


















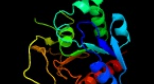

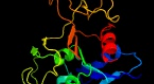







# Phyre2

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 Description RVBD0255c\_cobQ1\_306374\_307858  
 Date Tue Jul 23 14:50:31 BST 2019  
 Unique Job ID a9623830b1d66896

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fqbE_</a>	 Alignment		100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> cobyric acid synthase; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus pneumoniae r6
2	<a href="#">c5n9mA_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cobyric acid synthase; <b>PDBTitle:</b> crystal structure of gatd - a glutamine amidotransferase from2 staphylococcus aureus involved in peptidoglycan amidation
3	<a href="#">c3fmfA_</a>	 Alignment		100.0	22	<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
4	<a href="#">c2qmoA_</a>	 Alignment		100.0	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
5	<a href="#">d1byia_</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
6	<a href="#">c4a0rB_</a>	 Alignment		100.0	18	<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 from2 arabidopsis thaliana bound to dethiobiotin (dtb).
7	<a href="#">c4a0gC_</a>	 Alignment		99.9	16	<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.
8	<a href="#">c3of5A_</a>	 Alignment		99.9	15	<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
9	<a href="#">d1q7ra_</a>	 Alignment		99.9	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
10	<a href="#">d2nv0a1</a>	 Alignment		99.9	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
11	<a href="#">d2abwa1</a>	 Alignment		99.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)

12	<a href="#">c2issF</a>	Alignment		99.9	21	<b>PDB header:</b> lyase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> structure of the plp synthase holoenzyme from thermotoga maritima
13	<a href="#">c2ywdA</a>	Alignment		99.9	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of glutamine amidotransferase
14	<a href="#">c2ywjA</a>	Alignment		99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
15	<a href="#">d1ka9h</a>	Alignment		99.8	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
16	<a href="#">d1k9vf</a>	Alignment		99.8	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
17	<a href="#">d2afhe1</a>	Alignment		99.8	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
18	<a href="#">c1jvnB</a>	Alignment		99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
19	<a href="#">c5u03C</a>	Alignment		99.8	19	<b>PDB header:</b> ligase, protein fibril <b>Chain:</b> C: <b>PDB Molecule:</b> ctp synthase 1; <b>PDBTitle:</b> cryo-em structure of the human ctp synthase filament
20	<a href="#">c2ad5B</a>	Alignment		99.7	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
21	<a href="#">d1cp2a</a>	Alignment	not modelled	99.7	13	<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
22	<a href="#">c1vcnA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ctp synthetase; <b>PDBTitle:</b> crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
23	<a href="#">d1jvna2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
24	<a href="#">d1hyqa</a>	Alignment	not modelled	99.7	20	<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
25	<a href="#">c1hyqA</a>	Alignment	not modelled	99.7	20	<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
26	<a href="#">c4rz3B</a>	Alignment	not modelled	99.7	15	<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
27	<a href="#">c3nvaB</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> dimeric form of ctp synthase from sulfolobus solfataricus
28	<a href="#">c3vx3A</a>	Alignment	not modelled	99.7	18	<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
						<b>PDB header:</b> transcription

