










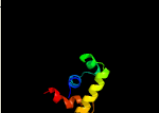












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0890c_(-)_989951_992599
Date	Fri Jul 26 01:50:48 BST 2019
Unique Job ID	075abb721d251202

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		100.0	11	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	23	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	32	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	21	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	23	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	30	PDB header: transcription Chain: C; PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
7	c2a5yB_	 Alignment		99.8	15	PDB header: apoptosis Chain: B; PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
8	c3iytG_	 Alignment		99.7	14	PDB header: apoptosis Chain: G; PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
9	c1z6tC_	 Alignment		99.7	19	PDB header: apoptosis Chain: C; PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
10	c5juyB_	 Alignment		99.7	19	PDB header: apoptosis Chain: B; PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
11	c3c3wB_	 Alignment		99.7	38	PDB header: transcription Chain: B; PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr

12	c4if4A_	Alignment		99.7	30	PDB header: transcription Chain: A; PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the magnesium and beryllofluoride-activated vrrar2 from staphylococcus aureus
13	c5f64C_	Alignment		99.7	34	PDB header: transcription regulator Chain: C; PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
14	c4yn8A_	Alignment		99.7	34	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
15	c1zljE_	Alignment		99.7	38	PDB header: transcription Chain: E; PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
16	c5hevC_	Alignment		99.7	36	PDB header: transcription Chain: C; PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the beryllofluoride-activated liar from2 enterococcus faecium
17	c4hyeB_	Alignment		99.7	29	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
18	c5o8yG_	Alignment		99.7	28	PDB header: transcription Chain: G; PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
19	c3klnC_	Alignment		99.7	35	PDB header: transcription Chain: C; PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
20	d1p4wa_	Alignment		99.7	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)
21	c6jqsA_	Alignment	not modelled	99.7	36	PDB header: dna binding protein Chain: A; PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
22	c2krfB_	Alignment	not modelled	99.7	32	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
23	c3cloC_	Alignment	not modelled	99.7	29	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
24	c1zn2A_	Alignment	not modelled	99.6	36	PDB header: transcription regulator Chain: A; PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
25	c1rnlA_	Alignment	not modelled	99.6	40	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
26	d1a04a1	Alignment	not modelled	99.6	38	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	d1l3la1	Alignment	not modelled	99.6	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)
28	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) 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
29	c6ideA_	Alignment	not modelled	99.6	31	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
30	c2rnjA_	Alignment	not modelled	99.6	31	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
31	c1x3uA_	Alignment	not modelled	99.6	44	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
32	d1yioa1	Alignment	not modelled	99.6	36	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)
33	c3iz8D_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
34	c1vt4I_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
35	c1vt4K_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
36	c3iz8B_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
37	c1vt4P_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
38	c1vt4N_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
39	c1vt4M_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
40	c3iz8F_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
41	c3iz8H_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
42	c1vt4J_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
43	c1vt4L_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
44	c3iz8G_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
45	c3iz8A_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
46	c1vt4O_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
47	c3iz8C_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
48	c3iz8E_	Alignment	not modelled	99.6	16	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
49	c2jpcA_	Alignment	not modelled	99.5	34	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
50	c5xt2C_	Alignment	not modelled	99.5	41	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
51	c6j5tC_	Alignment	not modelled	99.4	16	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
52	c2fnaA_	Alignment	not modelled	99.4	12	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
53	c2qenA_	Alignment	not modelled	99.3	15	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
54	c5udbA_	Alignment	not modelled	99.2	10	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
55	c4kxfF_	Alignment	not modelled	99.1	19	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition

						mechanism
56	c4kxP	Alignment	not modelled	99.1	19	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
57	c2v1uA	Alignment	not modelled	99.1	12	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the apopyrum pernix orc1 protein in complex2 with dna
58	c2qbyB	Alignment	not modelled	99.0	12	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)
59	d2fnaa2	Alignment	not modelled	99.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
60	c4xgcE	Alignment	not modelled	99.0	17	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
61	c1fnnB	Alignment	not modelled	99.0	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
62	c2qbyA	Alignment	not modelled	99.0	10	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)
63	c4xgcA	Alignment	not modelled	98.8	12	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
64	c5ujmE	Alignment	not modelled	98.8	15	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
65	c5uj7C	Alignment	not modelled	98.8	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
66	c6b5bA	Alignment	not modelled	98.8	22	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlr4-flagellin inflammasome
67	c5uj7B	Alignment	not modelled	98.7	8	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
68	c5zr1A	Alignment	not modelled	98.6	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
69	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
70	c6npyA	Alignment	not modelled	98.5	20	PDB header: immune system Chain: A: PDB Molecule: nacht, lrr and pyd domains-containing protein 3; PDBTitle: cryo-em structure of nlr3 bound to nek7
71	c1kgsA	Alignment	not modelled	98.5	13	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
72	d1fnaa2	Alignment	not modelled	98.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
73	c5udb9	Alignment	not modelled	98.5	10	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
74	c5udbE	Alignment	not modelled	98.5	19	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
75	c4xgcD	Alignment	not modelled	98.5	11	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
76	c5yudA	Alignment	not modelled	98.3	18	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: flagellin derivative in complex with the nlr protein naip5
77	d1ttya	Alignment	not modelled	98.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
78	c3q9sA	Alignment	not modelled	98.3	28	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of rra(1-215) from deinococcus radiodurans
79	c6blbA	Alignment	not modelled	98.3	18	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 PDB header: protein transport

80	c2zamA	Alignment	not modelled	98.3	16	Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
81	c3b9pA	Alignment	not modelled	98.2	14	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
82	c1xwiA	Alignment	not modelled	98.2	15	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
83	c1xxhB	Alignment	not modelled	98.2	22	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
84	c2chvE	Alignment	not modelled	98.2	10	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnp complex
85	c1sxC	Alignment	not modelled	98.2	12	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)
86	c6s2pN	Alignment	not modelled	98.2	22	PDB header: plant protein Chain: N: PDB Molecule: nrc1; PDBTitle: structure of the nb-arc domain from the tomato immune receptor nrc1
87	d2p7vb1	Alignment	not modelled	98.2	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
88	c1ny5A	Alignment	not modelled	98.2	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
89	c1w5sB	Alignment	not modelled	98.2	24	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
90	c1sxA	Alignment	not modelled	98.2	13	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)
91	c1in8A	Alignment	not modelled	98.2	21	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
92	c3d8bB	Alignment	not modelled	98.1	16	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
93	c1iqpF	Alignment	not modelled	98.1	10	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
94	c3te6A	Alignment	not modelled	98.1	15	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
95	c2chgB	Alignment	not modelled	98.1	11	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
96	d1smyf2	Alignment	not modelled	98.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
97	d1hz4a	Alignment	not modelled	98.1	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MaT domain III
98	c1sxD	Alignment	not modelled	98.1	10	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)
99	c6opcF	Alignment	not modelled	98.1	11	PDB header: motor protein Chain: F: PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
100	d1sxd2	Alignment	not modelled	98.1	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
101	c6nyyC	Alignment	not modelled	98.1	15	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
102	c3vfdA	Alignment	not modelled	98.0	19	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
103	d1rp3a2	Alignment	not modelled	98.0	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
104	d1sxa2	Alignment	not modelled	98.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	d1sxc2	Alignment	not modelled	98.0	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
						PDB header: membrane protein/transcription

106	c3vepA	Alignment	not modelled	98.0	23	Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
107	c4z8xC	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
108	c3hugA	Alignment	not modelled	98.0	28	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
109	d1or7a1	Alignment	not modelled	98.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
110	c2kjqA	Alignment	not modelled	98.0	16	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.
111	c1sxB	Alignment	not modelled	98.0	9	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)
112	d1njfa	Alignment	not modelled	98.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	c2o8xA	Alignment	not modelled	98.0	24	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
114	c4l16A	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
115	d1ku7a	Alignment	not modelled	97.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
116	d1in4a2	Alignment	not modelled	97.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
117	c6c03A	Alignment	not modelled	97.9	22	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
118	d1xsva	Alignment	not modelled	97.9	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
119	c4lcbA	Alignment	not modelled	97.9	14	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
120	c1xp8A	Alignment	not modelled	97.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s