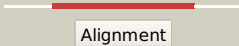





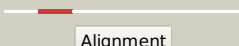

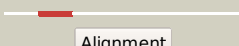

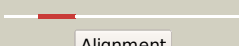

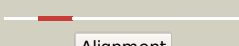

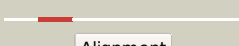









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2488c (-) _2797477_2800890
Date	Wed Aug 7 12:50:11 BST 2019
Unique Job ID	1823635e53a8bf4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		100.0	15	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	d1fx2a_	 Alignment		100.0	31	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
3	c6fhtB_	 Alignment		100.0	24	PDB header: lyase Chain: B; PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylyl/guanylate cyclase in its dark adapted pr form
4	c1y10C_	 Alignment		100.0	19	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
5	d1fx4a_	 Alignment		100.0	32	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
6	c4yusA_	 Alignment		99.9	15	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylyl cyclase; PDBTitle: crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
7	c4wp3E_	 Alignment		99.9	30	PDB header: lyase Chain: E; PDB Molecule: ma1120; PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
8	c4cIIA_	 Alignment		99.9	18	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
9	c3iytG_	 Alignment		99.9	18	PDB header: apoptosis Chain: G; PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
10	c5nbyA_	 Alignment		99.9	17	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenylyl cyclase; PDBTitle: structure of a bacterial light-regulated adenylyl cylcase
11	c3mr7B_	 Alignment		99.9	26	PDB header: hydrolase Chain: B; PDB Molecule: adenylate/guanylate cyclase/hydrolase, alpha/beta fold PDBTitle: crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi

12	c1z6tC_	Alignment		99.9	20	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
13	c5juyB_	Alignment		99.9	19	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
14	c1ybuA_	Alignment		99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenyl cyclase rv1900c chd, in complex2 with a substrate analog.
15	c6r4pA_	Alignment		99.9	19	PDB header: membrane protein Chain: A: PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenyl cyclase bound to an2 activated stimulatory g protein
16	c1wc6B_	Alignment		99.9	23	PDB header: lyase Chain: B: PDB Molecule: adenylate cyclase; PDBTitle: soluble adenyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
17	c5o5kC_	Alignment		99.9	22	PDB header: membrane protein Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenyl cyclase soluble domain
18	c3et6A_	Alignment		99.9	24	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
19	d1wc1a_	Alignment		99.9	23	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
20	c2w01C_	Alignment		99.9	27	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
21	c6r4oA_	Alignment	not modelled	99.9	19	PDB header: membrane protein Chain: A: PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
22	c1cjkA_	Alignment	not modelled	99.9	16	PDB header: lyase/lyase/signaling protein Chain: A: PDB Molecule: adenylate cyclase, type v; PDBTitle: complex of gs-alpha with the catalytic domains of mammalian adenyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
23	c3uvjC_	Alignment	not modelled	99.9	23	PDB header: lyase Chain: C: PDB Molecule: guanylate cyclase soluble subunit alpha-3; PDBTitle: crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
24	c3r5gB_	Alignment	not modelled	99.9	22	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenyl cyclase cyab from p. aeruginosa
25	c2a5yB_	Alignment	not modelled	99.9	16	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
26	c2wz1B_	Alignment	not modelled	99.9	21	PDB header: lyase Chain: B: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: structure of the catalytic domain of human soluble guanylate cyclase 12 beta 3.
27	d1azsa_	Alignment	not modelled	99.9	17	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
28	c1yk9A_	Alignment	not modelled	99.9	25	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenyl cyclase rv1625c

29	d1azsb_	Alignment	not modelled	99.8	16	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
30	c3iz8D_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
31	c3iz8G_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
32	c1vt4N_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
33	c3iz8F_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
34	c3iz8A_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
35	c1vt4P_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
36	c1vt4J_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
37	c1vt4M_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
38	c1vt4K_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
39	c3iz8C_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
40	c1vt4L_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
41	c3iz8H_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
42	c3iz8E_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
43	c3iz8B_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
44	c1vt4I_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
45	c1vt4O_	Alignment	not modelled	99.8	20	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
46	c2qenA_	Alignment	not modelled	99.8	16	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
47	c6a0aA_	Alignment	not modelled	99.8	19	PDB header: lyase Chain: A: PDB Molecule: bacterio-rhodopsin/guanylyl cyclase 1 fusion protein; PDBTitle: monomeric crystal structure of the e497/c566d double mutant of the2 guanylyl cyclase domain of the rhogc fusion protein from the aquatic3 fungus blastocladiella emersonii
48	c4lfuA_	Alignment	not modelled	99.8	25	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
49	c2fnaA_	Alignment	not modelled	99.8	14	PDB header: atp-binding protein Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolbus2 solfataricus p2 at 2.00 a resolution
50	c2q0oA_	Alignment	not modelled	99.8	26	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
51	c3sztB_	Alignment	not modelled	99.8	28	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
52	c1h0mD_	Alignment	not modelled	99.7	19	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
53	c3qp5C_	Alignment	not modelled	99.7	27	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
54	c2qbyB_	Alignment	not modelled	99.7	13	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)
55	c1dlfE_	Alignment	not modelled	99.6	22	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator;

