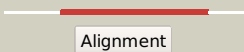

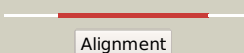

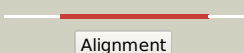

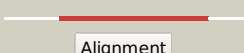





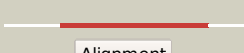

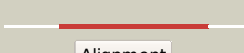









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3888c_(-)_4371859_4372884
Date	Sat Aug 10 22:05:07 BST 2019
Unique Job ID	e3225354c8cdc543

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2afhe1	 Alignment		100.0	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
2	c3endA	 Alignment		100.0	15	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
3	d1cp2a	 Alignment		100.0	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
4	c3ea0B	 Alignment		100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
5	c5j1jA	 Alignment		100.0	18	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
6	c4rz3B	 Alignment		100.0	19	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
7	c3q9lB	 Alignment		100.0	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
8	d1iona	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
9	c3ez6B	 Alignment		100.0	15	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
10	d1g3qa	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
11	c1hyqA	 Alignment		100.0	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus

12	d1hyqa_	Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
13	c2ozeA_	Alignment		100.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
14	c6iucC_	Alignment		100.0	15	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
15	c3fkqA_	Alignment		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
16	c6nonB_	Alignment		100.0	16	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcdA
17	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
18	c3vx3A_	Alignment		100.0	18	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [hife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
19	c2ph1A_	Alignment		100.0	16	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
20	c6g2gA_	Alignment		100.0	16	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
21	c2bekB_	Alignment	not modelled	100.0	16	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
22	c4v02B_	Alignment	not modelled	100.0	19	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
23	c3k9gA_	Alignment	not modelled	100.0	17	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
24	c3la6P_	Alignment	not modelled	100.0	16	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
25	c3cioA_	Alignment	not modelled	100.0	16	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
26	c3ezfA_	Alignment	not modelled	100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
27	c3pg5A_	Alignment	not modelled	100.0	22	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
28	c4ru8C_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp

29	c2xj9B	Alignment	not modelled	99.9	17	PDB header: replication Chain: B: PDB Molecule: mpiz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
30	c4pfsA	Alignment	not modelled	99.9	21	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
31	c2vedA	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
32	c2wojD	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
33	c3zq6D	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
34	c4dzzB	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
35	c2wooC	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
36	c6bs3A	Alignment	not modelled	99.9	21	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
37	d1byia	Alignment	not modelled	99.9	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
38	d1ihua2	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
39	c3cwqB	Alignment	not modelled	99.9	19	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
40	c5zmfA	Alignment	not modelled	99.9	20	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
41	d1ihua1	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
42	c3ug7D	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
43	c5bwkA	Alignment	not modelled	99.9	18	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
44	c1ii0A	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
45	c6bs5B	Alignment	not modelled	99.9	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
46	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
47	c3io3A	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
48	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
49	c2qmoA	Alignment	not modelled	99.8	11	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
50	c3igfB	Alignment	not modelled	99.8	19	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
51	c3fmfA	Alignment	not modelled	99.8	16	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	c2qy9A	Alignment	not modelled	99.4	15	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
53	c5l3qB	Alignment	not modelled	99.4	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
						PDB header: protein transport

