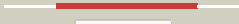

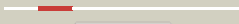





















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1358 (-)_1526618_1530097
Date	Wed Jul 31 22:05:46 BST 2019
Unique Job ID	58c4605aa09be113

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		100.0	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	c6fhtB_	 Alignment		100.0	22	PDB header: lyase Chain: B; PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
3	d1fx2a_	 Alignment		100.0	29	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
4	c1y10C_	 Alignment		100.0	22	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state
5	d1fx4a_	 Alignment		100.0	31	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
6	c4yusA_	 Alignment		100.0	20	PDB header: lyase Chain: A; PDB Molecule: family 3 adenylate cyclase; PDBTitle: crystal structure of photoactivated adenylyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
7	c4wp3E_	 Alignment		100.0	26	PDB header: lyase Chain: E; PDB Molecule: ma1120; PDBTitle: crystal structure of adenylyl cyclase from mycobacterium avium ma11202 wild type
8	c5nbyA_	 Alignment		100.0	17	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenylyl cyclase; PDBTitle: structure of a bacterial light-regulated adenylyl cyclase
9	c3mr7B_	 Alignment		100.0	29	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
10	c4cIIA_	 Alignment		100.0	16	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
11	c1wc6B_	 Alignment		99.9	27	PDB header: lyase Chain: B; PDB Molecule: adenylate cyclase; PDBTitle: soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate

12	c5o5kC_	Alignment		99.9	23	PDB header: membrane protein Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain
13	c2wz1B_	Alignment		99.9	16	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.
14	c3iytG_	Alignment		99.9	19	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
15	c3et6A_	Alignment		99.9	21	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
16	c6r4pA_	Alignment		99.9	13	PDB header: membrane protein Chain: A: PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenylyl cyclase bound to an2 activated stimulatory g protein
17	c2w01C_	Alignment		99.9	25	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
18	d1wc1a_	Alignment		99.9	25	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
19	c1z6tC_	Alignment		99.9	22	PDB header: apoptosis Chain: C: PDB Molecule: apoptotic protease activating factor 1; PDBTitle: structure of the apoptotic protease-activating factor 12 bound to adp
20	c1ybuA_	Alignment		99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
21	c1cjkA_	Alignment	not modelled	99.9	17	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 adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
22	c3r5gB_	Alignment	not modelled	99.9	26	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
23	c6r4oA_	Alignment	not modelled	99.9	23	PDB header: membrane protein Chain: A: PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a truncated adenylyl cyclase bound to mant-gtp, forskolin2 and an activated stimulatory galphas protein
24	c3uvjC_	Alignment	not modelled	99.9	18	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.
25	d1azsa_	Alignment	not modelled	99.9	16	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
26	c5juyB_	Alignment	not modelled	99.9	18	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
27	c1yk9A_	Alignment	not modelled	99.9	21	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
28	d1azsb_	Alignment	not modelled	99.9	15	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain

29	c2a5yB_	Alignment	not modelled	99.9	17	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
30	c6a0aA_	Alignment	not modelled	99.9	17	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
31	c4lfuA_	Alignment	not modelled	99.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
32	c3sztB_	Alignment	not modelled	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
33	c2q0aA_	Alignment	not modelled	99.8	29	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
34	c3iz8F_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
35	c1vt4J_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
36	c1vt4I_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
37	c3iz8C_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
38	c3iz8E_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
39	c1vt4K_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
40	c3iz8H_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
41	c1vt4N_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
42	c1vt4L_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
43	c1vt4P_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
44	c3iz8D_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
45	c3iz8B_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
46	c3iz8G_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
47	c3iz8A_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
48	c1vt4M_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
49	c1vt4O_	Alignment	not modelled	99.8	17	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
50	c1h0mD_	Alignment	not modelled	99.8	20	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
51	c3qp5C_	Alignment	not modelled	99.8	25	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
52	c2qenA_	Alignment	not modelled	99.8	12	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
53	c3c3wB_	Alignment	not modelled	99.8	30	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
54	c2fnaA_	Alignment	not modelled	99.8	11	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 PDB header: transcription regulator

55	c5f64C_	Alignment	not modelled	99.7	27	Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
56	c4if4A_	Alignment	not modelled	99.7	33	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vrrar2 from staphylococcus aureus
57	c1zljE_	Alignment	not modelled	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
58	c5hevC_	Alignment	not modelled	99.7	34	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrrar; PDBTitle: crystal structure of the berylliofluoride-activated liar from2 enterococcus faecium
59	c4yn8A_	Alignment	not modelled	99.7	39	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
60	c4hyeB_	Alignment	not modelled	99.7	28	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
61	d1p4wa_	Alignment	not modelled	99.7	25	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)
62	c5o8yG_	Alignment	not modelled	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.
63	c1zn2A_	Alignment	not modelled	99.7	34	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
64	c3klnC_	Alignment	not modelled	99.7	34	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
65	c2krfB_	Alignment	not modelled	99.7	34	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
66	c6jqsA_	Alignment	not modelled	99.7	33	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
67	c1rn1A_	Alignment	not modelled	99.7	39	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
68	c3cloC_	Alignment	not modelled	99.7	32	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
69	d1a04a1	Alignment	not modelled	99.7	37	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)
70	d1l31a1	Alignment	not modelled	99.7	23	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)
71	c6ideA_	Alignment	not modelled	99.7	23	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
72	d1fsea_	Alignment	not modelled	99.7	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)
73	c2rnjA_	Alignment	not modelled	99.7	36	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrrar; PDBTitle: nmr structure of the s. aureus vrrar dna binding domain
74	d1yioa1	Alignment	not modelled	99.7	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)
75	c1x3uA_	Alignment	not modelled	99.7	34	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
76	d1hz4a_	Alignment	not modelled	99.6	11	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MalT domain III
77	c2qbyB_	Alignment	not modelled	99.6	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)
78	c5xt2C_	Alignment	not modelled	99.6	31	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
79	c2jpcA_	Alignment	not modelled	99.6	30	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
80	c6j5tC_	Alignment	not modelled	99.6	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
81	c1fnbB	Alignment	not modelled	99.6	14	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
82	c4xgcE	Alignment	not modelled	99.6	15	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
83	c5udbA	Alignment	not modelled	99.6	8	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
84	c2qbyA	Alignment	not modelled	99.6	13	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)
85	d2fnaa2	Alignment	not modelled	99.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c2v1uA	Alignment	not modelled	99.5	16	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
87	c6s2pN	Alignment	not modelled	99.4	20	PDB header: plant protein Chain: N: PDB Molecule: nrc1; PDBTitle: structure of the nb-arc domain from the tomato immune receptor nrc1
88	c5uj7C	Alignment	not modelled	99.3	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
89	c5uj7B	Alignment	not modelled	99.3	10	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	c4xgcD	Alignment	not modelled	99.2	18	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
91	c5udb9	Alignment	not modelled	99.2	12	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
92	c5ujmE	Alignment	not modelled	99.2	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
93	c4xgcA	Alignment	not modelled	99.2	10	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
94	c4kxfF	Alignment	not modelled	99.1	17	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
95	c4kxfP	Alignment	not modelled	99.1	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
96	d1fnaa2	Alignment	not modelled	99.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c1w5sB	Alignment	not modelled	99.0	20	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
98	c3pfiB	Alignment	not modelled	99.0	15	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
99	c6blbA	Alignment	not modelled	99.0	14	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
100	c1sxjC	Alignment	not modelled	98.9	13	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	c2chvE	Alignment	not modelled	98.9	15	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
102	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
103	c1in8A	Alignment	not modelled	98.8	17	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
104	c3gw4B	Alignment	not modelled	98.8	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.

105	c1sxD_	Alignment	not modelled	98.8	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)
106	d1njfa_	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
107	c5zr1A_	Alignment	not modelled	98.7	9	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
108	d1sxd2_	Alignment	not modelled	98.7	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	d1sxb2_	Alignment	not modelled	98.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	c1iqpF_	Alignment	not modelled	98.7	11	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
111	c4ui9O_	Alignment	not modelled	98.7	12	PDB header: cell cycle Chain: O: PDB Molecule: anaphase-promoting complex subunit 5; PDBTitle: atomic structure of the human anaphase-promoting complex
112	d1w5sa2_	Alignment	not modelled	98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
113	d1sxc2_	Alignment	not modelled	98.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
114	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
115	c6e111_	Alignment	not modelled	98.7	16	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
116	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
117	c6b5bA_	Alignment	not modelled	98.6	21	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlrc4-flagellin inflammasome
118	c1hqCB_	Alignment	not modelled	98.6	14	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
119	c6em8H_	Alignment	not modelled	98.6	21	PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
120	c1kgsA_	Alignment	not modelled	98.6	17	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