

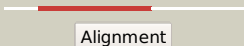

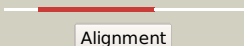







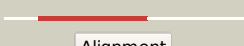











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1204c_(-)_1346942_1348630
Date	Wed Jul 31 22:05:29 BST 2019
Unique Job ID	c2087b917d63d093

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		100.0	13	PDB header: signaling protein Chain: C: PDB Molecule: tetratricopeptide repeat sensor ph0952; PDBTitle: crystal structure of the signal transduction atpase with numerous2 domains (stand) protein with a tetratricopeptide repeat sensor ph09523 from pyrococcus horikoshii
2	c2a5yB_	 Alignment		99.7	14	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
3	c3iytG_	 Alignment		99.7	12	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
4	c1z6tC_	 Alignment		99.7	13	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
5	c5juyB_	 Alignment		99.7	13	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
6	c3iz8C_	 Alignment		99.6	14	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
7	c3iz8G_	 Alignment		99.6	14	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
8	c3iz8A_	 Alignment		99.6	14	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
9	c3iz8D_	 Alignment		99.6	14	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
10	c1vt4N_	 Alignment		99.6	14	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
11	c3iz8B_	 Alignment		99.6	14	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome

12	c1vt4M_	Alignment		99.6	14	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
13	c1vt4L_	Alignment		99.6	14	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
14	c1vt4K_	Alignment		99.6	14	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
15	c3iz8E_	Alignment		99.6	14	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
16	c3iz8H_	Alignment		99.6	14	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
17	c1vt4J_	Alignment		99.6	14	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
18	c1vt4O_	Alignment		99.6	14	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
19	c3iz8F_	Alignment		99.6	14	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
20	c1vt4P_	Alignment		99.6	14	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
21	c1vt4I_	Alignment	not modelled	99.6	14	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
22	c2qenA_	Alignment	not modelled	99.4	13	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
23	c2fnaA_	Alignment	not modelled	99.4	9	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
24	c2qbyB_	Alignment	not modelled	99.3	14	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
25	c5udbA_	Alignment	not modelled	99.3	13	PDB header: replication Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
26	c4xgcE_	Alignment	not modelled	99.3	12	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
27	c1fnbB_	Alignment	not modelled	99.2	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
28	d2fnaa2	Alignment	not modelled	99.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain PDB header: immune system

29	c4kxfP	Alignment	not modelled	99.2	13	Chain: P; PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
30	c6j5tC	Alignment	not modelled	99.2	17	PDB header: plant protein Chain: C; PDB Molecule: disease resistance rpp13-like protein 4; PDBTitle: reconstitution and structure of a plant nlr resistosome conferring immunity
31	c2qbyA	Alignment	not modelled	99.2	9	PDB header: replication/dna Chain: A; PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
32	c5udb9	Alignment	not modelled	99.1	15	PDB header: replication Chain: 9; PDB Molecule: cell division control protein 6; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
33	c4kxfF	Alignment	not modelled	99.1	13	PDB header: immune system Chain: F; PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
34	c5uj7B	Alignment	not modelled	99.1	16	PDB header: dna binding protein Chain: B; PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
35	c2v1uA	Alignment	not modelled	99.1	15	PDB header: replication Chain: A; PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
36	c5ujmE	Alignment	not modelled	99.0	12	PDB header: replication Chain: E; PDB Molecule: origin recognition complex subunit 5; PDBTitle: structure of the active form of human origin recognition complex and2 its atpase motor module
37	c5uj7C	Alignment	not modelled	99.0	13	PDB header: dna binding protein Chain: C; PDB Molecule: origin recognition complex subunit 4; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
38	c3pe3D	Alignment	not modelled	99.0	14	PDB header: transferase Chain: D; PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
39	c2chgB	Alignment	not modelled	98.9	15	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
40	c2chvE	Alignment	not modelled	98.9	13	PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnp complex
41	c6npyA	Alignment	not modelled	98.9	15	PDB header: immune system Chain: A; PDB Molecule: nacht, lrr and pyd domains-containing protein 3; PDBTitle: cryo-em structure of nlrp3 bound to nek7
42	c5dseC	Alignment	not modelled	98.8	16	PDB header: protein binding Chain: C; PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
43	c1sxC	Alignment	not modelled	98.8	14	PDB header: replication Chain: C; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
44	d1a5ta2	Alignment	not modelled	98.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
45	c4xgcD	Alignment	not modelled	98.8	9	PDB header: dna binding protein Chain: D; PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
46	c1sxB	Alignment	not modelled	98.8	10	PDB header: replication Chain: B; PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
47	d1fnna2	Alignment	not modelled	98.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
48	c4d18J	Alignment	not modelled	98.8	9	PDB header: signaling protein Chain: J; PDB Molecule: cop9 signalosome complex subunit 2; PDBTitle: crystal structure of the cop9 signalosome
49	d1sxC2	Alignment	not modelled	98.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
50	c3pvsA	Alignment	not modelled	98.7	13	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
51	c3te6A	Alignment	not modelled	98.7	9	PDB header: gene regulation Chain: A; PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
52	c1iqpF	Alignment	not modelled	98.7	14	PDB header: replication Chain: F; PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
53	c1jr3E	Alignment	not modelled	98.7	14	PDB header: transferase Chain: E; PDB Molecule: dna polymerase iii, delta' subunit; PDBTitle: crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
						PDB header: motor protein

