RNA-associated protein 21; ribosome biogenesis, UTPB complex, 90S preribosome, small SU processome, protein binding; HET: FLC; 2.10a [Saccharomyces cerevisiae]  
 Probab=100.00 E-value=3e-31 Score=256.38 Aligned\_cols=299 Identities=12% Similarity=0.144 Sum\_probs=0.0

[illegible]





No 81       

☐ [3odt\\_A](#) Protein DOA1; ubiquitin, nuclear protein; HET: MSE MES; 1.35A {Saccharomyces cerevisiae}  
Probab=100.00 E-value=1.7e-31 Score=234.17 Aligned\_cols=282 Identities=17% Similarity=0.182 Sum\_probs=0.0

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Q ss pred CcCeEEEEEECCCCEEEEeCCCeEEEEEECCCCCceEeeeecccccEEEEEEcCCCCCEEEEEeCCCeEEFeec

No 86      

☐ >1r5m\_A\_SIR4-interacting protein SIF2; transcription corepressor, WD40 repeat, beta propeller; 1.55A  
 {Saccharomyces cerevisiae}  
 Probab=100.00 E-value=3.5e-31 Score=240.93 Aligned cols=277 Identities=15% Similarity=0.190 Sum probs=0.0

Q ss_pred	CCcccCCcCeEEEECCCCCEEEECcCCeEEEECCCCCceEeecccccEEEEECccccCEEEECcCCCEEEECcCCCE		
Q Fri_Mar_04_23:	1 MQPFDGGHDDVLVDVDFYGRHVATCSSDQHlKVFkDKDTSNWELSDSWRAHDSSIVAIWDASPYGRlIASASyDKT	80	(349)
Q Consensus	1 h-v-s-d-l-t-s-d-v-iwd-h-v-v-v-las-s-dg-+.+.+.+. .. ++++ + ++++ ++ .+. ++  ...+.+.+. .. ++++ + ++++ ++++ .+	80	(349)
T Consensus	100 h-v-s-l-dg-v-vw-l-d	172	(425)
T 1r5m_A	100 LSASSGKTTNGVTCLAWSHDGNSlVTGVGELRLWNKTGA----LlNVlNfHRAPiSVSVKWNK--DGTHlISMDVENV	172	(425)
T ss_dssp	CC-----CBCEEEEEECTTSSEEEEEETTSCEEEETTSCE-----EEEECCCCCEEEEEECT--TSSEEEEEETTC		
T ss_pred	hhhhhccCCCEEEEEcCCCCEEEEcCCCCEEEECCCC----eEEecCCCCEEEEECc--CCCEEEEEcCCCE		
Q ss_pred	EEEEccCCCCcccc-----ccEEEEEcCCCCEEE		
Q Fri_Mar_04_23:	81 VKLWEEDPDQEECSGR-----RWNKlCLTNDsKGSlyS	113	(349)
Q Consensus	81 v-lwd-++ + .+.+.+.+.v-++ + .+.+.+. . .+.+	113	(349)
T Consensus	173 i-lwd-g-i-d-i-d	252	(425)
T 1r5m_A	173 TlLwNlSGlTVMQHFELKETGGSSlNAENHSGDGLGVDEWVDDDKFVlPGPKAIFVYQITeKTPTGKlIGHHGPlSV	252	(425)
T ss_dssp	EEEEETTTTEEEEECC-----CCBSCCEEETTEEEECGGGEEEEETTCSSCEEEECSSCEEE		
T ss_pred	EEEECCCCceeeeeecccCccccceeecccCCcEEEEECcCCCEEEEECCCCEEEEcCCCCEEEecCCCceEE		
Q ss_pred	EEECcCCCCEEEEECcCCEEEECCCCCceeecccccEEEEcCCcCCCCceEEEEcccCCCCCceEEcCCc-eE		
Q Fri_Mar_04_23:	114 VKFAPAHlGLKLCLGNDGILRLYDALePSDLRSWTLTSEMKVLSlPPANHLQSDfCLSWCPsRfSPeKlAVSALEQ-AI	192	(349)
Q Consensus	114 -p--l-d-i-iwd-++ + +.+.++++ .+. ++ + .+.+.+.+.+.+.+.+.+. + ...+++++.+++.+	192	(349)
T Consensus	253 l-dg-i-i-d-v-l-d-i	313	(425)
T 1r5m_A	253 lEFNDTl--NKLlLSASDDGTlRlWHGGNGNSQNCF-----YGHQSIVSASVWG--DDKVIscMDGsvR	313	(425)
T ss_dssp	EEETTT--TTEEEETTSCEEEECSSBSCEEE-----CCSSCEEEEEET--TTEEEETTSSEE		
T ss_pred	EEECc--CEEEEEcCCEEEEECcCCcccch-----hccccEEEEEEcC--CcEEEEcCCCE		
Q ss_pred	EEEEcCCCtEEEEECcCCCCceEEEECCCCCCEEEECcCCCCEEEEECcCCCCcccccccccccccccccccc		
Q Fri_Mar_04_23:	193 lYQRGDKGLHVAAlPGHKSllRlSISWAPSlGRWYQlLiATGCKDGRlRlFkTlKlSLPASEESlTNSNMFdNSADVDM	272	(349)
Q Consensus	193 i-l-d-i-v-s-sp-las-s-d-v-vwd-++ + ...+.+.+. .. ++++ + +++.+ ++++ . .++ + .....	272	(349)
T Consensus	313 i-d-i-dg-v-iwd	384	(425)
T 1r5m_A	314 lWSlKQN--TlLLAlSVdGVPIFAGRISODG--QKYAVAFMDGQVNVYDLKklNSKRSlyGNRdGllNPlPlP--	384	(425)

```
T ss_dssp      EEEETTT---EEEEEECTTCEEEEEECTTS---SEEEEEETTSCEEEEECHHHHC-----CEECCE--
T ss_pred      EEECCCC---CeeEEecCCCCeEEEECCCC---CEEEecCCCEEEEECCcCcccccceecCCcccccccccc--

Q ss_pred      cccccccccccccccccccceeeecCCCCeEEEECCCCCEEEecCCCEEEEEec
Q Fri_Mar_04_23: 273 DAQGRSDSNTEKAEQLQSNLQVELLEHDDHNGEVSWNLGTGLTSLASAGDDGKVLWKAT 334 (349)
Q Consensus    273 -----h---i~v~spdg~las-s-D~v~lW~-----334 (349)
                  .....+|...|+++|+|+|++|+|+|.+.|+|+|+.
T Consensus    385 -----v-----s-dg~l-----dg-v-i-----424 (425)
T 1r5m_A       385 -----YASYQSSQDNDYIFDLSWNCAGNKISVAYSLEQGSVVAIP 424 (425)
T ss_dssp      -----EEEECCTTCCCEEEEEECTTSSEEEEESSSCCEEEEC
T ss_pred      -----ceeeeccccCCceEEEEcCCCCeEEEEecCCCEEEecC
```

