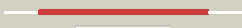























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1708_(-)_1936367_1937323
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	9f12ead9fa2c148a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ez6B_	 Alignment		100.0	20	PDB header: dna binding protein Chain: B; PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adt complex:tetragonal form
2	c6iucC_	 Alignment		100.0	37	PDB header: dna binding protein/dna Chain: C; PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
3	c2ozeA_	 Alignment		100.0	22	PDB header: dna binding protein Chain: A; PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
4	c6nonB_	 Alignment		100.0	23	PDB header: dna binding protein Chain: B; PDB Molecule: coobyric acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
5	d2afhe1	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
6	c2bekB_	 Alignment		100.0	43	PDB header: chromosome segregation Chain: B; PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
7	c4pfsA_	 Alignment		100.0	45	PDB header: ligase Chain: A; PDB Molecule: coobyric acid a,c-diamide synthase; PDBTitle: crystal structure of coobyric acid a,c-diamide synthase from2 mycobacterium smegmatis
8	d1iona_	 Alignment		100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
9	c3q9lB_	 Alignment		100.0	20	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
10	d1cp2a_	 Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
11	c3endA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein

12	c4rz3B_	Alignment		100.0	20	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
13	c5j1jA_	Alignment		100.0	22	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
14	d1g3qa_	Alignment		100.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
15	c3ezfA_	Alignment		100.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
16	c3ea0B_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
17	c6g2gA_	Alignment		100.0	15	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
18	c3kjqB_	Alignment		100.0	20	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
19	c1hyqA_	Alignment		100.0	21	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
20	d1hyqa_	Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
21	c2xj9B_	Alignment	not modelled	100.0	23	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
22	c4v02B_	Alignment	not modelled	100.0	23	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
23	c4ru8C_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with ampnp
24	c4dzzB_	Alignment	not modelled	100.0	25	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
25	c3cwqB_	Alignment	not modelled	100.0	26	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
26	c3fkqA_	Alignment	not modelled	100.0	13	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
27	c3vx3A_	Alignment	not modelled	100.0	21	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
						PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein;

28	c2ph1A	Alignment	not modelled	100.0	17	PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
29	c3pg5A	Alignment	not modelled	100.0	26	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
30	c3k9gA	Alignment	not modelled	100.0	28	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
31	d1byia	Alignment	not modelled	100.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
32	c3cioA	Alignment	not modelled	100.0	15	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
33	c6bs3A	Alignment	not modelled	100.0	15	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
34	c2wojD	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
35	c3zq6D	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
36	c3la6P	Alignment	not modelled	100.0	18	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
37	c2wooC	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
38	c5bwkA	Alignment	not modelled	99.9	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
39	c3ug7D	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
40	c2vedA	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
41	c3of5A	Alignment	not modelled	99.9	10	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
42	c5zmfA	Alignment	not modelled	99.9	16	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
43	d1ihua2	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
44	d1ihua1	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
45	c3io3A	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
46	c6bs5B	Alignment	not modelled	99.9	23	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
47	c3ibgF	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
48	c1ii0A	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
49	c3igfB	Alignment	not modelled	99.9	18	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
50	c2qmoA	Alignment	not modelled	99.9	13	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
51	c3fmfA	Alignment	not modelled	99.9	11	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	99.5	16	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	c2qy9A	Alignment	not modelled	99.4	20	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
54	c1zu4A_	Alignment	not modelled	99.4	21	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
55	c3dm5A_	Alignment	not modelled	99.4	14	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.
56	c1vmaA_	Alignment	not modelled	99.3	19	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
57	c5l3rC_	Alignment	not modelled	99.3	19	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
58	c2iy3A_	Alignment	not modelled	99.3	20	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal regognition particle
59	c2og2A_	Alignment	not modelled	99.3	23	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
60	c2j7pA_	Alignment	not modelled	99.3	20	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
61	c2j37W_	Alignment	not modelled	99.3	17	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
62	c3b9qA_	Alignment	not modelled	99.2	22	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
63	c2cnwF_	Alignment	not modelled	99.2	18	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
64	c4ak9A_	Alignment	not modelled	99.2	18	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
65	c2q9cA_	Alignment	not modelled	99.2	21	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
66	c1qzwC_	Alignment	not modelled	99.2	19	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
67	c6cy1B_	Alignment	not modelled	99.2	20	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
68	c5gafi_	Alignment	not modelled	99.2	22	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
69	c5l3sF_	Alignment	not modelled	99.2	19	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	c2yhsA_	Alignment	not modelled	99.2	20	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
71	c2v3cC_	Alignment	not modelled	99.1	13	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
72	c3dmdA_	Alignment	not modelled	99.1	19	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
73	c2j289_	Alignment	not modelled	98.9	23	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
74	c2px0D_	Alignment	not modelled	98.3	28	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
75	d1qzxa3	Alignment	not modelled	98.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c2npiB_	Alignment	not modelled	98.2	10	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
77	d1j8yf2	Alignment	not modelled	98.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
78	c1j8yF_	Alignment	not modelled	98.0	20	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
						Fold: P-loop containing nucleoside triphosphate hydrolases

