























# Phyre2

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Description	RVBD2787_(-)_3095121_3096884
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Unique Job ID	fa5fa8faf8f38997

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ea0B_</a>	 Alignment		100.0	19	<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 tls
2	<a href="#">d2afhe1</a>	 Alignment		100.0	15	<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
3	<a href="#">d1cp2a_</a>	 Alignment		100.0	11	<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
4	<a href="#">c3endA_</a>	 Alignment		100.0	15	<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
5	<a href="#">d1iona_</a>	 Alignment		100.0	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
6	<a href="#">c3q9lB_</a>	 Alignment		100.0	16	<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
7	<a href="#">c5i1jA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-amppnp complex
8	<a href="#">c4rz3B_</a>	 Alignment		100.0	17	<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 flhg
9	<a href="#">d1g3qa_</a>	 Alignment		100.0	23	<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
10	<a href="#">c2ozeA_</a>	 Alignment		100.0	12	<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
11	<a href="#">c1hyqA_</a>	 Alignment		100.0	22	<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

12	<a href="#">d1hyqa_</a>	Alignment		100.0	22	<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="#">c3ez6B_</a>	Alignment		100.0	15	<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
14	<a href="#">c6iucC_</a>	Alignment		100.0	18	<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
15	<a href="#">c3fkqA_</a>	Alignment		100.0	12	<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
16	<a href="#">c3kjqB_</a>	Alignment		100.0	17	<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
17	<a href="#">c4v02B_</a>	Alignment		100.0	22	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> minc:mind cell division protein complex, aquifex aeolicus
18	<a href="#">c6nonB_</a>	Alignment		100.0	15	<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
19	<a href="#">c6g2gA_</a>	Alignment		100.0	17	<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="#">c3vx3A_</a>	Alignment		100.0	19	<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
21	<a href="#">c3k9gA_</a>	Alignment	not modelled	100.0	14	<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
22	<a href="#">c2ph1A_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c2bekB_</a>	Alignment	not modelled	100.0	22	<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
24	<a href="#">c3ezfA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
25	<a href="#">c2xj9B_</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">c3pg5A_</a>	Alignment	not modelled	100.0	21	<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
27	<a href="#">c3cioA_</a>	Alignment	not modelled	100.0	13	<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
28	<a href="#">c3la6P_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <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="#">c4ru8C</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with amppnp
30	<a href="#">c2wojD</a>	Alignment	not modelled	100.0	19	<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
31	<a href="#">c4pfsA</a>	Alignment	not modelled	100.0	19	<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 from 2 mycobacterium smegmatis
32	<a href="#">c3zq6D</a>	Alignment	not modelled	99.9	16	<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
33	<a href="#">c2wooC</a>	Alignment	not modelled	99.9	18	<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
34	<a href="#">d1ihua2</a>	Alignment	not modelled	99.9	16	<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
35	<a href="#">c4dzzB</a>	Alignment	not modelled	99.9	16	<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
36	<a href="#">c2vedA</a>	Alignment	not modelled	99.9	17	<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
37	<a href="#">d1byia</a>	Alignment	not modelled	99.9	16	<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="#">c3cwqB</a>	Alignment	not modelled	99.9	17	<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
39	<a href="#">c5bwkA</a>	Alignment	not modelled	99.9	21	<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 from 2 s.cerevisiae
40	<a href="#">c6bs3A</a>	Alignment	not modelled	99.9	16	<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 in 2 mycobacterium tuberculosis
41	<a href="#">c3ug7D</a>	Alignment	not modelled	99.9	17	<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
42	<a href="#">d1ihua1</a>	Alignment	not modelled	99.9	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
43	<a href="#">c5zmfA</a>	Alignment	not modelled	99.9	19	<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
44	<a href="#">c1ii0A</a>	Alignment	not modelled	99.9	18	<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
45	<a href="#">c4f3vB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> esx-1 secretion system protein eccA1; <b>PDBTitle:</b> crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
46	<a href="#">c3ibgF</a>	Alignment	not modelled	99.9	19	<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
47	<a href="#">c6bs5B</a>	Alignment	not modelled	99.9	17	<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 in 2 mycobacterium tuberculosis
48	<a href="#">c3io3A</a>	Alignment	not modelled	99.9	17	<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
49	<a href="#">c2qmoA</a>	Alignment	not modelled	99.8	10	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dethiobiotin synthetase; <b>PDBTitle:</b> crystal structure of dethiobiotin synthetase (biot) from helicobacter2 pylori
50	<a href="#">c3of5A</a>	Alignment	not modelled	99.8	11	<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
51	<a href="#">c3igfB</a>	Alignment	not modelled	99.8	14	<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
52	<a href="#">c3fmfA</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 mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
53	<a href="#">c2qy9A</a>	Alignment	not modelled	99.4	14	<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
						<b>PDB header:</b> protein transport