No 87         

☐ >4jsn\_D Target of rapamycin complex subunit LST8; helical repeat, kinase, WD40 repeat, protein kinase, raptor, transferase; 3.20A {Homo sapiens} PDB: 4jsp\_D\* 4jsv\_D\* 4jsx\_D\* 4jt5\_D\* 4jt6\_D\*  
Probab=100.00 E-value=3.4e-31 Score=233.47 Aligned\_cols=272 Identities=16% Similarity=0.196 Sum\_probs=0.0

```
Q ss_pred      cccCCCCcCEEEEECCCCCEEEecCCcEEEEECCCCCceEeeeccccceEEEECCCCCCCCCEEEecCCCEEE
Q Fri_Mar_04_23: 3 PFDSGHDDLHVHVVYDFYGRHVATCSSDQHVKVFKLDKDTSNWELSDSWRAHDSSIVAIWASPEYGRITIASASYDKTVK 82 (349)
Q Consensus    3 -----h~v~s-d~l-t-s-D~v~iwd-----h~v~v~las-s-Dg~v~82 (349)
                  ..+.+.|...|.+++|+|+++.+. .|++|+|+..... ..+.+.|...|.+++|+| +|++|+|+|.+++|+
T Consensus    36 -----v-----l-----i~iwd-----h~v~v~dg~l-s-s-D~v~110 (326)
T 4jsn_D       36 RTVQHQSQVNVALVTPDRSMIAAGYQ-HIRMYDLNSNPN--PITSYDGVNKNIASVGFHE--DGRWMTGGEDCTAR 110 (326)
T ss_dssp      EEEECTTSCCEEEECTTSSEEEEECBS-CEEEESSSCSCC--CSEEECCCCSEEEEEECT--TSSSEEEETTSEEE
T ss_pred      EEECCCCCEEEEECCCCEEecCCC-cEEEEECCCCcc--ceEeccccCCceEEEEcC--CCCEEEECCEEEEC
```

```
Q ss_pred      EeeccCccccccccceEEEEcCCCCeEEEEcCCCCeEEEEcCCCEEEEECCCCCcceeecccccEEEEecCCC
Q Fri_Mar_04_23: 83 LWEEDPDQEECSGRRWNKLCITLNDKSGSLYSVKFAPAHGLKLACLGNDGILRLYDALEPSDLRSWTLTSEMKNVLSITPPA 162 (349)
Q Consensus    83 lwd~p~v~p~l~d~i~iwd-----p~l~d~i~iwd-----162 (349)
                  +|+|.+.+. .+.+.|...|.+++|+|+ +.+++++.|+|.++|+|++..... .
T Consensus    111 iwd-----v-----p~l~g~dg~i~iwd-----167 (326)
T 4jsn_D       111 IWLRLSRNLQ-----CORIFQVNPAINCVCLHPN--QAEILVGDQSGAIHIWDLKTDHNEQLI-----P 167 (326)
T ss_dssp      EEEETTSCTSS-----CSEEEECSSCEEEEEECTT--SSEEEETTTSCEEEETTTCCEEEEC-----S
T ss_pred      EEECCCCce-----EEEEecCCCeEEEEcCC--CEEEECcCCCEEEECcCCcceeEec-----c
```

```
Q ss_pred      cccccceEEEEccCCCCceEEecCCc-eEEEEcCC----CcEEEEECcCCCCceEEEECCCCCCCCceEEEEcC
Q Fri_Mar_04_23: 163 NHLQSDPCLSWCPSRFSPKLAVALQEQ-AITYQRKGD---GLHVAAKLPGHKSLIRISWAPSIGRWYQLIATGCK 236 (349)
Q Consensus    163 -----i-----h~v~v~sp~las-s~236 (349)
                  .+.+.+.+.+.| ++.+++++.+. +++|+|. .+.+.+.+.|...|.+++|+|++ .|++++.
T Consensus    168 -----i~s~l~dg~i~vw-----h~v~v~sp~l~s~s~240 (326)
T 4jsn_D       168 EPEVSI TSAHIDP---DASYMAAVNSTGNCYVWNLGTGGIGDEVTLQIPKTKIPAHTRYALQCRFSPDS---TLLATCSA 240 (326)
T ss_dssp      STTSCEEEEECT--TSSSEEEETTSCCEEEEECCCCGGSCCEEEEEECSSCCEEEEEECTTS--SEEEET
T ss_pred      CCCcCEEEEECC--CCCEEEEEcCCCCEEEEECCCCcccccccccccccccccccccceEEEECCCC--CEEEECcC
```

```
Q ss_pred      CCCEEEEECcC-----ccccccccccccccccccccccccccccccccccccccccccccccccceeeecCCCCc
Q Fri_Mar_04_23: 237 DGRIRIFKITEK-----LSPLASEELTNSNMFNSADVMDAQGRSDSNTEKAEQLQSNLQVELLEHDDHNGE 306 (349)
Q Consensus    237 d~v~vwd-----h~v~v~sp~las-s~306 (349)
                  |++|++|+|. .+.+.+.+.+.|+++++.+.+.+. .+.|.+.+.+.+.+.|...
T Consensus    241 D~i~iwd-----v~lwd~g~gH~314 (326)
T 4jsn_D       241 DQCKIWRITSNFSMLTELSIKSNPGESSRGWGWGAFSGDSQYIVTASSDNL-----ARLWCVTGEIKREYGGHQA 314 (326)
T ss_dssp      TTEEEETTTCCEEEEECCSSTTSCCEEEEEECTTSSEEEETTSE-----EEETTTTCCEEEEECCSSC
T ss_pred      CCeEEEECCCCceeeeccccCCCCCCCCcEEEEECCCCCEEEccCCCC-----EEEEccCCceeeecCccce
```

```
Q ss_pred      EEEEEECcC
Q Fri_Mar_04_23: 307 VWSVSWNL 315 (349)
Q Consensus    307 i~v~v~spd 315 (349)
                  |++|+|+|.
T Consensus    315 V~v~f~f~ 323 (326)
T 4jsn_D       315 VVCLAFNDS 323 (326)
T ss_dssp      EEEEEEEcC
T ss_pred      EEEEEecC
```