55	c1zjE_	Alignment	not modelled	99.6	33	PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar;
56	c4if4A_	Alignment	not modelled	99.6	29	PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus PDB header: transcription
57	c3c3wB_	Alignment	not modelled	99.6	33	Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr PDB header: transcription
58	c5f64C_	Alignment	not modelled	99.6	28	Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri PDB header: transcription
59	c5hevC_	Alignment	not modelled	99.6	34	Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from 2 enterococcus faecium
60	d1p4wa_	Alignment	not modelled	99.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators) PDB header: dna binding protein
61	c4yn8A_	Alignment	not modelled	99.6	35	Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
62	c1fnnB_	Alignment	not modelled	99.6	19	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
63	c6j5tC_	Alignment	not modelled	99.6	17	PDB header: plant protein Chain: C: PDB Molecule: disease resistance rpp13-like protein 4; PDBTitle: reconstitution and structure of a plant nlr resistosome conferring2 immunity
64	c6jqsA_	Alignment	not modelled	99.6	35	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
65	c4hyeB_	Alignment	not modelled	99.6	30	PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
66	c5o8yG_	Alignment	not modelled	99.6	28	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
67	c3cloC_	Alignment	not modelled	99.6	30	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
68	c2krfB_	Alignment	not modelled	99.6	29	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
69	c3kinC_	Alignment	not modelled	99.6	35	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
70	c1rnlA_	Alignment	not modelled	99.6	37	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
71	c2qbyA_	Alignment	not modelled	99.6	15	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)
72	d1l3la1	Alignment	not modelled	99.6	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
73	d1a04a1	Alignment	not modelled	99.6	34	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
74	d1fsea_	Alignment	not modelled	99.6	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
75	c1zn2A_	Alignment	not modelled	99.5	33	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
76	c1x3uA_	Alignment	not modelled	99.5	37	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
77	c6ideA_	Alignment	not modelled	99.5	31	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
78	c4xgcE_	Alignment	not modelled	99.5	16	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
79	c2rnlA_	Alignment	not modelled	99.5	31	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
80	c2x1uA_	Alignment	not modelled	99.5	18	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog;

80	c2v1uA	Alignment	not modelled	99.5	18	PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
81	d2fnaa2	Alignment	not modelled	99.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
82	d1yioa1	Alignment	not modelled	99.5	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
83	c2jpcA	Alignment	not modelled	99.5	32	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
84	d1hz4a	Alignment	not modelled	99.5	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
85	c5xt2C	Alignment	not modelled	99.4	38	PDB header: dna binding protein Chain: C: PDB Molecule: response regulator fixj; PDBTitle: crystal structures of full-length fixj from b. japonicum crystallized2 in space group p212121
86	c5udbA	Alignment	not modelled	99.4	12	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
87	c6s2pN	Alignment	not modelled	99.3	24	PDB header: plant protein Chain: N: PDB Molecule: nrc1; PDBTitle: structure of the nb-arc domain from the tomato immune receptor nrc1
88	c1w5sB	Alignment	not modelled	99.3	20	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
89	c5uj7B	Alignment	not modelled	99.3	13	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
90	c5uj7C	Alignment	not modelled	99.2	16	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
91	c5ujmE	Alignment	not modelled	99.2	13	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
92	d1fnna2	Alignment	not modelled	99.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	c4kxfF	Alignment	not modelled	99.1	16	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
94	c4kxfP	Alignment	not modelled	99.1	16	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
95	c5udb9	Alignment	not modelled	99.1	14	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
96	c4xgcD	Alignment	not modelled	99.1	20	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
97	c4xgcA	Alignment	not modelled	99.0	16	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
98	c6blbA	Alignment	not modelled	98.9	17	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
99	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
100	c1sxjC	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)
101	c3pfiB	Alignment	not modelled	98.8	16	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
102	d1w5sa2	Alignment	not modelled	98.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	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
104	c3pvsA	Alignment	not modelled	98.7	17	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli

					mgsa
105	c2chvE_	Alignment	not modelled	98.6	14 PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
106	d1sxb2	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
107	c1sxb_	Alignment	not modelled	98.6	13 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)
108	c1in8A_	Alignment	not modelled	98.6	22 PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
109	c5udbE_	Alignment	not modelled	98.6	17 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
110	d1r6bx2	Alignment	not modelled	98.6	17 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	c6npyA_	Alignment	not modelled	98.6	18 PDB header: immune system Chain: A; PDB Molecule: nacht, Irr and pyd domains-containing protein 3; PDBTitle: cryo-em structure of nlrp3 bound to nek7
112	d1sxc2	Alignment	not modelled	98.6	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	c5khrO_	Alignment	not modelled	98.6	17 PDB header: cell cycle Chain: O; PDB Molecule: anaphase-promoting complex subunit 5; PDBTitle: model of human anaphase-promoting complex/cyclosome complex (apc152 deletion mutant) in complex with the e2 ube2c/ubch10 poised for3 ubiquitin ligation to substrate (apc/c-cdc20-substrate-ube2c)
114	c1iqpF_	Alignment	not modelled	98.6	16 PDB header: replication Chain: F; PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
115	c1xxhB_	Alignment	not modelled	98.6	19 PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
116	c6b5bA_	Alignment	not modelled	98.5	19 PDB header: immune system Chain: A; PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
117	d1sxd2	Alignment	not modelled	98.5	10 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
118	d1njfa_	Alignment	not modelled	98.5	13 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
119	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
120	c6em8H_	Alignment	not modelled	98.5	16 PDB header: chaperone Chain: H; PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised