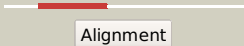

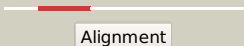

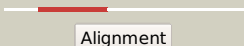

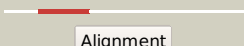

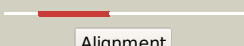

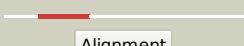

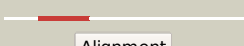










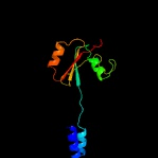
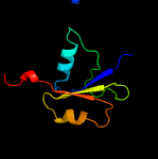

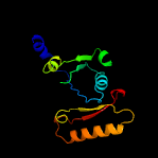

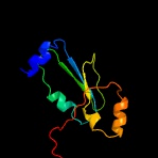




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0209 (-) _249038_250123
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	97bd0ef7117be43b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5izkB_</a>	 Alignment		97.9	22	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdp
2	<a href="#">c3gehA_</a>	 Alignment		97.8	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
3	<a href="#">c5izmA_</a>	 Alignment		97.8	26	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdpnp
4	<a href="#">c4kzD_</a>	 Alignment		97.7	24	<b>PDB header:</b> translation <b>Chain:</b> D; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
5	<a href="#">c3j8gX_</a>	 Alignment		97.7	24	<b>PDB header:</b> ribosome <b>Chain:</b> X; <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
6	<a href="#">c4b3xA_</a>	 Alignment		97.7	28	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> bacterial translation initiation factor if2 (1-363), apo form
7	<a href="#">c3wbkB_</a>	 Alignment		97.6	21	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
8	<a href="#">c1g7tA_</a>	 Alignment		97.6	28	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if2/eif5b; <b>PDBTitle:</b> x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp
9	<a href="#">d2c78a3</a>	 Alignment		97.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
10	<a href="#">c2qa5A_</a>	 Alignment		97.4	28	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> septin-2; <b>PDBTitle:</b> crystal structure of sept2 g-domain
11	<a href="#">c2qagA_</a>	 Alignment		97.4	21	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> septin-2; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7

12	<a href="#">c2qagC_</a>	Alignment		97.3	27	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7
13	<a href="#">d1tq4a_</a>	Alignment		97.3	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
14	<a href="#">c4n3nA_</a>	Alignment		97.3	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein, <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form
15	<a href="#">c3j4jA_</a>	Alignment		97.3	26	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map
16	<a href="#">d2p67a1</a>	Alignment		97.3	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
17	<a href="#">c2qagB_</a>	Alignment		97.3	23	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> septin-6; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7
18	<a href="#">c2j3eA_</a>	Alignment		97.3	28	<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 of 2 chloroplast translocon components atoc33 and pstoc159
19	<a href="#">c3md0A_</a>	Alignment		97.3	23	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine/ornithine transport system atpase; <b>PDBTitle:</b> crystal structure of arginine/ornithine transport system atpase from 2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
20	<a href="#">c2qthA_</a>	Alignment		97.3	18	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of a gtp-binding protein from the hyperthermophilic 2 archaeon sulfobolus solfataricus in complex with gdp
21	<a href="#">c4upyB_</a>	Alignment	not modelled	97.3	21	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> eif5b; <b>PDBTitle:</b> mammalian 80s hcv-ires initiation complex with eif5b pre-like state
22	<a href="#">c1zo1l_</a>	Alignment	not modelled	97.2	27	<b>PDB header:</b> translation/rna <b>Chain:</b> I: <b>PDB Molecule:</b> translation initiation factor 2; <b>PDBTitle:</b> if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
23	<a href="#">c1d2eA_</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu (ef-tu); <b>PDBTitle:</b> crystal structure of mitochondrial ef-tu in complex with gdp
24	<a href="#">c3t5dC_</a>	Alignment	not modelled	97.1	28	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of septin 7 in complex with gdp
25	<a href="#">c1mkyA_</a>	Alignment	not modelled	97.1	26	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein enga; <b>PDBTitle:</b> structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains
26	<a href="#">c2e87A_</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1320; <b>PDBTitle:</b> crystal structure of hypothetical gtp-binding protein ph1320 from 2 pyrococcus horikoshii ot3, in complex with gdp
27	<a href="#">c3ftqA_</a>	Alignment	not modelled	97.0	32	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> septin-2; <b>PDBTitle:</b> crystal structure of septin 2 in complex with gppnhp and 2 mg2+
28	<a href="#">c3izyP_</a>	Alignment	not modelled	97.0	29	<b>PDB header:</b> rna, ribosomal protein <b>Chain:</b> P: <b>PDB Molecule:</b> translation initiation factor if-2, mitochondrial; <b>PDBTitle:</b> mammalian mitochondrial translation initiation factor 2 <b>PDB header:</b> translation

29	<a href="#">c5fg3A_</a>	Alignment	not modelled	97.0	28	<b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of gdp-bound aif5b from aeropyrum pernix
30	<a href="#">c5irrB_</a>	Alignment	not modelled	97.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> septin-like protein; <b>PDBTitle:</b> crystal structure of septin gtpase domain from chlamydomonas2 reinhardtii
31	<a href="#">d1h65a_</a>	Alignment	not modelled	97.0	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
32	<a href="#">c1skqB_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> the crystal structure of sulfolobus solfataricus elongation factor 1-2 alpha in complex with magnesium and gdp
33	<a href="#">c1wb1C_</a>	Alignment	not modelled	97.0	23	<b>PDB header:</b> protein synthesis <b>Chain:</b> C: <b>PDB Molecule:</b> translation elongation factor selb; <b>PDBTitle:</b> crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp
34	<a href="#">c5ar1A_</a>	Alignment	not modelled	96.9	25	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 11; <b>PDBTitle:</b> crystal structure of cdc11 from saccharomyces cerevisiae
35	<a href="#">c1xzqA_</a>	Alignment	not modelled	96.9	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna modification gtpase trme; <b>PDBTitle:</b> structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
36	<a href="#">c3qq5A_</a>	Alignment	not modelled	96.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefe]-hydrogenase maturation protein hydF
37	<a href="#">d2dy1a2</a>	Alignment	not modelled	96.8	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
38	<a href="#">c4nc1B_</a>	Alignment	not modelled	96.8	21	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein; <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
39	<a href="#">c2hjqA_</a>	Alignment	not modelled	96.7	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein enga; <b>PDBTitle:</b> the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp
40	<a href="#">c2wwwB_</a>	Alignment	not modelled	96.7	21	<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
41	<a href="#">c5ady6_</a>	Alignment	not modelled	96.6	21	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> gtpase hflx; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with hflx
42	<a href="#">c2qptA_</a>	Alignment	not modelled	96.6	31	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> eh domain-containing protein-2; <b>PDBTitle:</b> crystal structure of an ehd atpase involved in membrane remodelling
43	<a href="#">c3j81k_</a>	Alignment	not modelled	96.6	20	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> es10; <b>PDBTitle:</b> cryoem structure of a partial yeast 48s preinitiation complex
44	<a href="#">c3geiB_</a>	Alignment	not modelled	96.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from chlorobium tepidum in complex2 with gcp
45	<a href="#">c4yqfA_</a>	Alignment	not modelled	96.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> septin-9; <b>PDBTitle:</b> gtpase domain of human septin 9
46	<a href="#">c3agjC_</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> translation/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
47	<a href="#">c5k0yS_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> translation <b>Chain:</b> S: <b>PDB Molecule:</b> eukaryotic initiation factor 2 gamma subunit (eif2-gamma); <b>PDBTitle:</b> m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face
48	<a href="#">c3j2k7_</a>	Alignment	not modelled	96.4	20	<b>PDB header:</b> ribosome/translation <b>Chain:</b> 7: <b>PDB Molecule:</b> eukaryotic polypeptide chain release factor 3; <b>PDB Fragment:</b> unp residues 147-584; <b>PDBTitle:</b> cryo-em structure of the mammalian erf1-erf3-associated termination2 complex
49	<a href="#">c3sopB_</a>	Alignment	not modelled	96.3	27	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neuronal-specific septin-3; <b>PDBTitle:</b> crystal structure of human septin 3 gtpase domain
50	<a href="#">c3p1jC_</a>	Alignment	not modelled	96.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
51	<a href="#">c2bvnB_</a>	Alignment	not modelled	96.3	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:gdpnp in complex with the antibiotic enacyloxin iia
52	<a href="#">d2bv3a2</a>	Alignment	not modelled	96.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
53	<a href="#">c5dn8A_</a>	Alignment	not modelled	96.2	26	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp. <b>PDB header:</b> hydrolase