29	<a href="#">c511jA_</a>	Alignment	not modelled	99.7	18	<b>Chain:</b> A: <b>PDB Molecule:</b> site-determining protein; <b>PDBTitle:</b> structure of flen-ampnp complex
30	<a href="#">c4gudA_</a>	Alignment	not modelled	99.7	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> imidazole glycerol phosphate synthase subunit hish; <b>PDBTitle:</b> crystal structure of amidotransferase hish from vibrio cholerae
31	<a href="#">c2ph1A_</a>	Alignment	not modelled	99.7	14	<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
32	<a href="#">c4zdiE_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> ctp synthase; <b>PDBTitle:</b> crystal structure of the m. tuberculosis ctp synthase pyrg (apo form)
33	<a href="#">d1t3ta2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
34	<a href="#">d1iona_</a>	Alignment	not modelled	99.6	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="#">d1g3qa_</a>	Alignment	not modelled	99.6	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
36	<a href="#">c3kjgB_</a>	Alignment	not modelled	99.6	19	<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
37	<a href="#">c3endA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase <b>PDBTitle:</b> crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
38	<a href="#">c3ea0B_</a>	Alignment	not modelled	99.6	11	<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
39	<a href="#">c3d54D_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylformylglycinamide synthase 1; <b>PDBTitle:</b> structure of purlqs from thermotoga maritima
40	<a href="#">d1o1ya_</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
41	<a href="#">c3i7nA_</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of smu.1228c
42	<a href="#">c6g2gA_</a>	Alignment	not modelled	99.5	16	<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
43	<a href="#">c3i83A_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amido transferase; <b>PDBTitle:</b> crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
44	<a href="#">c3cioA_</a>	Alignment	not modelled	99.5	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
45	<a href="#">c4pfsA_</a>	Alignment	not modelled	99.4	16	<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
46	<a href="#">c3la6P_</a>	Alignment	not modelled	99.4	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
47	<a href="#">c2ozeA_</a>	Alignment	not modelled	99.4	9	<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
48	<a href="#">c6iucC_</a>	Alignment	not modelled	99.4	13	<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
49	<a href="#">d1gpma2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
50	<a href="#">c4v02B_</a>	Alignment	not modelled	99.4	14	<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
51	<a href="#">c3q9lB_</a>	Alignment	not modelled	99.4	12	<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
52	<a href="#">c2bekB_</a>	Alignment	not modelled	99.4	18	<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
53	<a href="#">c3fkqA_</a>	Alignment	not modelled	99.4	15	<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
54	<a href="#">c2vedA_</a>	Alignment	not modelled	99.4	13	<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
55	<a href="#">c4dzzB</a>	Alignment	not modelled	99.4	19	<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
56	<a href="#">c6nonB</a>	Alignment	not modelled	99.3	14	<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
57	<a href="#">d1wl8a1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
58	<a href="#">d2a9va1</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
59	<a href="#">c1gpmD</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> transferase (glutamine amidotransferase) <b>Chain:</b> D: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> escherichia coli gmp synthetase complexed with amp and pyrophosphate
60	<a href="#">c3k9gA</a>	Alignment	not modelled	99.3	13	<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
61	<a href="#">d1i7qb</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
62	<a href="#">c3uowB</a>	Alignment	not modelled	99.3	9	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthetase; <b>PDBTitle:</b> crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
63	<a href="#">d1s1ma1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
64	<a href="#">d1qdlb</a>	Alignment	not modelled	99.3	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
65	<a href="#">c2xj9B</a>	Alignment	not modelled	99.2	16	<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
66	<a href="#">c2wooc</a>	Alignment	not modelled	99.2	16	<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
67	<a href="#">d1vcoa1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
68	<a href="#">c3zq6D</a>	Alignment	not modelled	99.2	17	<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
69	<a href="#">d1ihua2</a>	Alignment	not modelled	99.2	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
70	<a href="#">c5zmfA</a>	Alignment	not modelled	99.2	17	<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
71	<a href="#">d1i1qb</a>	Alignment	not modelled	99.2	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)
72	<a href="#">c2vpiA</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase; <b>PDBTitle:</b> human gmp synthetase - glutaminase domain
73	<a href="#">c5tw7E</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
74	<a href="#">c2ywcC</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
75	<a href="#">c2lxnA</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit a; <b>PDBTitle:</b> solution nmr structure of glutamine amido transferase subunit of2 gaunosine monophosphate synthetase from methanocaldococcus jannaschii
76	<a href="#">c6qurA</a>	Alignment	not modelled	99.1	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaminase; <b>PDBTitle:</b> mapping the allosteric communication network of aminodeoxychorismate2 synthase
77	<a href="#">c3ug7D</a>	Alignment	not modelled	99.1	15	<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
78	<a href="#">c2wojD</a>	Alignment	not modelled	99.1	14	<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
79	<a href="#">c3tqiB</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
80	<a href="#">c3dm5A</a>	Alignment	not modelled	99.1	23	<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.