54	c1zu4A_	Alignment	not modelled	99.3	18	Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsyl from mycoplasma mycoides-space2 group p21212
55	c2cnwF_	Alignment	not modelled	99.2	17	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyl; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyl
56	c1vmaA_	Alignment	not modelled	99.2	19	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: crystal structure of cell division protein ftsyl (tm0570) from2 thermotoga maritima at 1.60 a resolution
57	c5l3rC_	Alignment	not modelled	99.2	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 ftsyl from2 arabidopsis thaliana
58	c3dm5A_	Alignment	not modelled	99.2	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.
59	c2og2A_	Alignment	not modelled	99.2	15	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsyl from arabidopsis2 thaliana
60	c2iy3A_	Alignment	not modelled	99.2	13	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
61	c5gafi_	Alignment	not modelled	99.2	16	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
62	c3b9qA_	Alignment	not modelled	99.2	15	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyl from arabidopsis thaliana
63	c2j7pA_	Alignment	not modelled	99.2	15	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyl
64	c6cy1B_	Alignment	not modelled	99.2	18	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsyl; PDBTitle: crystal structure of signal recognition particle receptor ftsyl from2 elizabethkingia anophelis
65	c2yhsA_	Alignment	not modelled	99.2	14	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: structure of the e. coli srp receptor ftsyl
66	c2j37W_	Alignment	not modelled	99.2	15	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
67	c5l3sF_	Alignment	not modelled	99.1	22	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsyl; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsyl
68	c2q9cA_	Alignment	not modelled	99.1	19	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: structure of ftsyl:gmppnp with mgcl complex
69	c1qzwC_	Alignment	not modelled	99.0	17	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
70	c4ak9A_	Alignment	not modelled	99.0	17	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsyl from physcomitrella patens
71	c3dmdA_	Alignment	not modelled	98.9	20	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
72	c2v3cC_	Alignment	not modelled	98.9	20	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
73	c2j289_	Alignment	not modelled	98.7	20	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	98.6	17	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	98.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d2qm8a1	Alignment	not modelled	98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c4ohvA_	Alignment	not modelled	98.1	13	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
78	d1j8yf2	Alignment	not modelled	98.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	d1vmaa2	Alignment	not modelled	97.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

80	c4xc8B	Alignment	not modelled	97.8	16	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)
81	c2npiB	Alignment	not modelled	97.7	14	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
82	c1j8yF	Alignment	not modelled	97.7	21	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
83	c4nkrB	Alignment	not modelled	97.7	19	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
84	c2f1rA	Alignment	not modelled	97.5	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
85	d2qy9a2	Alignment	not modelled	97.5	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	d1okkd2	Alignment	not modelled	97.4	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c3cr8C	Alignment	not modelled	97.4	15	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
88	d1ls1a2	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	d1xjca	Alignment	not modelled	97.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
90	c1xjqA	Alignment	not modelled	97.2	14	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
91	d1nija1	Alignment	not modelled	97.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
92	c3bgwD	Alignment	not modelled	97.1	10	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
93	d1x6va3	Alignment	not modelled	97.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
94	c2h5eB	Alignment	not modelled	97.1	19	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
95	d1nlfa	Alignment	not modelled	97.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
96	c1xnjB	Alignment	not modelled	97.1	15	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
97	c2recB	Alignment	not modelled	97.1	24	PDB header: helicase PDB COMPND:
98	c1xp8A	Alignment	not modelled	97.0	27	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
99	c3c8uA	Alignment	not modelled	97.0	7	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
100	c4zc0A	Alignment	not modelled	97.0	12	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
101	c3tr5C	Alignment	not modelled	97.0	11	PDB header: translation Chain: C: PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
102	c5hcnA	Alignment	not modelled	96.9	23	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
103	c4a0gC	Alignment	not modelled	96.9	11	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
104	c6bbmA	Alignment	not modelled	96.8	19	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
105	d2p67a1	Alianment	not modelled	96.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
106	c4xgcE_	Alignment	not modelled	96.7	15	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
107	c1u9iA_	Alignment	not modelled	96.7	12	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
108	c2wwwB_	Alignment	not modelled	96.7	14	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
109	d1sq5a_	Alignment	not modelled	96.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
110	c1w78A_	Alignment	not modelled	96.6	16	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
111	d1odfa_	Alignment	not modelled	96.6	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
112	d1xp8a1	Alignment	not modelled	96.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
113	c4zciA_	Alignment	not modelled	96.5	15	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
114	c4wiaA_	Alignment	not modelled	96.5	16	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
115	c1fnbB_	Alignment	not modelled	96.5	15	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
116	c2q6tB_	Alignment	not modelled	96.5	15	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
117	d1rz3a_	Alignment	not modelled	96.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
118	c2vosA_	Alignment	not modelled	96.4	12	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
119	c4fn5A_	Alignment	not modelled	96.4	16	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
120	c2gksB_	Alignment	not modelled	96.4	13	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