No 88         

☐ >5a9q\_2 Nucleoporin NUP37; transport protein; 23.00A {Homo sapiens}  
Probab=100.00 E-value=7.1e-32 Score=237.09 Aligned\_cols=285 Identities=14% Similarity=0.212 Sum\_probs=0.0

```
Q ss_pred      CCcCEEEEEEC-----CCCEEEEEcCCCEe---EEEECCCCC---ceEeeeccccceEEEECCCCCCCC-----
Q Fri_Mar_04_23: 7 GHDDLHVHVVYDF-----YGRHVATCSSDQHII---KVFKLKDTSTNWELSDSWRAHDSSIVAIWASPEYGR-----70 (349)
Q Consensus    7 -----h~v~s~d~l-t-s-D~v~iwd-----h~v~v~las-s~70 (349)
                  +|.+.|.+++|+|++++|++|+|.|++|+|+..... ..+.+.|...|.+++|+|++ +++
T Consensus    14 -----v-----l~d~i~i~iw-----90 (326)
T 5a9q_2       14 DCEDYVHVVEFNPFGNGDSGNLIAYGGNNYVVGTCFQEEADVIGIQYKTLRTFPH-HGVRVGDIASWP---ETRLDSL 90 (326)
T ss_dssp      ECSSCCCCEEECSSCSSTTSSEEEECSSSEEEEEECCTTSCCSCCEEEEEEC--CSCEEEEEECT--TCCESSC
T ss_pred      ccCEEEEEEcCCcCccCCCEEEcCCCCEEEEEeccccccccCccceEEEEc-cCCCEEEEECC--Ccccccc
```

```
Q ss_pred      --EEEEECcCEEEecCccccccccccceEEEEcCCCCeEEEEcC-CCCCeEEEEcCCCEEEEECCCCCce
Q Fri_Mar_04_23: 71 ---IASASYDKTVKLWEEDPDQEECSGRRWNKLCITLNDKSGSLYSVKFAP-AHLGLKLACLGNDGILRLYDALEPSDLR 146 (349)
Q Consensus    71 -----las-s-Dg~v~lwd-----p~l~d~i~iwd-----146 (349)
                  +|++++.|.+.|++|+++ .....+.+.+.+.|...|.+++|+| + +.++++.|.+.|++|+|+ +.....
T Consensus    91 -----l~d~i~i~iw-----l~d~i~i~iw-----160 (326)
T 5a9q_2       91 PVIKFCTSAADMKIRLFTSD-----LQDKNEYKVLGHTDFINGLVDFPKE--GQETIASVSDHDTCTRIWNL-EGVQTA 160 (326)
```

No 89

☐ >Salu\_D Coatomer subunit beta'; transport protein, structural protein, COPI, coate vesicles; 13.00A {Mus musculus} PDB: [5alv\\_D](#) [5alw\\_D](#) [5alx\\_D](#) [5aly\\_D](#)  
 Probab=100.0 E-value=6.3e-31 Score=261.82 Aligned cols=288 Identities=13% Similarity=0.200 Sum\_probs=0.0



