

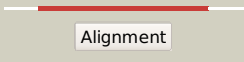

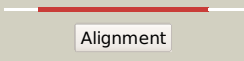

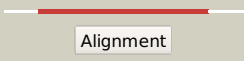

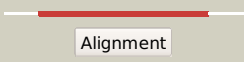

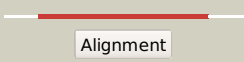
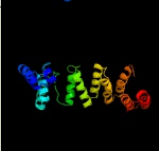
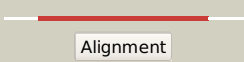

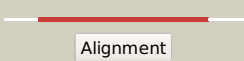

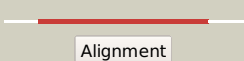

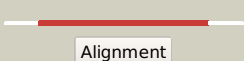

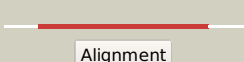
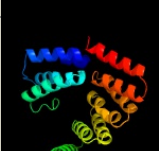

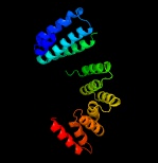



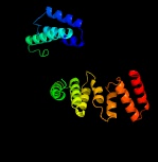

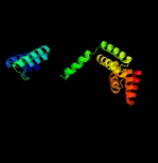



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1203c_(-)_1346327_1346911
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	fd807a4384d53786

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pe3D_	 Alignment		99.8	16	PDB header: transferase Chain: D; PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcnac transferase and its complex with a peptide2 substrate
2	c6c95A_	 Alignment		99.8	11	PDB header: transferase Chain: A; PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit; PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
3	c5ganJ_	 Alignment		99.8	13	PDB header: transcription Chain: J; PDB Molecule: pre-mrna-splicing factor 6; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
4	c4bujF_	 Alignment		99.8	12	PDB header: hydrolase Chain: F; PDB Molecule: superkiller protein 3; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
5	c5dseC_	 Alignment		99.8	16	PDB header: protein binding Chain: C; PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
6	c5nnrD_	 Alignment		99.7	10	PDB header: transferase Chain: D; PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
7	c2xpiA_	 Alignment		99.7	13	PDB header: cell cycle Chain: A; PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
8	c4kvmA_	 Alignment		99.7	9	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
9	c5xw7B_	 Alignment		99.7	16	PDB header: biosynthetic protein Chain: B; PDB Molecule: cellulose synthase subunit c; PDBTitle: crystal structure of the flexible tandem repeat domain of bacterial2 cellulose synthase subunit c
10	c3cvpA_	 Alignment		99.7	12	PDB header: transport protein Chain: A; PDB Molecule: peroxisome targeting signal 1 receptor pex5; PDBTitle: structure of peroxisomal targeting signal 1 (pts1) binding domain of2 trypanosoma brucei peroxin 5 (tbpex5)complexed to pts1 peptide (10-3 skl)
11	c1fchB_	 Alignment		99.7	11	PDB header: signaling protein Chain: B; PDB Molecule: peroxisomal targeting signal 1 receptor; PDBTitle: crystal structure of the pts1 complexed to the tpr region2 of human pex5

12	c5zypA_	Alignment		99.7	15	PDB header: transcription Chain: A: PDB Molecule: rna polymerase-associated protein ctr9,rna polymerase ii- PDBTitle: structure of the yeast ctr9/paf1 complex
13	c5jqyA_	Alignment		99.7	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and factor x substrate3 peptide fragment(39mer-4ser)
14	c4r7sA_	Alignment		99.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat protein; PDBTitle: crystal structure of a tetratricopeptide repeat protein (parmer_03812)2 from parabacteroides merdae atcc 43184 at 2.39 a resolution
15	c4hnxA_	Alignment		99.7	19	PDB header: transferase Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata acetyltransferase complex bound to ppppp
16	c2ho1B_	Alignment		99.6	13	PDB header: protein binding Chain: B: PDB Molecule: type 4 fimbrial biogenesis protein pilf; PDBTitle: functional characterization of pseudomonas aeruginosa pilf
17	c4ui9C_	Alignment		99.6	10	PDB header: cell cycle Chain: C: PDB Molecule: cell division cycle protein 23 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
18	c5tqbB_	Alignment		99.6	16	PDB header: ribosomal protein Chain: B: PDB Molecule: assembly chaperone of ribosomal protein l4 (acl4); PDBTitle: crystal structure of assembly chaperone of ribosomal protein l4 (acl4)2 in complex with ribosomal protein l4 (rpl4)
19	c3uq3A_	Alignment		99.6	14	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein sti1; PDBTitle: tpr2ab-domain:phsp90-complex of yeast sti1
20	c6b85J_	Alignment		99.6	21	PDB header: membrane protein Chain: J: PDB Molecule: tmhc4_r; PDBTitle: crystal structure of transmembrane protein tmhc4_r
21	d1fcha_	Alignment	not modelled	99.6	10	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
22	c3iegB_	Alignment	not modelled	99.6	19	PDB header: chaperone Chain: B: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of p58(lpk) tpr domain at 2.5 a
23	c2vq2A_	Alignment	not modelled	99.6	13	PDB header: structural protein Chain: A: PDB Molecule: putative fimbrial biogenesis and twitching motility PDBTitle: crystal structure of pilw, widely conserved type iv pilus biogenesis2 factor
24	c5zyqA_	Alignment	not modelled	99.6	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase-associated protein ctr9 homolog,rna PDBTitle: the structure of human paf1/ctr9 complex
25	c3hymB_	Alignment	not modelled	99.6	16	PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
26	c4eqfA_	Alignment	not modelled	99.6	11	PDB header: protein binding/transport protein Chain: A: PDB Molecule: pex5-related protein; PDBTitle: trip8b-1a#206-567 interacting with the carboxy-terminal seven residues2 of hcn2
27	c4zlhB_	Alignment	not modelled	99.6	12	PDB header: metal binding protein Chain: B: PDB Molecule: lipopolysaccharide assembly protein b; PDBTitle: structure of the lapb cytoplasmic domain at 2 angstroms
28	c5efrA_	Alignment	not modelled	99.6	13	PDB header: cell adhesion Chain: A: PDB Molecule: bama-bamd fusion protein; PDBTitle: crystal structure of a bama-bamd fusion

29	d1xnfa_	Alignment	not modelled	99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
30	c5dseA_	Alignment	not modelled	99.6	15	PDB header: protein binding Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
31	c4abnA_	Alignment	not modelled	99.6	15	PDB header: gene regulation Chain: A: PDB Molecule: tetratricopeptide repeat protein 5; PDBTitle: crystal structure of full length mouse strap (ttc5)
32	d1w3ba_	Alignment	not modelled	99.5	17	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
33	c5o9zG_	Alignment	not modelled	99.5	16	PDB header: splicing Chain: G: PDB Molecule: pre-mrna-processing factor 6; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for 2 activation (b complex)
34	c4ui9K_	Alignment	not modelled	99.5	15	PDB header: cell cycle Chain: K: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
35	c6af0A_	Alignment	not modelled	99.5	13	PDB header: transcription Chain: A: PDB Molecule: ctr9 protein; PDBTitle: structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila
36	c4xi0E_	Alignment	not modelled	99.5	14	PDB header: protein binding Chain: E: PDB Molecule: magnetosome protein mama; PDBTitle: mama 41-end from desulfurovibrio magneticus rs-1
37	c2q7fA_	Alignment	not modelled	99.5	12	PDB header: protein binding Chain: A: PDB Molecule: yrrb protein; PDBTitle: crystal structure of yrrb: a tpr protein with an unusual peptide-2 binding site
38	c6gmhQ_	Alignment	not modelled	99.5	17	PDB header: transcription Chain: Q: PDB Molecule: ctr9,rna polymerase-associated protein ctr9 homolog,rna PDBTitle: structure of activated transcription complex pol ii-dsif-paf-spt6
39	c4i17A_	Alignment	not modelled	99.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a tpr repeats protein (bf2334) from bacteroides2 fragilis nctc 9343 at 1.50 a resolution
40	c4f3vB_	Alignment	not modelled	99.5	12	PDB header: protein transport Chain: B: PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
41	c3urzB_	Alignment	not modelled	99.5	12	PDB header: protein binding Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative protein binding protein (bacova_03105)2 from bacteroides ovatus atcc 8483 at 2.19 a resolution
42	c4uzyA_	Alignment	not modelled	99.5	12	PDB header: motor protein Chain: A: PDB Molecule: flagellar associated protein; PDBTitle: crystal structure of the chlamydomonas ift70 and ift52 complex
43	c4ynvA_	Alignment	not modelled	99.5	14	PDB header: chaperone Chain: A: PDB Molecule: acl4; PDBTitle: assembly chaperone of rpl4 (acl4) (residues 28-338)
44	c3q75A_	Alignment	not modelled	99.5	7	PDB header: transferase Chain: A: PDB Molecule: farnesyltransferase alpha subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpt-ii and tkcvvm peptide
45	c5gmkd_	Alignment	not modelled	99.5	13	PDB header: rna binding protein/rna Chain: D: PDB Molecule: u5 snrna; PDBTitle: cryo-em structure of the catalytic step i spliceosome (c complex) at2 3.4 angstrom resolution
46	c2y4tA_	Alignment	not modelled	99.5	18	PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
47	c2pl2A_	Alignment	not modelled	99.5	20	PDB header: protein binding Chain: A: PDB Molecule: hypothetical conserved protein ttc0263; PDBTitle: crystal structure of ttc0263: a thermophilic tpr protein in thermus2 thermophilus hb27
48	c4hotA_	Alignment	not modelled	99.5	17	PDB header: rna binding protein/rna Chain: A: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: crystal structure of full-length human ifit5 with 5'-triphosphate2 oligoadenine
49	c2r5sB_	Alignment	not modelled	99.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp0806; PDBTitle: the crystal structure of a domain of protein vp0806 (unknown function)2 from vibrio parahaemolyticus rimd 2210633
50	c3draA_	Alignment	not modelled	99.5	8	PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
51	c4houB_	Alignment	not modelled	99.5	21	PDB header: rna binding protein Chain: B: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: crystal structure of n-terminal human ifit1
52	c4d18J_	Alignment	not modelled	99.5	7	PDB header: signaling protein Chain: J: PDB Molecule: cop9 signalosome complex subunit 2; PDBTitle: crystal structure of the cop9 signalosome
53	c3fp4A_	Alignment	not modelled	99.4	13	PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
54	d1hz4a_	Alignment	not modelled	99.4	14	Fold: alpha-alpha superhelix Superfamily: TPR-like

