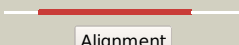

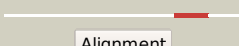

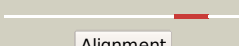

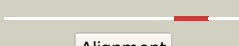









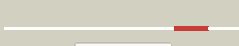







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0339c_(-)_405950_408448
Date	Tue Jul 23 14:50:40 BST 2019
Unique Job ID	a8a3d72275957dac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		99.9	12	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	c4lfuA_	 Alignment		99.8	20	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
3	c2q0oA_	 Alignment		99.8	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
4	c3sztB_	 Alignment		99.8	26	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
5	c1h0mD_	 Alignment		99.8	10	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
6	c3qp5C_	 Alignment		99.8	29	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
7	c3c3wB_	 Alignment		99.7	29	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
8	c5o8yG_	 Alignment		99.7	24	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
9	c3klnC_	 Alignment		99.7	24	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
10	c1zljE_	 Alignment		99.7	30	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
11	c4if4A_	 Alignment		99.7	24	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vrar2 from staphylococcus aureus

12	c4yn8A_	Alignment		99.7	33	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
13	c5f64C_	Alignment		99.7	29	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
14	c2krfB_	Alignment		99.7	22	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
15	c3cloC_	Alignment		99.7	31	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
16	c5hevC_	Alignment		99.7	28	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
17	c1zn2A_	Alignment		99.7	28	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
18	d1p4wa_	Alignment		99.7	24	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)
19	c4hyeB_	Alignment		99.7	25	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
20	c6jqsA_	Alignment		99.7	38	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
21	c1rnlA_	Alignment	not modelled	99.7	31	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
22	d1l3la1	Alignment	not modelled	99.6	11	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)
23	c6ideA_	Alignment	not modelled	99.6	34	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
24	d1a04a1	Alignment	not modelled	99.6	30	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)
25	d1fsea_	Alignment	not modelled	99.6	42	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)
26	d1yioa1	Alignment	not modelled	99.6	28	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)
27	c1x3uA_	Alignment	not modelled	99.6	36	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
28	c2rniA_	Alignment	not modelled	99.6	27	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain

29	c2jpcA	Alignment	not modelled	99.6	36	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
30	c5xt2C	Alignment	not modelled	99.5	33	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
31	c3iytG	Alignment	not modelled	99.0	16	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
32	c1kgsA	Alignment	not modelled	98.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding response regulator d; PDBTitle: crystal structure at 1.50 a of an ompr/phob homolog from thermotoga2 maritima
33	c1z6tC	Alignment	not modelled	98.5	14	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
34	d1ttya	Alignment	not modelled	98.4	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
35	c3q9sA	Alignment	not modelled	98.4	28	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
36	d2p7vb1	Alignment	not modelled	98.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
37	c5x06G	Alignment	not modelled	98.3	17	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
38	d1smyf2	Alignment	not modelled	98.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
39	c2fnaA	Alignment	not modelled	98.3	21	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
40	d1rp3a2	Alignment	not modelled	98.2	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
41	c2qenA	Alignment	not modelled	98.2	17	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
42	d1or7a1	Alignment	not modelled	98.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
43	c3vepA	Alignment	not modelled	98.2	26	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
44	c5juyB	Alignment	not modelled	98.1	15	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
45	c3hugA	Alignment	not modelled	98.1	26	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rslA2 in complex with -35 promoter binding domain of sigI
46	c5fgmA	Alignment	not modelled	98.1	23	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
47	c2o8xA	Alignment	not modelled	98.1	36	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
48	d1ku7a	Alignment	not modelled	98.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
49	d1xsva	Alignment	not modelled	98.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
50	c6c03A	Alignment	not modelled	98.1	16	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
51	c2kjqA	Alignment	not modelled	98.1	15	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.
52	d1ku3a	Alignment	not modelled	98.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
53	d2fnaa2	Alignment	not modelled	98.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
54	c2t0vA	Alignment	not modelled	98.0	10	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator;

54	c3vya_	Alignment	not modelled	98.0	19	PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr PDB header: dna binding protein
55	c4xgcE_	Alignment	not modelled	98.0	23	Chain: E; PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
56	c3mzyA_	Alignment	not modelled	98.0	33	PDB header: rna binding protein Chain: A; PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
57	c1rp3G_	Alignment	not modelled	98.0	27	PDB header: transcription Chain: G; PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
58	c5jpmF_	Alignment	not modelled	97.9	26	PDB header: transcription, transferase/dna/rna Chain: F; PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
59	c2a5yB_	Alignment	not modelled	97.9	14	PDB header: apoptosis Chain: B; PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
60	c5zx3F_	Alignment	not modelled	97.9	26	PDB header: transcription Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
61	c3vdoA_	Alignment	not modelled	97.9	26	PDB header: dna binding protein/protein binding Chain: A; PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rskA from mycobacterium3 tuberculosis
62	c2lfwA_	Alignment	not modelled	97.9	16	PDB header: signaling protein Chain: A; PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
63	c5uxxC_	Alignment	not modelled	97.9	35	PDB header: dna binding protein/unknown function Chain: C; PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
64	c2ja1A_	Alignment	not modelled	97.8	16	PDB header: transferase Chain: A; PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
65	c5tw1F_	Alignment	not modelled	97.8	23	PDB header: transcription activator/transferase/dna Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpa
66	c6dvdF_	Alignment	not modelled	97.8	26	PDB header: transferase/dna Chain: F; PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor l) with 6 nt spacer and bromine3 labelled in position "-11
67	c1fnnB_	Alignment	not modelled	97.8	23	PDB header: cell cycle Chain: B; PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
68	d1s7oa_	Alignment	not modelled	97.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
69	c4kxfP_	Alignment	not modelled	97.8	17	PDB header: immune system Chain: P; PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
70	c5wurB_	Alignment	not modelled	97.8	31	PDB header: metal binding protein Chain: B; PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
71	c1or7A_	Alignment	not modelled	97.8	28	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
72	c2oqrA_	Alignment	not modelled	97.8	27	PDB header: transcription,signaling protein Chain: A; PDB Molecule: sensory transduction protein regx3; PDBTitle: the structure of the response regulator regx3 from mycobacterium2 tuberculosis
73	c4s05B_	Alignment	not modelled	97.7	17	PDB header: transcription/dna Chain: B; PDB Molecule: dna-binding transcriptional regulator basr; PDBTitle: crystal structure of klebsiella pneumoniae pmra in complex with pmra2 box dna
74	c2q1zA_	Alignment	not modelled	97.7	19	PDB header: transcription Chain: A; PDB Molecule: rpoe, ecf sige; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
75	c1sxiC_	Alignment	not modelled	97.7	16	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)
76	c5xe7A_	Alignment	not modelled	97.7	19	PDB header: dna binding protein Chain: A; PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
77	c5uj7B_	Alignment	not modelled	97.7	15	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
78	c4cxfA_	Alignment	not modelled	97.7	37	PDB header: transcription Chain: A; PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry

79	c4kxf_	Alignment	not modelled	97.7	18	PDB header: immune system Chain: F; PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
80	c6c05F_	Alignment	not modelled	97.6	26	PDB header: transcription Chain: F; PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
81	c3pfiB_	Alignment	not modelled	97.6	14	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
82	c5udbA_	Alignment	not modelled	97.6	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
83	c2hqrA_	Alignment	not modelled	97.6	15	PDB header: signaling protein Chain: A; PDB Molecule: putative transcriptional regulator; PDBTitle: structure of a atypical orphan response regulator protein revealed a2 new phosphorylation-independent regulatory mechanism
84	c5ujmE_	Alignment	not modelled	97.6	27	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
85	c4a1fB_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: B; PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
86	c1ys7B_	Alignment	not modelled	97.5	19	PDB header: transcription regulator Chain: B; PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
87	c4xgcA_	Alignment	not modelled	97.5	17	PDB header: dna binding protein Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
88	c3cmvG_	Alignment	not modelled	97.5	27	PDB header: recombination Chain: G; PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
89	d1u94a1	Alignment	not modelled	97.4	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
90	c3bosA_	Alignment	not modelled	97.4	18	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
91	c2gwrA_	Alignment	not modelled	97.4	16	PDB header: signaling protein Chain: A; PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
92	c2chvE_	Alignment	not modelled	97.4	16	PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnpn complex
93	c5udb9_	Alignment	not modelled	97.4	24	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
94	c4b09F_	Alignment	not modelled	97.4	16	PDB header: transcription Chain: F; PDB Molecule: transcriptional regulatory protein baer; PDBTitle: structure of unphosphorylated baer dimer
95	c3t72o_	Alignment	not modelled	97.4	16	PDB header: transcription/dna Chain: O; PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
96	d1qvr3	Alignment	not modelled	97.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	d1njfa_	Alignment	not modelled	97.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	d2cg4a1	Alignment	not modelled	97.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
99	c3wodF_	Alignment	not modelled	97.4	21	PDB header: transferase/transcription Chain: F; PDB Molecule: rna polymerase sigma factor; PDBTitle: rna polymerase-gp39 complex
100	d1mo6a1	Alignment	not modelled	97.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
101	d1ny5a2	Alignment	not modelled	97.3	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	c1i9uH_	Alignment	not modelled	97.3	24	PDB header: transcription Chain: H; PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
103	c5z3qD_	Alignment	not modelled	97.3	25	PDB header: viral protein Chain: D; PDB Molecule: pv-2c; PDBTitle: crystal structure of a soluble fragment of poliovirus 2c atpase (2.552 angstrom) PDB header: plant protein

104	c6j5tC	Alignment	not modelled	97.3	13	Chain: C; PDB Molecule: disease resistance rpp13-like protein 4; PDBTitle: reconstitution and structure of a plant nlr resistosome conferring2 immunity
105	c2cnwF	Alignment	not modelled	97.3	30	PDB header: signal recognition Chain: F; PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
106	c3pvsA	Alignment	not modelled	97.3	23	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
107	c2v1uA	Alignment	not modelled	97.3	24	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
108	c2z4rB	Alignment	not modelled	97.3	21	PDB header: dna binding protein Chain: B; PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
109	d1qzxa3	Alignment	not modelled	97.3	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
110	c2qybB	Alignment	not modelled	97.3	16	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)
111	d1hz4a	Alignment	not modelled	97.2	12	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MatI domain III
112	c5uj7C	Alignment	not modelled	97.2	18	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
113	c2chgB	Alignment	not modelled	97.2	20	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
114	c1ojfF	Alignment	not modelled	97.2	31	PDB header: response regulator Chain: F; PDB Molecule: transcriptional regulatory protein zrar; PDBTitle: crystal structure of a sigma54-activator suggests the mechanism for2 the conformational switch necessary for sigma54 binding
115	d1a5ta2	Alignment	not modelled	97.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
116	d1fnna2	Alignment	not modelled	97.2	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
117	c3uieB	Alignment	not modelled	97.2	18	PDB header: transferase/transferase inhibitor Chain: B; PDB Molecule: adenylyl-sulfate kinase 1, chloroplastic; PDBTitle: crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with amppnp and aps
118	c1xxbB	Alignment	not modelled	97.2	18	PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
119	c1sxA	Alignment	not modelled	97.2	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	c4ciuA	Alignment	not modelled	97.2	20	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb