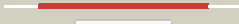



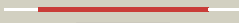

























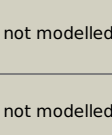


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3680_(-)_4119973_4121133
Date	Fri Aug 9 18:20:37 BST 2019
Unique Job ID	cf00c46fdb01429

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6bs5B_</a>	 Alignment		100.0	98	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> anion transporter; <b>PDBTitle:</b> crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
2	<a href="#">c5zmfA_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> atpase arsa1; <b>PDBTitle:</b> amppnp complex of c. reinhardtii arsa1
3	<a href="#">c1ii0A_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of the escherichia coli arsenite-translocating2 atpase
4	<a href="#">c3ug7D_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> arsenical pump-driving atpase; <b>PDBTitle:</b> crystal structure of get3 from methanocaldococcus jannaschii
5	<a href="#">c3zq6D_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> putative arsenical pump-driving atpase; <b>PDBTitle:</b> adp-alf4 complex of m. therm. trc40
6	<a href="#">c6bs3A_</a>	 Alignment		100.0	23	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative atpase rv3679; <b>PDBTitle:</b> crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
7	<a href="#">c2wooc_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> nucleotide-free form of s. pombe get3
8	<a href="#">c3igfB_</a>	 Alignment		100.0	19	<b>PDB header:</b> atp binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> all4481 protein; <b>PDBTitle:</b> crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
9	<a href="#">c3ibgF_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> atpase, subunit of the get complex; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus get3 with bound2 adp
10	<a href="#">c2wojD_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> adp-alf4 complex of s. cerevisiae get3
11	<a href="#">c5bwkA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase/transport <b>Chain:</b> A; <b>PDB Molecule:</b> atpase get3; <b>PDBTitle:</b> 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae

12	<a href="#">d1ihua1</a>	Alignment		100.0	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
13	<a href="#">d1ihua2</a>	Alignment		100.0	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
14	<a href="#">c3io3A</a>	Alignment		100.0	28	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> deha2d07832p; <b>PDBTitle:</b> get3 with adp from d. hansenii in closed form
15	<a href="#">c3kjbB</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> co dehydrogenase/acetyl-coa synthase complex, accessory <b>PDBTitle:</b> adp-bound state of cooc1
16	<a href="#">c3ez6B</a>	Alignment		99.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition protein a; <b>PDBTitle:</b> structure of para-adp complex:tetragonal form
17	<a href="#">c4ru8C</a>	Alignment		99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with amppnp
18	<a href="#">c6iucC</a>	Alignment		99.9	21	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> spooj regulator (soj); <b>PDBTitle:</b> structure of helicobacter pylori soj-atp complex bound to dna
19	<a href="#">c6g2gA</a>	Alignment		99.9	27	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytosolic fe-s cluster assembly factor cfd1; <b>PDBTitle:</b> fe-s assembly cfd1
20	<a href="#">d2afhe1</a>	Alignment		99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
21	<a href="#">c2ozeA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> orf delta'; <b>PDBTitle:</b> the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
22	<a href="#">c5j1jA</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-ampnp complex
23	<a href="#">c3endA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
24	<a href="#">c2ph1A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide-binding protein; <b>PDBTitle:</b> crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
25	<a href="#">c3pg5A</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
26	<a href="#">d1iona</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
27	<a href="#">c6nonB</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> cobyrinic acid ac-diamide synthase; <b>PDBTitle:</b> structure of cyanthece apo mcda <b>PDB header:</b> transferase