						Family: Transcription factor MalT domain III
55	c5wsqd	Alignment	not modelled	99.4	12	PDB header: rna binding protein/rna Chain: D: PDB Molecule: cu5 snrna; PDBTitle: cryo-em structure of the catalytic step ii spliceosome (c* complex) at2 4.0 angstrom resolution
56	c5udjA	Alignment	not modelled	99.4	20	PDB header: rna binding protein Chain: A: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: ifit1 monomeric mutant (I457e/I464e) with gppp-aaaa
57	c3as5A	Alignment	not modelled	99.4	11	PDB header: protein binding Chain: A: PDB Molecule: mama; PDBTitle: mama amb-1 p212121
58	c3vtxB	Alignment	not modelled	99.4	15	PDB header: protein binding Chain: B: PDB Molecule: mama; PDBTitle: crystal structure of mama protein
59	c3v6pA	Alignment	not modelled	99.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: dhax3; PDBTitle: crystal structure of the dna-binding domain of dhax3, a tal effector
60	d1dcea1	Alignment	not modelled	99.4	10	Fold: alpha-alpha superhelix Superfamily: Protein prenyltransferase Family: Protein prenyltransferase
61	c4n5cH	Alignment	not modelled	99.4	15	PDB header: protein binding Chain: H: PDB Molecule: cargo-transport protein ypp1; PDBTitle: crystal structure of ypp1
62	c5waqA	Alignment	not modelled	99.4	12	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein assembly factor bamd; PDBTitle: structure of bamd from neisseria gonorrhoeae
63	c3jb9R	Alignment	not modelled	99.4	13	PDB header: rna binding protein/rna Chain: R: PDB Molecule: pre-mrna-splicing factor cwf4; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
64	c3mv3B	Alignment	not modelled	99.4	11	PDB header: protein transport Chain: B: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
65	c4g1tB	Alignment	not modelled	99.4	17	PDB header: antiviral protein Chain: B: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: crystal structure of interferon-stimulated gene 54
66	c4rg6B	Alignment	not modelled	99.4	14	PDB header: protein binding Chain: B: PDB Molecule: cell division cycle protein 27 homolog; PDBTitle: crystal structure of apc3-apc16 complex
67	c3u4tA	Alignment	not modelled	99.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tpr repeat-containing protein; PDBTitle: crystal structure of the c-terminal part of the tpr repeat-containing2 protein q11t16_cyth3 from cytophaga hutchinsonii. northeast3 structural genomics consortium target chr11b.
68	c4uqzA	Alignment	not modelled	99.3	17	PDB header: protein transport Chain: A: PDB Molecule: hsie1; PDBTitle: coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
69	c5aioA	Alignment	not modelled	99.3	12	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 131 kda subunit; PDBTitle: crystal structure of t131 n-terminal tpr array
70	d1qsaa1	Alignment	not modelled	99.3	13	Fold: alpha-alpha superhelix Superfamily: Bacterial muramidases Family: Bacterial muramidases
71	c3mkrA	Alignment	not modelled	99.3	9	PDB header: transport protein Chain: A: PDB Molecule: coatomer subunit epsilon; PDBTitle: crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
72	c4ui9Y	Alignment	not modelled	99.3	13	PDB header: cell cycle Chain: Y: PDB Molecule: anaphase-promoting complex subunit 7; PDBTitle: atomic structure of the human anaphase-promoting complex
73	c4i2wA	Alignment	not modelled	99.3	14	PDB header: chaperone/protein binding Chain: A: PDB Molecule: protein unc-45; PDBTitle: crystal structure of the myosin chaperone unc-45 from c.elegans in2 complex with a hsp70 peptide
74	c1tnoL	Alignment	not modelled	99.3	4	PDB header: transferase Chain: I: PDB Molecule: geranylgeranyltransferase type i alpha subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a gppp analog and a kkskstkcvim peptide derived from k-3 ras4b
75	c4a1sB	Alignment	not modelled	99.3	18	PDB header: cell cycle Chain: B: PDB Molecule: partner of inscuteable; PDBTitle: crystallographic structure of the pins:insc complex
76	c6aitD	Alignment	not modelled	99.3	18	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
77	c3ro2A	Alignment	not modelled	99.3	17	PDB header: protein binding Chain: A: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: structures of the lgn/numa complex
78	c5a7dB	Alignment	not modelled	99.3	17	PDB header: cell cycle Chain: B: PDB Molecule: pins; PDBTitle: tetrameric assembly of lgn with inscuteable
79	c5djsA	Alignment	not modelled	99.2	15	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnac transferase mutant - k341m
						PDB header: structural genomics, unknown function