54	<a href="#">c1zu4A_</a>	Alignment	not modelled	99.3	15	<b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
55	<a href="#">c5l3qB_</a>	Alignment	not modelled	99.3	13	<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
56	<a href="#">c5l3rC_</a>	Alignment	not modelled	99.2	14	<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
57	<a href="#">c1vmaA_</a>	Alignment	not modelled	99.2	15	<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
58	<a href="#">c2og2A_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
59	<a href="#">c2cnwF_</a>	Alignment	not modelled	99.1	16	<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
60	<a href="#">c6cy1B_</a>	Alignment	not modelled	99.1	15	<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
61	<a href="#">c2yhsA_</a>	Alignment	not modelled	99.1	15	<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
62	<a href="#">c3dm5A_</a>	Alignment	not modelled	99.1	14	<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.
63	<a href="#">c2j37W_</a>	Alignment	not modelled	99.1	12	<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
64	<a href="#">c5l3sF_</a>	Alignment	not modelled	99.1	17	<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
65	<a href="#">c3b9qA_</a>	Alignment	not modelled	99.0	13	<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
66	<a href="#">c2j7pA_</a>	Alignment	not modelled	99.0	15	<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
67	<a href="#">c2q9cA_</a>	Alignment	not modelled	99.0	15	<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
68	<a href="#">c5gafi_</a>	Alignment	not modelled	99.0	16	<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
69	<a href="#">c2iy3A_</a>	Alignment	not modelled	98.9	17	<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
70	<a href="#">c1qzwC_</a>	Alignment	not modelled	98.9	14	<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
71	<a href="#">c4ak9A_</a>	Alignment	not modelled	98.8	16	<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
72	<a href="#">c2v3cC_</a>	Alignment	not modelled	98.7	14	<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="#">c3dmdA_</a>	Alignment	not modelled	98.6	15	<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
74	<a href="#">c2j289_</a>	Alignment	not modelled	98.5	15	<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
75	<a href="#">c2px0D_</a>	Alignment	not modelled	98.3	16	<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+)
76	<a href="#">c2npiB_</a>	Alignment	not modelled	98.3	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein clp1; <b>PDBTitle:</b> clp1-atp-pcf11 complex
77	<a href="#">d2qm8a1</a>	Alignment	not modelled	98.1	16	<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
78	<a href="#">d1qza3</a>	Alignment	not modelled	98.1	15	<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="#">c4ohvA_</a>	Alignment	not modelled	98.1	15	<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+
80	<a href="#">d1vmaa2</a>	Alignment	not modelled	97.7	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="#">c5hcnA</a>	Alignment	not modelled	97.6	8 <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
82	<a href="#">c4a0gC</a>	Alignment	not modelled	97.5	16 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
83	<a href="#">d2p67a1</a>	Alignment	not modelled	97.4	19 <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
84	<a href="#">c4a0rB</a>	Alignment	not modelled	97.3	14 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylmethionine-8-amino-7-oxononoate <b>PDBTitle:</b> structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
85	<a href="#">c2recB</a>	Alignment	not modelled	97.2	19 <b>PDB header:</b> helicase <b>PDB COMPND:</b>
86	<a href="#">d2qy9a2</a>	Alignment	not modelled	97.2	23 <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
87	<a href="#">d1nija1</a>	Alignment	not modelled	97.1	12 <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="#">d1yrba1</a>	Alignment	not modelled	97.1	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
89	<a href="#">d1j8yf2</a>	Alignment	not modelled	97.1	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
90	<a href="#">c4xc8B</a>	Alignment	not modelled	97.0	12 <b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
91	<a href="#">c2h5eB</a>	Alignment	not modelled	97.0	20 <b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor rf-3; <b>PDBTitle:</b> crystal structure of e.coli polypeptide release factor rf3
92	<a href="#">c4xgcE</a>	Alignment	not modelled	97.0	13 <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
93	<a href="#">d1okkd2</a>	Alignment	not modelled	97.0	27 <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
94	<a href="#">c1xjqA</a>	Alignment	not modelled	96.9	12 <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
95	<a href="#">c4nkrB</a>	Alignment	not modelled	96.8	16 <b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> molybdopterin-guanine dinucleotide biosynthesis protein b; <b>PDBTitle:</b> the crystal structure of bacillus subtilis mobb
96	<a href="#">c4aurA</a>	Alignment	not modelled	96.8	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leoa; <b>PDBTitle:</b> leoa bacterial dynamin gtpase from etec
97	<a href="#">c1fnnB</a>	Alignment	not modelled	96.7	13 <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
98	<a href="#">d1xjca</a>	Alignment	not modelled	96.7	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
99	<a href="#">c3cr8C</a>	Alignment	not modelled	96.7	17 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenyltransferase, adenylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
100	<a href="#">c3bgwD</a>	Alignment	not modelled	96.6	9 <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
101	<a href="#">c1w78A</a>	Alignment	not modelled	96.6	13 <b>PDB header:</b> synthase <b>Chain:</b> A: <b>PDB Molecule:</b> folc bifunctional protein; <b>PDBTitle:</b> e.coli folc in complex with dhpp and adp
102	<a href="#">c2vyeA</a>	Alignment	not modelled	96.6	16 <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
103	<a href="#">c4zc0A</a>	Alignment	not modelled	96.6	11 <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
104	<a href="#">c6bbmA</a>	Alignment	not modelled	96.5	14 <b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase loader complex
105	<a href="#">c6qelB</a>	Alignment	not modelled	96.4	14 <b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> replicative dna helicase; <b>PDBTitle:</b> e. coli dnabc apo complex