28	<a href="#">c3la6P_</a>	Alignment	not modelled	99.9	19	<b>Chain:</b> P: <b>PDB Molecule:</b> tyrosine-protein kinase wzc; <b>PDBTitle:</b> octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
29	<a href="#">c3vx3A_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> adp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase involved in chromosome partitioning, para/mind <b>PDBTitle:</b> crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
30	<a href="#">c3cioA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> signaling protein, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein kinase etk; <b>PDBTitle:</b> the kinase domain of escherichia coli tyrosine kinase etk
31	<a href="#">c4rz3B_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> crystal structure of the mind-like atpase filhg
32	<a href="#">c3fkqA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc-like two-domain protein; <b>PDBTitle:</b> crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
33	<a href="#">c3k9gA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pf-32 protein; <b>PDBTitle:</b> crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
34	<a href="#">c3ezfA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
35	<a href="#">d1cp2a_</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
36	<a href="#">c3q9lB_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> cell cycle, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> septum site-determining protein mind; <b>PDBTitle:</b> the structure of the dimeric e.coli mind-atp complex
37	<a href="#">d1g3qa_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
38	<a href="#">c2vedA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> membrane protein capa1, protein tyrosine kinase; <b>PDBTitle:</b> crystal structure of the chimerical mutant capabk55m2 protein
39	<a href="#">c4v02B_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> mind:mind cell division protein complex, aquifex aeolicus
40	<a href="#">c4pfsA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyrinic acid a,c-diamide synthase; <b>PDBTitle:</b> crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
41	<a href="#">d1byia_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
42	<a href="#">c2bekB_</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> chromosome segregation <b>Chain:</b> B: <b>PDB Molecule:</b> segregation protein; <b>PDBTitle:</b> structure of the bacterial chromosome segregation protein soj
43	<a href="#">c3ea0B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase, para family; <b>PDBTitle:</b> crystal structure of para family atpase from chlorobium tepidum t1s
44	<a href="#">c3cwqB_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> para family chromosome partitioning protein; <b>PDBTitle:</b> crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
45	<a href="#">c4dzzB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partitioning protein parf; <b>PDBTitle:</b> structure of parf-adp, crystal form 1
46	<a href="#">c1hyqA_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division inhibitor (mind-1); <b>PDBTitle:</b> mind bacterial cell division regulator from a. fulgidus
47	<a href="#">d1hyqa_</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
48	<a href="#">c3of5A_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
49	<a href="#">c2qmoA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (bid) from helicobacter2 pylori
50	<a href="#">c2xj9B_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> mipz; <b>PDBTitle:</b> dimer structure of the bacterial cell division regulator mipz
51	<a href="#">c3fmfA_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
52	<a href="#">c5l3qB_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor subunit alpha; <b>PDBTitle:</b> structure of the gtpase heterodimer of human srp54 and sralpha
						<b>PDB header:</b> protein transport

53	<a href="#">c2og2A</a>	Alignment	not modelled	99.4	22	<b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
54	<a href="#">c3b9qA</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpftsyt from arabidopsis thaliana
55	<a href="#">c2cnwF</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> signal recognition <b>Chain:</b> F: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
56	<a href="#">c2qy9A</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
57	<a href="#">c1zu4A</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
58	<a href="#">c5l3rC</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
59	<a href="#">c1vmaA</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
60	<a href="#">c2j7pA</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
61	<a href="#">c2q9cA</a>	Alignment	not modelled	99.3	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmppnp with mgcl complex
62	<a href="#">c2yhsA</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
63	<a href="#">c2iy3A</a>	Alignment	not modelled	99.3	26	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
64	<a href="#">c4ak9A</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpftsyt; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
65	<a href="#">c6cy1B</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
66	<a href="#">c3dm5A</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
67	<a href="#">c1qzwC</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
68	<a href="#">c5l3sF</a>	Alignment	not modelled	99.2	23	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
69	<a href="#">c2j37W</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
70	<a href="#">c5gafi</a>	Alignment	not modelled	99.2	27	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> rnc in complex with srp
71	<a href="#">c3dmdA</a>	Alignment	not modelled	99.1	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
72	<a href="#">c2v3cC</a>	Alignment	not modelled	99.0	21	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
73	<a href="#">c2j289</a>	Alignment	not modelled	98.9	28	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
74	<a href="#">d1qzxa3</a>	Alignment	not modelled	98.7	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
75	<a href="#">d1vmaa2</a>	Alignment	not modelled	98.1	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
76	<a href="#">c2px0D</a>	Alignment	not modelled	98.0	30	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> flagellar biosynthesis protein flhf; <b>PDBTitle:</b> crystal structure of flhf complexed with gmppnp/mg(2+)
77	<a href="#">c4ohvA</a>	Alignment	not modelled	98.0	26	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein clpf-1; <b>PDBTitle:</b> c. elegans clp1 bound to amp-pnp, and mg2+
78	<a href="#">d2qy9a2</a>	Alignment	not modelled	98.0	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like