54	c4uzuA_	Alignment	not modelled	98.7	12	Chain: A: PDB Molecule: flagellar associated protein; PDBTitle: crystal structure of the chlamydomonas ift70 and ift52 complex
55	d1sxb2	Alignment	not modelled	98.7	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	c3gw4B_	Alignment	not modelled	98.7	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein from deinococcus2 radiodurans. northeast structural genomics consortium target drr162b.
57	c5zr1A_	Alignment	not modelled	98.7	13	PDB header: dna binding protein/dna Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
58	c1sxD_	Alignment	not modelled	98.6	9	PDB header: replication Chain: D: PDB Molecule: activator 1 41 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
59	c5yudA_	Alignment	not modelled	98.6	14	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: flagellin derivative in complex with the nlr protein naip5
60	d1iqa2	Alignment	not modelled	98.6	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
61	c6b5bA_	Alignment	not modelled	98.6	14	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
62	c5jqvA_	Alignment	not modelled	98.6	15	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)
63	c4xgcA_	Alignment	not modelled	98.6	18	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
64	d1r6bx2	Alignment	not modelled	98.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	c1w5sB_	Alignment	not modelled	98.6	11	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
66	c4hnxA_	Alignment	not modelled	98.6	11	PDB header: transferase Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata acetyltransferase complex bound to ppppp
67	d1sxd2	Alignment	not modelled	98.6	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	c4bujF_	Alignment	not modelled	98.6	12	PDB header: hydrolase Chain: F: PDB Molecule: superkiller protein 3; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
69	c5dseA_	Alignment	not modelled	98.6	17	PDB header: protein binding Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
70	c3pfiB_	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
71	c5nnrD_	Alignment	not modelled	98.5	11	PDB header: transferase Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
72	c3mv3B_	Alignment	not modelled	98.5	14	PDB header: protein transport Chain: B: PDB Molecule: coatamer subunit epsilon; PDBTitle: crystal structure of a-cop in complex with e-cop
73	c5kneA_	Alignment	not modelled	98.5	14	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
74	c6hftA_	Alignment	not modelled	98.5	9	PDB header: chaperone Chain: A: PDB Molecule: hsp70/hsp90 co-chaperone cns1; PDBTitle: hsp90 co-chaperone cns1 from saccharomyces cerevisiae (delta69)
75	d1w5sa2	Alignment	not modelled	98.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
76	d1hz4a_	Alignment	not modelled	98.5	13	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor Mat domain III
77	c5udbD_	Alignment	not modelled	98.5	9	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
78	c1xxhB_	Alignment	not modelled	98.5	16	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
						PDB header: hydrolase

79	c5kzfj_	Alignment	not modelled	98.5	19	Chain: J; PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
80	d1jbka_	Alignment	not modelled	98.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
81	c6e111_	Alignment	not modelled	98.5	17	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
82	c6c95A_	Alignment	not modelled	98.4	8	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
83	c3bosA_	Alignment	not modelled	98.4	20	PDB header: hydrolase regulator,dna binding protein Chain: A; PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
84	c4z8xC_	Alignment	not modelled	98.4	16	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
85	c4f3vB_	Alignment	not modelled	98.4	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
86	d1njfa_	Alignment	not modelled	98.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
87	c5vy9C_	Alignment	not modelled	98.4	15	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
88	c6blbA_	Alignment	not modelled	98.4	21	PDB header: hydrolase Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
89	c6djvE_	Alignment	not modelled	98.4	18	PDB header: chaperone Chain: E; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
90	c5kneD_	Alignment	not modelled	98.4	13	PDB header: chaperone Chain: D; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
91	d2hr2a1	Alignment	not modelled	98.4	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: CT2138-like
92	c1in8A_	Alignment	not modelled	98.4	21	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
93	c5gjqQ_	Alignment	not modelled	98.4	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
94	c1r6bX_	Alignment	not modelled	98.4	18	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
95	c4i2wA_	Alignment	not modelled	98.3	16	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
96	c1sxjE_	Alignment	not modelled	98.3	10	PDB header: replication Chain: E; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
97	c2qz4A_	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: A; PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
98	c1xwiA_	Alignment	not modelled	98.3	20	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
99	c2dhrC_	Alignment	not modelled	98.3	21	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
100	c5kneF_	Alignment	not modelled	98.3	14	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
101	c6djuA_	Alignment	not modelled	98.3	18	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
102	d1qvra2	Alignment	not modelled	98.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	c4b4tH_	Alignment	not modelled	98.3	21	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
						Fold: P-loop containing nucleoside triphosphate hydrolases

104	d1sxje2	Alignment	not modelled	98.3	10	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c5aioA	Alignment	not modelled	98.3	12	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 131 kda subunit; PDBTitle: crystal structure of t131 n-terminal tpr array
106	c3n71A	Alignment	not modelled	98.3	8	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
107	c5djsA	Alignment	not modelled	98.3	11	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcnae transferase mutant - k341m
108	c4kvmA	Alignment	not modelled	98.3	7	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
109	c6em8H	Alignment	not modelled	98.3	13	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
110	c3hu2C	Alignment	not modelled	98.3	18	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
111	c4b4tL	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
112	c6nyyC	Alignment	not modelled	98.3	19	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
113	c2zamA	Alignment	not modelled	98.3	22	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
114	c5ubvB	Alignment	not modelled	98.3	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
115	c3vfdA	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
116	c2xpiA	Alignment	not modelled	98.3	11	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
117	c2kjqA	Alignment	not modelled	98.2	18	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
118	c5udbE	Alignment	not modelled	98.2	12	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
119	c1sxiA	Alignment	not modelled	98.2	15	PDB header: replication Chain: A: PDB Molecule: activator 1 95 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
120	c4b4tM	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome