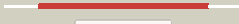



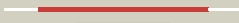



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1852_(ureG)_2100347_2101021
Date	Fri Aug 2 13:30:46 BST 2019
Unique Job ID	9d9eed54741d9e6e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5xktA_</a>	 Alignment		100.0	55	<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
2	<a href="#">c4hi0F_</a>	 Alignment		100.0	55	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> urease accessory protein ureg; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease accessory protein2 uref/h/g complex
3	<a href="#">c2hf9A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrogenase nickel incorporation <b>PDBTitle:</b> crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
4	<a href="#">c4lpsA_</a>	 Alignment		100.0	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein hypb; <b>PDBTitle:</b> crystal structure of hypb from helicobacter pylori in complex with2 nickel
5	<a href="#">d2qm8a1</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="#">c2wsmB_</a>	 Alignment		99.9	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hypb); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus
7	<a href="#">c5ady6_</a>	 Alignment		99.9	17	<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
8	<a href="#">c3nxsA_</a>	 Alignment		99.9	24	<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
9	<a href="#">c2e87A_</a>	 Alignment		99.9	18	<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 from2 pyrococcus horikoshii ot3, in complex with gdp
10	<a href="#">c3ievA_</a>	 Alignment		99.9	14	<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
11	<a href="#">c4csu9_</a>	 Alignment		99.9	16	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> gtpase obge/cgta; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with obge

12	<a href="#">c1xzqA_</a>	Alignment		99.9	17	<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
13	<a href="#">c2wwwB_</a>	Alignment		99.9	19	<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
14	<a href="#">c1lnzA_</a>	Alignment		99.9	14	<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
15	<a href="#">c1egaB_</a>	Alignment		99.9	22	<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
16	<a href="#">c1udxA_</a>	Alignment		99.9	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> the gtp-binding protein obg; <b>PDBTitle:</b> crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8
17	<a href="#">c1wf3A_</a>	Alignment		99.9	16	<b>PDB header:</b> hydrolase <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
18	<a href="#">d2p67a1</a>	Alignment		99.9	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
19	<a href="#">c2qthA_</a>	Alignment		99.9	16	<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 hyperthermophilic2 archaeon sulfobolus solfataricus in complex with gdp
20	<a href="#">c6em5b_</a>	Alignment		99.9	14	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 60s ribosomal protein l3; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
21	<a href="#">c3md0A_</a>	Alignment	not modelled	99.9	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 from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
22	<a href="#">c3gehA_</a>	Alignment	not modelled	99.9	21	<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
23	<a href="#">c3j65o_</a>	Alignment	not modelled	99.9	15	<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.
24	<a href="#">c4b3xA_</a>	Alignment	not modelled	99.9	15	<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
25	<a href="#">c3j8gX_</a>	Alignment	not modelled	99.9	15	<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
26	<a href="#">c2hjgA_</a>	Alignment	not modelled	99.9	16	<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
27	<a href="#">c3j4jA_</a>	Alignment	not modelled	99.9	17	<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
						<b>PDB header:</b> translation

28	<a href="#">c4kzD_</a>	Alignment	not modelled	99.9	17	<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)
29	<a href="#">c4xc8B_</a>	Alignment	not modelled	99.9	19	<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)
30	<a href="#">c1mkyA_</a>	Alignment	not modelled	99.9	15	<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
31	<a href="#">c5fg3A_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> translation <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
32	<a href="#">c5dn8A_</a>	Alignment	not modelled	99.9	19	<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.
33	<a href="#">c4upyB_</a>	Alignment	not modelled	99.9	17	<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
34	<a href="#">c4nclB_</a>	Alignment	not modelled	99.9	18	<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
35	<a href="#">c4a9aB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> ribosome-interacting gtpase 1; <b>PDBTitle:</b> structure of rbg1 in complex with tma46 dfrp domain
36	<a href="#">c3izyP_</a>	Alignment	not modelled	99.9	18	<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
37	<a href="#">c3wbkB_</a>	Alignment	not modelled	99.9	11	<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
38	<a href="#">c1g7tA_</a>	Alignment	not modelled	99.9	22	<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
39	<a href="#">c4zu9A_</a>	Alignment	not modelled	99.9	16	<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
40	<a href="#">c4dheA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of a probable gtp-binding protein engb from2 burkholderia thailandensis
41	<a href="#">d1yrba1</a>	Alignment	not modelled	99.8	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
42	<a href="#">c1zoi1_</a>	Alignment	not modelled	99.8	16	<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
43	<a href="#">c3a1vB_</a>	Alignment	not modelled	99.8	14	<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
44	<a href="#">c5hcnA_</a>	Alignment	not modelled	99.8	19	<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
45	<a href="#">c3pqcA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp
46	<a href="#">c5ymxB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> signaling protein, hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mutual gliding-motility protein mgla; <b>PDBTitle:</b> myxococcus xanthus mgla in gdp bound conformation
47	<a href="#">c1wb1C_</a>	Alignment	not modelled	99.8	18	<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
48	<a href="#">c3k53B_</a>	Alignment	not modelled	99.8	15	<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
49	<a href="#">c1kk3A_</a>	Alignment	not modelled	99.8	17	<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+
50	<a href="#">c2ywfA_</a>	Alignment	not modelled	99.8	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
51	<a href="#">c3qq5A_</a>	Alignment	not modelled	99.8	21	<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
52	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
						<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b,