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Q ss_pred	eCCeEEEEccCcccccc-----ccEEEEECCCCcEEEECCcCC		
Q Fri_Mar_04_23:	76 SYDKTVKLWEEDPDQEECSGR-----RWKLCITNDKSGSLYSVKFAPAH	121 (349)	
Q Consensus	76 s-Dg-v-lwd-----v-----p-----	121 (349)	
T Consensus	258 ~d~i~iwd-----v-----g~i-----s-----	335 (611)	
T lnr0_A	258 SADKTIKIWNVATLKVKETIPVGTRIEDQQLGIWTKQALVSIANGFINFVNPELGSIDQVRYGHNKAITALSSAD--	335 (611)	
T ss_dssp	ETTSEEEEEETTTSEEEEECCSSGGGCEEEEECSCEEEETTCSEEEETTTSEEEEECCSSSCCTTSCCEEEECCTT--		
T ss_pred	eCCeEEEEccCccccccCccccceEEeCCCEEEEECCCEEEEEccCchhhhhccccceEEEECC--		
Q ss_pred	CcEEEEECCEEEEECCCCccee-----eccccEE		
Q Fri_Mar_04_23:	122 GLKLACLGNDILRLYDALEPSDLRSW-----TLTSEM	155 (349)	
Q Consensus	122 ~l~d~i~iwd-----v-----h-----	155 (349)	
T Consensus	336 ~l~d~i~iwd-----v-----d~i-----	415 (611)	
T lnr0_A	336 GKTLSADAEHINSWDISTGINSRVFPDVHATMITGIXTKSGDLPTVSWDDHLKVVPAAGSGVDSSKAVANKLSSQPL	415 (611)	
T ss_dssp	SSSEEEETTSCEEEETTCCEEECCSSCSCSSCEEEECTTSCSEEEETTTSEEEEECCSSSSCTTSCCEEECSCE		
T ss_pred	CCEEEECCCCCEEEECCEeccccccceEEEECCCEEEEECCCEEEEECCCECCCCccccccccccCCEe		
Q ss_pred	EeeCCcCcc-----cceeEEEEccCCCCcEEeCCc--eEEEEcCCcEEEEEEccCC		
Q Fri_Mar_04_23:	156 VLSIPPAHNL-----QSDFCISWCPSPRFSPKLAVALAQ--AIITYQRKDGKLVAAKLP	211 (349)	
Q Consensus	156 ~l~d~i~iwd-----v-----h-----	211 (349)	
T Consensus	416 ~s~g~l~i-----s-----l~d~i~iwd-----v-----	490 (611)	
T lnr0_A	416 GLAVSADGDAIAAACYKHIAIYSHGKLTVEPISVNSSCVALSN--DKQFVAVGGQDSKVHVYKLSGA--SVSEVKTIIVH	490 (611)	
T ss_dssp	EEEECTTSCSEEEESSEEEETTTSEEEEECCSEEEECT--TSCEEEETTTSEEEETTT--EEEEEEEC		
T ss_pred	eeEECCCCCEEEECcCEEECCCEeccccCCCEEEECc--CCCEEEECCEEEEECCc--cceecccc		
Q ss_pred	CCceEEEECCCCCCcEEEECCCCCEEEECcC-----cccccccccccccccccccccccccccccccccc		
Q Fri_Mar_04_23:	212 KSLIRISISWAPSIGRWYQLIATGCKDGRIRIFKITEK-----LSPLASSESLTNSNMFNDADVDMAQGRSDNTEKA	286 (349)	
Q Consensus	212 ~v~v~sp-----las~s~d~v~vwd-----	286 (349)	
T Consensus	491 ~v~s~l~i-----s-----h~v~s~d~l~s~d-----v	560 (611)	
T lnr0_A	491 PAEITSVAFSNG--AFLVATDQSRKVIPIYSVANNFELAHTNSWTFHTAKVACVSWSPDNVRLATGSLDNS--	560 (611)	
T ss_dssp	SSCEEEECTTSC--SEEEETTSCEEEEGGGTTESCCCCCCCCSSCEEEECTTSCSEEEETTTSC--E		
T ss_pred	CceEEEECCCC--CEEEECCEEEECcChHhhhhhhccccceEEEECCCCCEEEECCECC--E		
Q ss_pred	cccccc--ceeee--ccCCC--ceEEEECCCCCEEEECcCCCEEEEcCC		