81	<a href="#">c4ru8C</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of pnob8 para with amppnp
82	<a href="#">c1ii0A</a>	Alignment	not modelled	99.1	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
83	<a href="#">c3ez6B</a>	Alignment	not modelled	99.1	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
84	<a href="#">d1ihua1</a>	Alignment	not modelled	99.1	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
85	<a href="#">c2qy9A</a>	Alignment	not modelled	99.1	18	<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
86	<a href="#">c5bwkA</a>	Alignment	not modelled	99.1	13	<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
87	<a href="#">c3ibgF</a>	Alignment	not modelled	99.1	13	<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
88	<a href="#">c6bs5B</a>	Alignment	not modelled	99.0	23	<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
89	<a href="#">c1zu4A</a>	Alignment	not modelled	99.0	18	<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
90	<a href="#">c3fijD</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> lin1909 protein; <b>PDBTitle:</b> crystal structure of a uncharacterized protein lin1909
91	<a href="#">c6cy1B</a>	Alignment	not modelled	99.0	20	<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
92	<a href="#">c2yhsA</a>	Alignment	not modelled	99.0	19	<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
93	<a href="#">c5l3qB</a>	Alignment	not modelled	99.0	18	<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
94	<a href="#">c2iy3A</a>	Alignment	not modelled	99.0	20	<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
95	<a href="#">c5l3rC</a>	Alignment	not modelled	98.9	19	<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
96	<a href="#">c6bs3A</a>	Alignment	not modelled	98.9	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 in2 mycobacterium tuberculosis
97	<a href="#">c2j37W</a>	Alignment	not modelled	98.9	15	<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
98	<a href="#">c3io3A</a>	Alignment	not modelled	98.9	15	<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
99	<a href="#">c3l4eA</a>	Alignment	not modelled	98.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized peptidase lmo0363; <b>PDBTitle:</b> 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
100	<a href="#">c2og2A</a>	Alignment	not modelled	98.9	18	<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
101	<a href="#">c5l3sF</a>	Alignment	not modelled	98.9	16	<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
102	<a href="#">c2q9cA</a>	Alignment	not modelled	98.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmpnp with mgcl complex
103	<a href="#">c2v3cC</a>	Alignment	not modelled	98.9	17	<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
104	<a href="#">c3b9qA</a>	Alignment	not modelled	98.9	21	<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
105	<a href="#">c2vx0B</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> human gmp synthetase in complex with xmp
106	<a href="#">c2v3cC</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein;



106	<a href="#">c26bnA_</a>	Alignment	not modelled	98.9	22	<b>PDBTitle:</b> crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution <b>PDB header:</b> transport protein
107	<a href="#">c3dmdA_</a>	Alignment	not modelled	98.9	20	<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
108	<a href="#">c2cnwF_</a>	Alignment	not modelled	98.9	20	<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
109	<a href="#">c1qzWC_</a>	Alignment	not modelled	98.9	16	<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
110	<a href="#">c3r74B_</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> lyase, biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> anthranilate/para-aminobenzoate synthases component i; <b>PDBTitle:</b> crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
111	<a href="#">c1vmaA_</a>	Alignment	not modelled	98.8	20	<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
112	<a href="#">c5gafi_</a>	Alignment	not modelled	98.8	22	<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
113	<a href="#">c3cwqB_</a>	Alignment	not modelled	98.8	15	<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
114	<a href="#">c4ak9A_</a>	Alignment	not modelled	98.8	26	<b>PDB header:</b> protein transport <b>Chain:</b> A; <b>PDB Molecule:</b> cpfts2; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
115	<a href="#">c1keeH_</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> ligase <b>Chain:</b> H; <b>PDB Molecule:</b> carbamoyl-phosphate synthetase small chain; <b>PDBTitle:</b> inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
116	<a href="#">c6a4tB_</a>	Alignment	not modelled	98.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidase e; <b>PDBTitle:</b> crystal structure of peptidase e from deinococcus radiodurans r1
117	<a href="#">c2j7pA_</a>	Alignment	not modelled	98.7	19	<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
118	<a href="#">c3igfB_</a>	Alignment	not modelled	98.7	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
119	<a href="#">c2w7tA_</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> ligase <b>Chain:</b> A; <b>PDB Molecule:</b> putative cytidine triphosphate synthase; <b>PDBTitle:</b> trypanosoma brucei ctps - glutaminase domain with bound acivicin
120	<a href="#">d1a9xb2</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> Class I glutamine amidotransferases (GAT)