79	<a href="#">d1okkd2</a>	Alignment	not modelled	98.0	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
80	<a href="#">d1j8yf2</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
81	<a href="#">c1xp8A</a>	Alignment	not modelled	97.9	25	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> reca protein; <b>PDBTitle:</b> deinococcus radiodurans reca in complex with atp-gamma-s
82	<a href="#">c2recB</a>	Alignment	not modelled	97.9	31	<b>PDB header:</b> helicase <b>PDB COMPND:</b>
83	<a href="#">c3hr8A</a>	Alignment	not modelled	97.9	29	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
84	<a href="#">c2npiB</a>	Alignment	not modelled	97.9	26	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein clp1; <b>PDBTitle:</b> clp1-atp-pcf11 complex
85	<a href="#">c1j8yF</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
86	<a href="#">d1g64b</a>	Alignment	not modelled	97.9	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
87	<a href="#">d1ls1a2</a>	Alignment	not modelled	97.8	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
88	<a href="#">d1g5ta</a>	Alignment	not modelled	97.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
89	<a href="#">d1xp8a1</a>	Alignment	not modelled	97.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
90	<a href="#">c4nkrB</a>	Alignment	not modelled	97.8	27	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> smolydopterin-guanine dinucleotide biosynthesis protein b; <b>PDBTitle:</b> the crystal structure of bacillus subtilis mobb
91	<a href="#">c4nmnA</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
92	<a href="#">c2zroA</a>	Alignment	not modelled	97.7	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> msreca adp form iv
93	<a href="#">c4wiaA</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flagella-related protein h; <b>PDBTitle:</b> crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
94	<a href="#">c5hcnA</a>	Alignment	not modelled	97.6	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gpn-loop gtpase 1; <b>PDBTitle:</b> gpn-loop gtpase npa3 in complex with gmppcp
95	<a href="#">c4zc0A</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> structure of a dodecameric bacterial helicase
96	<a href="#">c3bgwD</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> the structure of a dnab-like replicative helicase and its interactions2 with primase
97	<a href="#">d1mo6a1</a>	Alignment	not modelled	97.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
98	<a href="#">c3cmvG</a>	Alignment	not modelled	97.5	32	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
99	<a href="#">c4a1fB</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
100	<a href="#">d1tf7a2</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
101	<a href="#">c4ydsA</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagella-related protein h; <b>PDBTitle:</b> flah from sulfobolbus acidocaldarius with atp and mg-ion
102	<a href="#">c5x06G</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> replication <b>Chain:</b> G: <b>PDB Molecule:</b> dnaa regulatory inactivator hda; <b>PDBTitle:</b> dna replication regulation protein
103	<a href="#">c2ztsB</a>	Alignment	not modelled	97.4	33	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ph0186; <b>PDBTitle:</b> crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
104	<a href="#">c4a0gC</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
105	<a href="#">d1u94a1</a>	Alianment	not modelled	97.3	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

						<b>Family:</b> RecA protein-like (ATPase-domain)
106	<a href="#">c2f1rA_</a>	Alignment	not modelled	97.3	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis <b>PDBTitle:</b> crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
107	<a href="#">d1ubea1</a>	Alignment	not modelled	97.3	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
108	<a href="#">c3tqcB_</a>	Alignment	not modelled	97.3	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the pantothenate kinase (coaa) from coxiella burnetii
109	<a href="#">c3upuC_</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent dna helicase dda; <b>PDBTitle:</b> crystal structure of the t4 phage sf1b helicase dda
110	<a href="#">c1xnjB_</a>	Alignment	not modelled	97.3	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
111	<a href="#">c2w0mA_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> sso2452; <b>PDBTitle:</b> crystal structure of sso2452 from sulfolobus solfataricus p2
112	<a href="#">c1xjqA_</a>	Alignment	not modelled	97.3	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> adp complex of human paps synthetase 1
113	<a href="#">c2vyeA_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> crystal structure of the dnaC-ssdna complex
114	<a href="#">c1fnnB_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
115	<a href="#">c5he8J_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> protein binding <b>Chain:</b> J: <b>PDB Molecule:</b> helicase loader; <b>PDBTitle:</b> bacterial initiation protein
116	<a href="#">c3bh0A_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnab-like replicative helicase; <b>PDBTitle:</b> atpase domain of g40p
117	<a href="#">c4a0rB_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononanoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from Arabidopsis thaliana bound to dethiobiotin (dtb).
118	<a href="#">c4xgcE_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> crystal structure of the eukaryotic origin recognition complex
119	<a href="#">c6qe1B_</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex
120	<a href="#">d1nija1</a>	Alignment	not modelled	97.2	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like