Q Fri_Mar_04_23:	287 ELQSNLQ-VELLSE-HDDHN-GEVWSVSWNLGTILSSAGDDGKVRWKATY	335 (349)	
Q Consensus	287 ~h~i~v~spdg~las~s~D~v~iW-----	335 (349)	
T Consensus	561 ~v~w~h~v-----h~v-----l~s~dg~i~W-----	611 (611)	
T lnr0_A	561 IVWNMKNPSDHPITIKGAHAMSSVNSVIWL-NETTIVSAGQDSNIKFWNVPF	611 (611)	
T ss_dssp	EEETTCCTSCCEETTSSTTSCSEEEEEE-ETTEEEETTSCEEEEC		
T ss_pred	EEEECCCCceeeccccCccceEEEEEC-CCCEEEECCEEEECCEEEECcC		
Q ss_pred	CcccCCcCeEEEECCCCCEEEECcCCEEEECCEEEECcCCEEEEcCC		
Q Fri_Mar_04_23:	2 QPFGSGHDDLVDVVDYDFYGRHVATCSSDQHIKVKFLDKDT-----SNWELSDSWRAHDSIVAIDWASPEYG--RI	71 (349)	
Q Consensus	2 ~h~v~s~d~l~t~s~D~v~iwd-----h~v~v-----	71 (349)	
T Consensus	9 ~gH~V~l~s~Dg~v~vw-----l~s~Dg~v~vw-----	83 (397)	
T lsq9_A	9 ANAGKAHADIFSVSACN--SPTVSCSDGYLKVWNLKLDNENPKDKSYSHFVKHSGLHHVVLQA--IER--DAFELCL	83 (397)	
T ss_dssp	EEESSSSCEEEEECS--SEEEETTSCEEEESBCCTTCGGGGEEEECTTCEEEEEEBE--TTEEEEE		
T ss_pred	ceccccCCCEEEECc--CeEEEECCCEEEECcCccccccccceccccCccceEEEE-eCC--CCcCE		
Q ss_pred	EEEECCCEEEecCccccccccce-----EEEC-----CCCCEEEEEECc-CCCC--cEEEEECCEEE		
Q Fri_Mar_04_23:	72 IASASYDKTVKLWEEDPDQEECSGRWKNK-----LCTLN-----DSKGLYSVKFAP-AHLG-----LKLACLGNDILR	135 (349)	
Q Consensus	72 las~s~Dg~v~lwd-----v-----p-----	135 (349)	
T Consensus	84 ~l~s~dg~i~vw-----v-----l~s~dg~i~v-----	151 (397)	
T lsq9_A	84 VATTFSFGDLLFYRITR-----EDETCKVIFEKLDLLDSMKKHSFWALKWGSAN--DRLLSHRLVATDVKGTTY	151 (397)	
T ss_dssp	EEEEETTSCEEEEEE-----CTTTCCEEEECSCCTTGGSCEEEEECC-----CEEEETTSCEEE		
T ss_pred	EEECcCCCCCEEEECc-----CccccccccceccccceEEEEECcC--CCCCcEEEEECCEEE		
Q ss_pred	EEECcCcc-----eccccEEEEcCCcCcc-----cceeEEEEccCCCCcEEeCCc--eEEEEcCCcEE		
Q Fri_Mar_04_23:	136 LYDALPSDL-----RSWTLTSEMKVLSIPPAHNL--QSDFCISWCPSPRFSPKLAVALAQ--AIITYQRKDGKLVH	203 (349)	
Q Consensus	136 ~iwd-----i-----	203 (349)	
T Consensus	152 ~iwd-----h~p~v-----l~d~i~iwd-----	218 (397)	
T lsq9_A	152 IWKFHFPADENSLTLNWSPTLELQGTVES-----PMTPSQFATSVDIS--RG-LIATGFNNGTVQISELSTL--R	218 (397)	
T ss_dssp	EEEESSSSHHHHHTTCCCCEEEEEEEC-----SSSSCCCCEEEECT--TS-EEEEETTSCEEEETTTT--E		
T ss_pred	EEECcCcccccccccccccecccccecc-----ccccceEEEEEC--Cc-eEEEECCCEEEEECCCC--c		
Q ss_pred	EEEEccC-----CCCceEEEECCCCCCcEEEEECcC--CCEEEEECcC--cccc-----cccccc		
Q Fri_Mar_04_23:	204 VAAKLPG-----HKSILIRISISWAPSIGRWYQLIATGCKD--GRIRIFKITEK--LSPLA-----SESLT	259 (349)	
Q Consensus	204 ~h~v~v~sp-----las~s~d~v~vwd-----	259 (349)	

