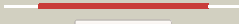



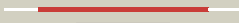



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3679 (-) _4118954_4119976
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	1399c81af9e6780e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6bs3A_	 Alignment		100.0	100	PDB header: unknown function Chain: A; PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
2	c6bs5B_	 Alignment		100.0	24	PDB header: unknown function Chain: B; PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
3	c5zmfA_	 Alignment		100.0	19	PDB header: hydrolase/transport protein Chain: A; PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
4	c1ii0A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
5	c3ug7D_	 Alignment		100.0	23	PDB header: hydrolase Chain: D; PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
6	c3zq6D_	 Alignment		100.0	22	PDB header: hydrolase Chain: D; PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
7	c3igfB_	 Alignment		100.0	20	PDB header: atp binding protein Chain: B; PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
8	c2wooc_	 Alignment		100.0	24	PDB header: hydrolase Chain: C; PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
9	c2wojD_	 Alignment		100.0	21	PDB header: hydrolase Chain: D; PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
10	d1ihua1	 Alignment		100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
11	c5bwkA_	 Alignment		100.0	20	PDB header: hydrolase/transport Chain: A; PDB Molecule: atpase get3; PDBTitle: 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae

12	c3ibgF_	Alignment		100.0	24	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
13	d2afhe1	Alignment		100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
14	d1ihua2	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
15	c3io3A_	Alignment		100.0	24	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
16	d1cp2a_	Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
17	c3endA_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
18	c3kjqB_	Alignment		100.0	17	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
19	c6iucC_	Alignment		100.0	17	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
20	c5j1jA_	Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
21	c4rz3B_	Alignment	not modelled	100.0	18	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
22	c6g2gA_	Alignment	not modelled	100.0	17	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
23	c3ez6B_	Alignment	not modelled	100.0	12	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
24	c6nonB_	Alignment	not modelled	100.0	16	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
25	d1iona_	Alignment	not modelled	100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
26	c2ozeA_	Alignment	not modelled	100.0	12	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
27	c3ea0B_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
28	d1g3ga_	Alignment	not modelled	100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
29	c2hskB_	Alignment	not modelled	100.0	19	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein;

29	c2vebB	Alignment	not modelled	100.0	19	PDBTitle: structure of the bacterial chromosome segregation protein soj
30	c4ru8C	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
31	c3vx3A	Alignment	not modelled	100.0	19	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
32	c2ph1A	Alignment	not modelled	99.9	20	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
33	c4v02B	Alignment	not modelled	99.9	20	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
34	c3q9lB	Alignment	not modelled	99.9	19	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
35	c3pg5A	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
36	c1hyqA	Alignment	not modelled	99.9	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
37	d1hyqa	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
38	c3cwqB	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: para family chromosome partitioning protein; PDBTitle: crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
39	c3la6P	Alignment	not modelled	99.9	19	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
40	c4pfsA	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
41	c3ezfA	Alignment	not modelled	99.9	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
42	c3cioA	Alignment	not modelled	99.9	20	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
43	c3k9gA	Alignment	not modelled	99.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
44	c2xj9B	Alignment	not modelled	99.9	17	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
45	c4dzzB	Alignment	not modelled	99.9	15	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
46	c3fkqA	Alignment	not modelled	99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
47	c2vedA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
48	d1byia	Alignment	not modelled	99.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	c3of5A	Alignment	not modelled	99.9	14	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
50	c2qmoA	Alignment	not modelled	99.9	13	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (bid) from helicobacter2 pylori
51	c3fmfA	Alignment	not modelled	99.8	20	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
52	c5l3qB	Alignment	not modelled	99.7	18	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
53	c2og2A	Alignment	not modelled	99.5	20	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2