79	d1vmaa2	Alignment	not modelled	98.0	31	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	c5hcnA	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
81	c2obnA	Alignment	not modelled	97.9	19	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
82	d2qy9a2	Alignment	not modelled	97.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	d1okkd2	Alignment	not modelled	97.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
84	c4ohvA	Alignment	not modelled	97.8	24	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
85	c2f1rA	Alignment	not modelled	97.7	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
86	d2qm8a1	Alignment	not modelled	97.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c4nkrB	Alignment	not modelled	97.5	16	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
88	d1ls1a2	Alignment	not modelled	97.5	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	c2recB	Alignment	not modelled	97.4	22	PDB header: helicase PDB COMPND:
90	d1mo6a1	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
91	c1xp8A	Alignment	not modelled	97.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
92	d1xjca	Alignment	not modelled	97.1	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
93	c4xc8B	Alignment	not modelled	97.1	15	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)
94	d1xp8a1	Alignment	not modelled	97.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
95	c4fn5A	Alignment	not modelled	96.9	19	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
96	c1xnjB	Alignment	not modelled	96.9	23	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
97	c4zciA	Alignment	not modelled	96.9	21	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
98	d1x6va3	Alignment	not modelled	96.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'-phosphosulfate kinase (APS kinase)
99	d1np6a	Alignment	not modelled	96.8	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c3bgwD	Alignment	not modelled	96.8	14	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
101	c4zc0A	Alignment	not modelled	96.8	16	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
102	c1xjqA	Alignment	not modelled	96.7	20	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
103	c3hr8A	Alignment	not modelled	96.7	21	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
104	c2zroA	Alignment	not modelled	96.7	23	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
105	d1u94a1	Alignment	not modelled	96.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain) PDB header: transferase

106	c3cr8C_	Alignment	not modelled	96.6	33	Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
107	d1ubea1	Alignment	not modelled	96.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
108	c4a1fB_	Alignment	not modelled	96.6	16	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
109	c6n39A_	Alignment	not modelled	96.6	16	PDB header: transferase Chain: A: PDB Molecule: dephospho-coa kinase; PDBTitle: crystal structure of an dephospho-coa kinase coae from mycobacterium2 paratuberculosis
110	c2gksB_	Alignment	not modelled	96.6	28	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
111	c3uieB_	Alignment	not modelled	96.5	26	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
112	c3c8uA_	Alignment	not modelled	96.5	28	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
113	c4wiaA_	Alignment	not modelled	96.5	14	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
114	c3vr1B_	Alignment	not modelled	96.5	13	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
115	d1nija1	Alignment	not modelled	96.4	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
116	c2q6tB_	Alignment	not modelled	96.4	14	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
117	c4nmnA_	Alignment	not modelled	96.4	17	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
118	c5x06G_	Alignment	not modelled	96.4	21	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
119	d1rz3a_	Alignment	not modelled	96.4	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
120	c3bh0A_	Alignment	not modelled	96.3	14	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p