80	c3gw4B_	Alignment	not modelled	99.2	15	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
81	c5xi8A_	Alignment	not modelled	99.2	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: structure and function of the tpr domain
82	c2yhca_	Alignment	not modelled	99.2	13	PDB header: membrane protein Chain: A: PDB Molecule: upf0169 lipoprotein yfio; PDBTitle: structure of bamd from e. coli
83	d1d8da_	Alignment	not modelled	99.2	9	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
84	c5mqfO_	Alignment	not modelled	99.2	13	PDB header: splicing Chain: O: PDB Molecule: crooked neck-like protein 1; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
85	d2ooea1	Alignment	not modelled	99.2	16	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: HAT/Suf repeat
86	c3v6tA_	Alignment	not modelled	99.2	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dhax3; PDBTitle: crystal structure of the dna-bound dhax3, a tal effector, at 1.852 angstrom
87	c6hftA_	Alignment	not modelled	99.2	11	PDB header: chaperone Chain: A: PDB Molecule: hsp70/hsp90 co-chaperone cns1; PDBTitle: hsp90 co-chaperone cns1 from saccharomyces cerevisiae (delta69)
88	c2hyza_	Alignment	not modelled	99.2	17	PDB header: de novo protein Chain: A: PDB Molecule: synthetic consensus tpr protein; PDBTitle: crystal structure of an 8 repeat consensus tpr superhelix (orthorhombic2 crystal form)
89	c4ebaC_	Alignment	not modelled	99.2	12	PDB header: structural protein/rna binding protein Chain: C: PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of the rna14-rna15 complex
90	c3qdnA_	Alignment	not modelled	99.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin protein; PDBTitle: putative thioredoxin protein from salmonella typhimurium
91	c5fzqB_	Alignment	not modelled	99.2	17	PDB header: unknown function Chain: B: PDB Molecule: designed tpr protein; PDBTitle: designed tpr protein m4n
92	d2hr2a1	Alignment	not modelled	99.2	19	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
93	c3qkyA_	Alignment	not modelled	99.2	14	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfio; PDBTitle: crystal structure of rhodothermus marinus bamd
94	d2h6fa1	Alignment	not modelled	99.2	8	Fold: alpha-alpha superhelix Superfamily: Protein prenylyltransferase Family: Protein prenylyltransferase
95	d1hh8a_	Alignment	not modelled	99.2	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
96	c5c9sB_	Alignment	not modelled	99.2	10	PDB header: gene regulation Chain: B: PDB Molecule: rrna biogenesis protein rrp5; PDBTitle: crystal structure of the c-terminal domain of rrp5
97	c3zn3A_	Alignment	not modelled	99.2	13	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit 8; PDBTitle: n-terminal domain of s. pombe cdc23 apc subunit
98	c4lngA_	Alignment	not modelled	99.2	9	PDB header: transferase Chain: A: PDB Molecule: caax farnesyltransferase alpha subunit ram2; PDBTitle: aspergillus fumigatus protein farnesyltransferase complex with2 farnesyldiphosphate and tipfarnib
99	c4nrhB_	Alignment	not modelled	99.2	8	PDB header: chaperone/protein binding Chain: B: PDB Molecule: chaperone sycd; PDBTitle: copn-scc3 complex
100	c5y88l_	Alignment	not modelled	99.1	9	PDB header: splicing Chain: I: PDB Molecule: pre-mrna-splicing factor clf1; PDBTitle: cryo-em structure of the intron-lariat spliceosome ready for2 disassembly from s.cerevisiae at 3.5 angstrom
101	c5a6cB_	Alignment	not modelled	99.1	18	PDB header: cell adhesion Chain: B: PDB Molecule: g-protein-signaling modulator 2, afadin; PDBTitle: concomitant binding of afadin to lgn and f-actin directs2 planar spindle orientation
102	c3ly8A_	Alignment	not modelled	99.1	14	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional activator cadc; PDBTitle: crystal structure of mutant d471e of the periplasmic domain of cadc
103	c4ui9O_	Alignment	not modelled	99.1	15	PDB header: cell cycle Chain: O: PDB Molecule: anaphase-promoting complex subunit 5; PDBTitle: atomic structure of the human anaphase-promoting complex
104	c4gyoB_	Alignment	not modelled	99.1	12	PDB header: hydrolase Chain: B: PDB Molecule: response regulator aspartate phosphatase j; PDBTitle: crystal structure of rap protein complexed with competence and2 sporulation factor
105	c3sf4B_	Alignment	not modelled	99.1	18	PDB header: signaling protein/protein binding Chain: B: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: crystal structure of the complex between the conserved cell polarity2 proteins inscuteable and lgn
						PDB header: structural protein