54	<a href="#">c1wf3A</a>	Alignment	not modelled	96.1	35	<b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
55	<a href="#">c1kk3A</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eif2gamma; <b>PDBTitle:</b> structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+
56	<a href="#">c2h5eB</a>	Alignment	not modelled	95.9	22	<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
57	<a href="#">c1s0uA</a>	Alignment	not modelled	95.9	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
58	<a href="#">c3wyaA</a>	Alignment	not modelled	95.9	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
59	<a href="#">c1egaB</a>	Alignment	not modelled	95.8	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gtp-binding protein era); <b>PDBTitle:</b> crystal structure of a widely conserved gtpase era
60	<a href="#">c3i8sC</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
61	<a href="#">c3lx8A</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron uptake transporter protein b; <b>PDBTitle:</b> crystal structure of gdp-bound nfeob from s. thermophilus
62	<a href="#">c3a1vB</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structure of the cytosolic domain of t. maritima feob2 iron transporter in apo form
63	<a href="#">c5mvfA</a>	Alignment	not modelled	95.8	24	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> eh domain-containing protein 4; <b>PDBTitle:</b> active structure of ehd4 complexed with adp
64	<a href="#">c4zu9A</a>	Alignment	not modelled	95.7	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor selb; <b>PDBTitle:</b> crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
65	<a href="#">c3ibyA</a>	Alignment	not modelled	95.7	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of cytosolic domain of l. pneumophila feob
66	<a href="#">c3j65o</a>	Alignment	not modelled	95.7	20	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l15; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
67	<a href="#">c2elfA</a>	Alignment	not modelled	95.6	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein translation elongation factor 1a; <b>PDBTitle:</b> crystal structure of the selb-like elongation factor ef-pyl from2 methanosarcina mazei
68	<a href="#">d1n0ua2</a>	Alignment	not modelled	95.6	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
69	<a href="#">d1jnya3</a>	Alignment	not modelled	95.4	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
70	<a href="#">c3lxwA</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase imap family member 1; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 1
71	<a href="#">c1lnzA</a>	Alignment	not modelled	95.2	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> spo0b-associated gtp-binding protein; <b>PDBTitle:</b> structure of the obg gtp-binding protein
72	<a href="#">c3vr1B</a>	Alignment	not modelled	95.1	27	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> crystal structure analysis of the translation factor rf3
73	<a href="#">c3vr5C</a>	Alignment	not modelled	95.1	28	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> v-type sodium atpase catalytic subunit a; <b>PDBTitle:</b> crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
74	<a href="#">c5h7iB</a>	Alignment	not modelled	95.1	26	<b>PDB header:</b> translation/ribosomal protein <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 2-50s ribosomal protein l12 <b>PDBTitle:</b> complex of elongation factor 2-50s ribosomal protein l12
75	<a href="#">c4crnP</a>	Alignment	not modelled	95.0	19	<b>PDB header:</b> translation <b>Chain:</b> P: <b>PDB Molecule:</b> erf3 in ribosome bound erf1-erf3-gdnpn complex; <b>PDBTitle:</b> cryo-em of a pretermination complex with erf1 and erf3
76	<a href="#">c4zciA</a>	Alignment	not modelled	95.0	27	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein typa/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/typa
77	<a href="#">d2qm8a1</a>	Alignment	not modelled	94.9	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
78	<a href="#">c2dpyA</a>	Alignment	not modelled	94.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> crystal structure of the flagellar type iii atpase flii
79	<a href="#">c3k53B</a>	Alignment	not modelled	94.9	29	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> crystal structure of nfeob from p. furiosus
80	<a href="#">c2c61A</a>	Alignment	not modelled	94.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-type atp synthase non-catalytic subunit b; <b>PDBTitle:</b> crystal structure of the non-catalytic b subunit of a-type2

