





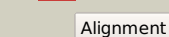





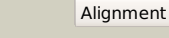

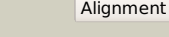

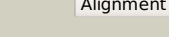







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0386 (-) _463412_466669
Date	Tue Jul 23 14:50:45 BST 2019
Unique Job ID	ea3b09aeb7d1bdd3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6mfvC_	 Alignment		100.0	16	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	26	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	c1y10C_	 Alignment		100.0	22	PDB header: lyase Chain: C; PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyllyl cyclase rv1264, holoenzyme, inhibited state
4	d1fx2a_	 Alignment		100.0	36	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
5	d1fx4a_	 Alignment		100.0	36	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 adenyllyl cyclase of a2 cyanobacteriaoscillatoria acuminata in hexagonal form
7	c5nbyA_	 Alignment		100.0	20	PDB header: lyase Chain: A; PDB Molecule: beta subunit of photoactivated adenyllyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyllyl clycase
8	c4cIIA_	 Alignment		100.0	18	PDB header: lyase Chain: A; PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenyllyl cyclase in complex with2 bicarbonate
9	c4wp3E_	 Alignment		100.0	29	PDB header: lyase Chain: E; PDB Molecule: ma1120; PDBTitle: crystal structure of adenyllyl cyclase from mycobacterium avium ma11202 wild type
10	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
11	c1ybuA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenyllyl cyclase rv1900c chd, in complex2 with a substrate analog.

12	c1wc6B_	Alignment		100.0	21	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
13	c3r5gB_	Alignment		100.0	26	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
14	c2w01C_	Alignment		99.9	26	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
15	d1wc1a_	Alignment		99.9	21	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
16	c5o5kC_	Alignment		99.9	22	PDB header: membrane protein Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: x-ray structure of a bacterial adenylyl cyclase soluble domain
17	c6r4pA_	Alignment		99.9	22	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
18	c6r4oA_	Alignment		99.9	22	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
19	c1cjkA_	Alignment		99.9	18	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
20	c3uvjC_	Alignment		99.9	20	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.
21	c3et6A_	Alignment	not modelled	99.9	19	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
22	d1azsa_	Alignment	not modelled	99.9	18	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
23	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.
24	c1yk9A_	Alignment	not modelled	99.9	24	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenylyl cyclase rv1625c
25	c6aoaA_	Alignment	not modelled	99.9	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 blastocladia emersonii
26	d1azsb_	Alignment	not modelled	99.9	14	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
27	c3iytG_	Alignment	not modelled	99.9	16	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
28	c1z6tC_	Alignment	not modelled	99.9	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
29	c5juyB	Alignment	not modelled	99.8	18	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
30	c2a5yB	Alignment	not modelled	99.8	13	PDB header: apoptosis Chain: B: PDB Molecule: ced-4; PDBTitle: structure of a ced-4/ced-9 complex
31	c3iz8B	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
32	c1vt4L	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: L: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
33	c3iz8G	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
34	c3iz8A	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
35	c1vt4M	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
36	c1vt4P	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
37	c1vt4N	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: N: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
38	c1vt4O	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: O: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
39	c1vt4J	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
40	c3iz8E	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
41	c3iz8C	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
42	c3iz8D	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
43	c1vt4I	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: I: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
44	c3iz8F	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
45	c1vt4K	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
46	c3iz8H	Alignment	not modelled	99.7	18	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
47	c2qenA	Alignment	not modelled	99.7	13	PDB header: unknown function Chain: A: PDB Molecule: walker-type atpase; PDBTitle: the walker-type atpase paby2304 of pyrococcus abyssi
48	c4lfuA	Alignment	not modelled	99.7	24	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	99.7	13	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	c2q0aA	Alignment	not modelled	99.7	27	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	99.7	20	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	24	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	d1hz4a	Alignment	not modelled	99.7	15	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Transcription factor MaIT domain III
54	c3qp5C	Alignment	not modelled	99.6	31	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
55	c3c3wB	Alignment	not modelled	99.6	35	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr;

						PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
56	c1zljE	Alignment	not modelled	99.6	35	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
57	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.
58	c3klnC	Alignment	not modelled	99.5	35	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
59	c5f64C	Alignment	not modelled	99.5	36	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
60	c5hevC	Alignment	not modelled	99.5	33	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
61	c4if4A	Alignment	not modelled	99.5	29	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
62	c4yn8A	Alignment	not modelled	99.5	37	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
63	c1zn2A	Alignment	not modelled	99.5	34	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styf
64	d1p4wa	Alignment	not modelled	99.5	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)
65	c4hyeB	Alignment	not modelled	99.5	32	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	c6jqsA	Alignment	not modelled	99.5	30	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
67	c2qbyB	Alignment	not modelled	99.5	11	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)
68	c3cloC	Alignment	not modelled	99.5	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
69	c2krfB	Alignment	not modelled	99.5	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
70	c1rn1A	Alignment	not modelled	99.5	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	c1fnnB	Alignment	not modelled	99.5	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
72	d1l3la1	Alignment	not modelled	99.5	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)
73	d1a04a1	Alignment	not modelled	99.5	35	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	99.5	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)
75	c6j5tC	Alignment	not modelled	99.4	18	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
76	c2qbyA	Alignment	not modelled	99.4	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)
77	d1yioa1	Alignment	not modelled	99.4	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)
78	c6ideA	Alignment	not modelled	99.4	28	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
79	c2rniA	Alignment	not modelled	99.4	30	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
80	c1x3uA	Alignment	not modelled	99.4	39	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
81	c2v1uA_	Alignment	not modelled	99.4	17	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
82	c5udbA_	Alignment	not modelled	99.4	9	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	c2jpcA_	Alignment	not modelled	99.4	33	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
84	c4xgcE_	Alignment	not modelled	99.3	18	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
85	c5xt2C_	Alignment	not modelled	99.3	37	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	d2fnaa2	Alignment	not modelled	99.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
87	c6s2pN_	Alignment	not modelled	99.2	18	PDB header: plant protein Chain: N: PDB Molecule: nrc1; PDBTitle: structure of the nb-arc domain from the tomato immune receptor nrc1
88	c5ujmE_	Alignment	not modelled	99.2	14	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
89	c5uj7C_	Alignment	not modelled	99.1	15	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
90	c5uj7B_	Alignment	not modelled	99.1	9	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
91	c4xgcA_	Alignment	not modelled	99.1	10	PDB header: dna binding protein Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
92	c5udb9_	Alignment	not modelled	99.0	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
93	c4xgcD_	Alignment	not modelled	99.0	19	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
94	c3gw4B_	Alignment	not modelled	99.0	17	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.
95	c5gjgQ_	Alignment	not modelled	98.9	10	PDB header: hydrolase Chain: Q: PDB Molecule: 26s proteasome non-atpase regulatory subunit 11; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
96	c4kxfP_	Alignment	not modelled	98.9	17	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
97	c4kxfF_	Alignment	not modelled	98.9	17	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
98	c4ui9O_	Alignment	not modelled	98.9	14	PDB header: cell cycle Chain: O: PDB Molecule: anaphase-promoting complex subunit 5; PDBTitle: atomic structure of the human anaphase-promoting complex
99	d1fnaa2	Alignment	not modelled	98.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	c1w5sB_	Alignment	not modelled	98.8	20	PDB header: replication Chain: B: PDB Molecule: origin recognition complex subunit 2 orc2; PDBTitle: structure of the aeropyrum pernix orc2 protein (adp form)
101	c4d18J_	Alignment	not modelled	98.8	9	PDB header: signaling protein Chain: J: PDB Molecule: cop9 signalosome complex subunit 2; PDBTitle: crystal structure of the cop9 signalosome
102	c5khrO_	Alignment	not modelled	98.8	11	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)
103	c4cr3Q_	Alignment	not modelled	98.8	8	PDB header: hydrolase Chain: Q: PDB Molecule: 26s proteasome regulatory subunit rp6; PDBTitle: deep classification of a large cryo-em dataset defines the2 conformational landscape of the 26s proteasome
104	c3pfiB_	Alignment	not modelled	98.8	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
105	c2ifuA_	Alignment	not modelled	98.7	10	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: gamma-snap; PDBTitle: crystal structure of a gamma-snap from danio rerio
106	c1sxC_	Alignment	not modelled	98.7	15	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)
107	c6blbA_	Alignment	not modelled	98.7	16	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
108	c2chvE_	Alignment	not modelled	98.7	13	PDB header: dna-binding protein Chain: E: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnp complex
109	c2chgB_	Alignment	not modelled	98.6	14	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
110	c5zr1A_	Alignment	not modelled	98.6	11	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
111	c3ro3A_	Alignment	not modelled	98.6	14	PDB header: protein binding Chain: A: PDB Molecule: g-protein-signaling modulator 2; PDBTitle: crystal structure of lgn/minscuteable complex
112	c1in8A_	Alignment	not modelled	98.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
113	c4gyoB_	Alignment	not modelled	98.5	12	PDB header: hydrolase Chain: B: PDB Molecule: response regulator aspartate phosphatase j; PDBTitle: crystal structure of rap protein complexed with competence and2 sporulation factor
114	c1sxD_	Alignment	not modelled	98.5	12	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)
115	c1iqpF_	Alignment	not modelled	98.5	13	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
116	c4bujF_	Alignment	not modelled	98.5	7	PDB header: hydrolase Chain: F: PDB Molecule: superkiller protein 3; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
117	c4b4tQ_	Alignment	not modelled	98.5	8	PDB header: hydrolase Chain: Q: PDB Molecule: 26s proteasome regulatory subunit rpn6; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
118	c1xxhB_	Alignment	not modelled	98.5	13	PDB header: transferase Chain: B: PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
119	d1sxC2	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
120	c4yvaC_	Alignment	not modelled	98.4	12	PDB header: oxidoreductase/fluorescent protein Chain: C: PDB Molecule: protein fluorescent in blue light, chloroplastic; PDBTitle: crystal structure of flu-tpr in complex with the c-terminal region of2 glutr