106	c4e85B_	Alignment	not modelled	99.1	11	Chain: B: PDB Molecule: mrna 3'-end-processing protein rna14; PDBTitle: crystal structure of hat domain of rna14
107	c2uy1A_	Alignment	not modelled	99.1	7	PDB header: rna-binding protein Chain: A: PDB Molecule: cleavage stimulation factor 77; PDBTitle: crystal structure of cstf-77
108	c5gjqO_	Alignment	not modelled	99.1	10	PDB header: hydrolase Chain: Q: PDB Molecule: 26s proteasome non-atpase regulatory subunit 11; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
109	c5cwnA_	Alignment	not modelled	99.1	17	PDB header: de novo protein Chain: A: PDB Molecule: designed helical repeat protein; PDBTitle: crystal structure of de novo designed helical repeat protein dhr71
110	c5mqfM_	Alignment	not modelled	99.1	15	PDB header: splicing Chain: M: PDB Molecule: pre-mrna-splicing factor syf1; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of 2 splicing (c* complex)
111	c6ff7M_	Alignment	not modelled	99.1	15	PDB header: splicing Chain: M: PDB Molecule: pre-mrna-splicing factor syf1; PDBTitle: human bact spliceosome core structure
112	c2ifuA_	Alignment	not modelled	99.1	10	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
113	c4i1aA_	Alignment	not modelled	99.1	10	PDB header: hydrolase Chain: A: PDB Molecule: response regulator aspartate phosphatase i; PDBTitle: crystal structure of the apo form of rapi
114	c6g70A_	Alignment	not modelled	99.1	10	PDB header: splicing Chain: A: PDB Molecule: pre-mrna-processing factor 39; PDBTitle: structure of murine prpf39
115	c2c2lD_	Alignment	not modelled	99.0	15	PDB header: chaperone Chain: D: PDB Molecule: carboxy terminus of hsp70-interacting protein; PDBTitle: crystal structure of the chip u-box e3 ubiquitin ligase
116	c4cgwA_	Alignment	not modelled	99.0	10	PDB header: chaperone Chain: A: PDB Molecule: rna polymerase ii-associated protein 3; PDBTitle: second tpr of spaghetti (rpap3) bound to hsp90 peptide srmeevd
117	c5h7aA_	Alignment	not modelled	99.0	11	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin g-binding protein a; PDBTitle: crystal structure of a repeat protein with four protein a repeat2 module
118	c4gpkI_	Alignment	not modelled	99.0	12	PDB header: transcription, peptide binding protein Chain: I: PDB Molecule: npr; ; PDBTitle: crystal structure of npr in complex with its cognate peptide nprx
119	c6hpgA_	Alignment	not modelled	99.0	16	PDB header: plant protein Chain: A: PDB Molecule: outer envelope protein 64, mitochondrial; PDBTitle: arabidopsis om64 tpr domain
120	d1qgea_	Alignment	not modelled	99.0	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)