						atpase from m. mazei go1
81	<a href="#">c5gnuA_</a>	Alignment	not modelled	94.8	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin-1; <b>PDBTitle:</b> the structure of mini-mfn1 apo
82	<a href="#">d1f60a3</a>	Alignment	not modelled	94.7	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
83	<a href="#">c1mj1A_</a>	Alignment	not modelled	94.6	22	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 1.3 a cryo-em map of the coli 70s ribosome
84	<a href="#">c1zunB_</a>	Alignment	not modelled	94.6	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylate transferase, subunit <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
85	<a href="#">c5ksza_</a>	Alignment	not modelled	94.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial rho gtpase 1; <b>PDBTitle:</b> hmiro ef hand and cgtpase domains in the gmppcp-bound state
86	<a href="#">c3ievA_</a>	Alignment	not modelled	94.6	37	<b>PDB header:</b> nucleotide binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein era; <b>PDBTitle:</b> crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
87	<a href="#">c2w6jD_</a>	Alignment	not modelled	94.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta, mitochondrial; <b>PDBTitle:</b> low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
88	<a href="#">c5b0oB_</a>	Alignment	not modelled	94.4	24	<b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> structure of the flih-flii complex
89	<a href="#">c4fn5A_</a>	Alignment	not modelled	94.3	23	<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
90	<a href="#">c2jizD_</a>	Alignment	not modelled	94.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> the structure of f1-atpase inhibited by resveratrol.
91	<a href="#">c5syrA_</a>	Alignment	not modelled	94.1	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp synthase spa1/mxib; <b>PDBTitle:</b> crystal structure of atpase delta1-79 spa47 r350a
92	<a href="#">c4byxV_</a>	Alignment	not modelled	94.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b, probable <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
93	<a href="#">c3degC_</a>	Alignment	not modelled	94.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
94	<a href="#">c1r5nA_</a>	Alignment	not modelled	93.9	16	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptide chain release factor gtp- <b>PDBTitle:</b> crystal structure analysis of sup35 complexed with gdp
95	<a href="#">c2rdo7_</a>	Alignment	not modelled	93.9	25	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdnp) and rrf bound
96	<a href="#">d1zaka1</a>	Alignment	not modelled	93.9	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
97	<a href="#">c3zjcC_</a>	Alignment	not modelled	93.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 7; <b>PDBTitle:</b> crystal structure of gmppnp-bound human gimap7 I100q variant
98	<a href="#">c4byrP_</a>	Alignment	not modelled	93.8	25	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
99	<a href="#">c2plfA_</a>	Alignment	not modelled	93.7	23	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form.
100	<a href="#">c3nxsA_</a>	Alignment	not modelled	93.5	29	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase; <b>PDBTitle:</b> crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
101	<a href="#">c1zakB_</a>	Alignment	not modelled	93.4	30	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)
102	<a href="#">c6njpC_</a>	Alignment	not modelled	93.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> translocator escn; <b>PDBTitle:</b> structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system
103	<a href="#">d1ye8a1</a>	Alignment	not modelled	93.4	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)
104	<a href="#">c2dy1A_</a>	Alignment	not modelled	93.4	30	<b>PDB header:</b> signaling protein, translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of ef-g-2 from thermus thermophilus
105	<a href="#">c4wnrA_</a>	Alignment	not modelled	93.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich-repeat protein; <b>PDBTitle:</b> structure of methanosarcina barkeri roco2 roccordc bound to gdp
						<b>PDB header:</b> translation



106	<a href="#">c1g7cA_</a>	Alignment	not modelled	93.3	19	<b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> yeast eef1a:eef1ba in complex with gdpnp
107	<a href="#">c5bn4A_</a>	Alignment	not modelled	93.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> structure of a unique atp synthase neqa-neqb in complex with anp from2 nanoarchaeum equitans
108	<a href="#">c5xktA_</a>	Alignment	not modelled	93.2	48	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease accessory protein ureg; <b>PDBTitle:</b> klebsiella pneumoniae ureg in complex with gmppnp and nickel
109	<a href="#">c2lkcA_</a>	Alignment	not modelled	93.2	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> free b.st if2-g2
110	<a href="#">c3a5dM_</a>	Alignment	not modelled	93.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> v-type atp synthase beta chain; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
111	<a href="#">c2ak3B_</a>	Alignment	not modelled	93.2	39	<b>PDB header:</b> transferase (phosphotransferase) <b>Chain:</b> B: <b>PDB Molecule:</b> adenylate kinase isoenzyme-3; <b>PDBTitle:</b> the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
112	<a href="#">c2ywfA_</a>	Alignment	not modelled	93.2	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> crystal structure of gmppnp-bound lepa from aquifex aeolicus
113	<a href="#">c5ujmE_</a>	Alignment	not modelled	93.1	14	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> origin recognition complex subunit 5; <b>PDBTitle:</b> structure of the active form of human origin recognition complex and2 its atpase motor module
114	<a href="#">c2xexA_</a>	Alignment	not modelled	93.1	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of staphylococcus aureus elongation factor2 g
115	<a href="#">d1uj2a_</a>	Alignment	not modelled	93.0	26	<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="#">c3uieB_</a>	Alignment	not modelled	93.0	26	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> adenylyl-sulfate kinase 1, chloroplastic; <b>PDBTitle:</b> crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with amppnp and aps
117	<a href="#">c1ii0A_</a>	Alignment	not modelled	92.9	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
118	<a href="#">d2jdid3</a>	Alignment	not modelled	92.9	14	<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)
119	<a href="#">c4pzcC_</a>	Alignment	not modelled	92.8	32	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylate kinase; <b>PDBTitle:</b> the crystal structure of adenylate kinase from francisella tularensis2 subsp. tularensis schu s4
120	<a href="#">c3vx3A_</a>	Alignment	not modelled	92.8	37	<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