						thaliana
54	c2qy9A_	Alignment	not modelled	99.5	14	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
55	c1zu4A_	Alignment	not modelled	99.5	15	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
56	c2cnwF_	Alignment	not modelled	99.5	20	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
57	c1vmaA_	Alignment	not modelled	99.4	18	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
58	c3b9gA_	Alignment	not modelled	99.4	18	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
59	c5l3rC_	Alignment	not modelled	99.4	24	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
60	c2iy3A_	Alignment	not modelled	99.4	20	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
61	c3dm5A_	Alignment	not modelled	99.4	23	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
62	c2j7pA_	Alignment	not modelled	99.4	22	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
63	c1qzwC_	Alignment	not modelled	99.4	21	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
64	c6cy1B_	Alignment	not modelled	99.4	19	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
65	c2yhsA_	Alignment	not modelled	99.4	14	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
66	c4ak9A_	Alignment	not modelled	99.4	20	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
67	c2j37W_	Alignment	not modelled	99.4	17	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
68	c5gafi_	Alignment	not modelled	99.4	18	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
69	c5l3sF_	Alignment	not modelled	99.3	18	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
70	c2v3cC_	Alignment	not modelled	99.3	23	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
71	c2q9cA_	Alignment	not modelled	99.3	20	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
72	c2j289_	Alignment	not modelled	99.2	20	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
73	c3dmdA_	Alignment	not modelled	99.2	16	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
74	d1qzxa3	Alignment	not modelled	99.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	d1vmaa2	Alignment	not modelled	98.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c4ohvA_	Alignment	not modelled	98.4	31	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
77	c2npiB_	Alignment	not modelled	98.3	20	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
78	c2px0D_	Alignment	not modelled	98.3	20	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
79	c3hr8A_	Alignment	not modelled	98.3	18	PDB header: recombination Chain: A: PDB Molecule: protein reca;

						PDBTitle: crystal structure of thermotoga maritima reca
80	d1okkd2	Alignment	not modelled	98.2	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	c1xjqA	Alignment	not modelled	98.2	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
82	d2qy9a2	Alignment	not modelled	98.2	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	c5hcnA	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
84	c1xnjB	Alignment	not modelled	98.1	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
85	d1ls1a2	Alignment	not modelled	98.1	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	d1j8yf2	Alignment	not modelled	98.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c2gksB	Alignment	not modelled	98.0	38	PDB header: transferase Chain: B: PDB Molecule: bifunctional sat/aps kinase; PDBTitle: crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
88	c3cmvG	Alignment	not modelled	98.0	22	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
89	c4nkrB	Alignment	not modelled	97.9	16	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
90	c3cr8C	Alignment	not modelled	97.9	38	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
91	c3bgwD	Alignment	not modelled	97.8	20	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
92	c4zc0A	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
93	c1j8yF	Alignment	not modelled	97.7	17	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
94	c4a1fB	Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
95	c2q6tB	Alignment	not modelled	97.7	22	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
96	c4nmnA	Alignment	not modelled	97.7	18	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
97	d1u94a1	Alignment	not modelled	97.7	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
98	c4wiaA	Alignment	not modelled	97.6	19	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
99	c3uieB	Alignment	not modelled	97.6	34	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
100	c2f1rA	Alignment	not modelled	97.6	22	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
101	d1nija1	Alignment	not modelled	97.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
102	c2recB	Alignment	not modelled	97.6	20	PDB header: helicase PDB COMPND:
103	c3io5B	Alignment	not modelled	97.5	17	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvx recombinase core2 domain from enterobacteria phage t4
104	c1fnnB	Alignment	not modelled	97.5	12	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
105	c6qelB	Alignment	not modelled	97.5	28	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnab apo complex

106	d1mo6a1	Alignment	not modelled	97.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
107	c3c8uA	Alignment	not modelled	97.5	33	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
108	c5x06G	Alignment	not modelled	97.5	20	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
109	c2w0mA	Alignment	not modelled	97.5	17	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfobolus solfataricus p2
110	d1x6va3	Alignment	not modelled	97.5	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
111	c4ydsA	Alignment	not modelled	97.5	24	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfobolus acidocaldarius with atp and mg-ion
112	c1xp8A	Alignment	not modelled	97.4	20	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
113	d1ubea1	Alignment	not modelled	97.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
114	clu9iA	Alignment	not modelled	97.4	19	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
115	c6b8vA	Alignment	not modelled	97.4	28	PDB header: transferase Chain: A: PDB Molecule: adenylylsulfate kinase; PDBTitle: crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
116	d2qm8a1	Alignment	not modelled	97.4	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
117	d1rz3a	Alignment	not modelled	97.4	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
118	d1tf7a2	Alignment	not modelled	97.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	c4bzbB	Alignment	not modelled	97.4	23	PDB header: transferase Chain: B: PDB Molecule: bifunctional enzyme cysn/cysc; PDBTitle: structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp
120	c4xc8B	Alignment	not modelled	97.3	24	PDB header: isomerase Chain: B: PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)