No 94



☐ >lsq9\_A Antiviral protein SKI8; WD repeat, beta-transducin repeat, WD40 repeat, beta propeller, recombination; 1.90A {Saccharomyces cerevisiae} SCOP: b.69.4.1 PDB: 4buj\_C ls4u\_x Probab=100.00 E-value=2.1e-31 Score=240.55 Aligned\_cols=295 Identities=15% Similarity=0.176 Sum\_probs=0.0







No 96    

>4u7a\_A Ribosome biogenesis protein ERB1; WD40, rRNA binding, beta-propeller, Pro binding; 1.60A {Saccharomyces cerevisiae}

Probab=100.00 E-value=4.6e-31 Score=259.69 Aligned\_cols=289 Identities=18% Similarity=0.224 Sum\_probs=0.0

Q ss\_pred cccCCCCcEEEEEECCCCEEEEeCCcEEEECCCCCceEeeeecc-----cceEEEEEEcCCCCC-----EEEE

Q Fri\_Mar\_04\_23: 3 PFDSGHDDLVDVVVYFYGRHVAFCSSDQHKVFKLDKTSNWLSDSWRAH-----DSSIVLDWASPEYGR--ITAS 74 (349)

No 97       [PubMed](#)

☐ >[4i79\\_A](#) Nucleoporin NUP43; structural genomics consortium, SGC, WD40 repeat, cell cycle; 1.75A {Homo sapiens} Probab=100.00 E-value=1.3e-30 Score=235.85 Aligned cols=258 Identities=16% Similarity=0.225 Sum\_probs=0.0





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