106	<a href="#">c1xnjB_</a>	Alignment	not modelled	96.4	14	<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
107	<a href="#">c2f1rA_</a>	Alignment	not modelled	96.4	14	<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)
108	<a href="#">c2j3eA_</a>	Alignment	not modelled	96.3	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t7i23.11 protein; <b>PDBTitle:</b> dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
109	<a href="#">c2j69D_</a>	Alignment	not modelled	96.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> bacterial dynamin-like protein; <b>PDBTitle:</b> bacterial dynamin-like protein bdlp
110	<a href="#">c3n2aA_</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional folylpolyglutamate synthase/dihydrofolate <b>PDBTitle:</b> crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
111	<a href="#">c2wwwB_</a>	Alignment	not modelled	96.2	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> methylmalonic aciduria type a protein, <b>PDBTitle:</b> crystal structure of methylmalonic acidemia type a protein
112	<a href="#">c1j8yF_</a>	Alignment	not modelled	96.1	14	<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
113	<a href="#">c4fn5A_</a>	Alignment	not modelled	96.1	18	<b>PDB header:</b> translation/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g 1; <b>PDBTitle:</b> elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
114	<a href="#">c3pe3D_</a>	Alignment	not modelled	96.0	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-n-acetylglucosamine--peptide n- <b>PDBTitle:</b> structure of human o-glcnae transferase and its complex with a peptide2 substrate
115	<a href="#">d1rz3a_</a>	Alignment	not modelled	96.0	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Phosphoribulokinase/pantothenate kinase
116	<a href="#">d1x6va3</a>	Alignment	not modelled	96.0	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'phosphosulfate kinase (APS kinase)
117	<a href="#">d1ls1a2</a>	Alignment	not modelled	96.0	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
118	<a href="#">c2qbyA_</a>	Alignment	not modelled	96.0	14	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
119	<a href="#">c2bvnB_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdnpn in complex with the antibiotic enacyloxin iia
120	<a href="#">c1xp8A_</a>	Alignment	not modelled	95.9	18	<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