53	<a href="#">c4byxV_</a>	Alignment	not modelled	99.8	13	probable <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
54	<a href="#">c3i8sC_</a>	Alignment	not modelled	99.8	20	<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
55	<a href="#">c3lx8A_</a>	Alignment	not modelled	99.8	16	<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
56	<a href="#">c3j81k_</a>	Alignment	not modelled	99.8	17	<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
57	<a href="#">c5izkB_</a>	Alignment	not modelled	99.8	27	<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
58	<a href="#">c3ibyA_</a>	Alignment	not modelled	99.8	13	<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 I. pneumophila feob
59	<a href="#">d1svia_</a>	Alignment	not modelled	99.8	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
60	<a href="#">c4n3nA_</a>	Alignment	not modelled	99.8	18	<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
61	<a href="#">d1nija1</a>	Alignment	not modelled	99.8	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
62	<a href="#">c3wyaA_</a>	Alignment	not modelled	99.8	12	<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
63	<a href="#">c5izmA_</a>	Alignment	not modelled	99.8	23	<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
64	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
65	<a href="#">d1egaa1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
66	<a href="#">c5k0yS_</a>	Alignment	not modelled	99.8	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
67	<a href="#">c3degC_</a>	Alignment	not modelled	99.8	16	<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
68	<a href="#">d1zunb3</a>	Alignment	not modelled	99.8	17	<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="#">d2dy1a2</a>	Alignment	not modelled	99.8	24	<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="#">c5ee1A_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> obg-like atpase 1; <b>PDBTitle:</b> crystal structure of osychf1 at ph 7.85
71	<a href="#">c1nija_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
72	<a href="#">c5ucvA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of a ribosome biogenesis gtp-binding protein (ysxc)2 from neisseria gonorrhoeae with bound gdp
73	<a href="#">c1jalA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yichf protein; <b>PDBTitle:</b> yichf protein (hi0393)
74	<a href="#">c3t1tC_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gliding protein mgla; <b>PDBTitle:</b> mgla bound to gdp in p1 tetrameric arrangement
75	<a href="#">d1wf3a1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
76	<a href="#">c2wjjB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b homolog; <b>PDBTitle:</b> structure and function of the feob g-domain from2 methanococcus jannaschii
77	<a href="#">c4byrP_</a>	Alignment	not modelled	99.8	13	<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
78	<a href="#">c2ohfA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein 9; <b>PDBTitle:</b> crystal structure of human ola1 in complex with amppcp
						<b>PDB header:</b> ribosome

79	<a href="#">c4qjty_</a>	Alignment	not modelled	99.8	18	<b>Chain:</b> Y; <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of elongation factor 4 (ef4/lepa) bound to the 23S subunit of the 70S ribosome, 30S subunit of the 70S ribosome
80	<a href="#">c6bbqA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> cytohesin-3, adp-ribosylation factor 6; <b>PDBTitle:</b> model for extended volume of truncated monomeric cytohesin-3 (grp1; 2 amino acids 63-399) e161a arf6 q67l fusion protein
81	<a href="#">c2dwqB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> thermus thermophilus ychf gtp-binding protein
82	<a href="#">c2qu8A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> putative nucleolar gtp-binding protein 1; <b>PDBTitle:</b> crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
83	<a href="#">d1lnza2</a>	Alignment	not modelled	99.7	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
84	<a href="#">c2plfA_</a>	Alignment	not modelled	99.7	22	<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 archaeon 23S subunit of methanocaldococcus jasperi in the nucleotide-free form.
85	<a href="#">d2cxa1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
86	<a href="#">d2qn6a3</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
87	<a href="#">d1f60a3</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
88	<a href="#">c4wnrA_</a>	Alignment	not modelled	99.7	12	<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
89	<a href="#">d2gj8a1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
90	<a href="#">d1wb1a4</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
91	<a href="#">c2bvnB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> elongation factor <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdnp in complex with the antibiotic enacyloxin iia
92	<a href="#">c3o47A_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> hydrolase, hydrolase activator <b>Chain:</b> A; <b>PDB Molecule:</b> adp-ribosylation factor gtpase-activating protein 1, adp- <b>PDBTitle:</b> crystal structure of arfgap1-arf1 fusion protein
93	<a href="#">d1ni3a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
94	<a href="#">c1ni3A_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ychf gtp-binding protein; <b>PDBTitle:</b> structure of the schizosaccharomyces pombe ychf gtpase
95	<a href="#">c2dykB_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of n-terminal gtp-binding domain of enga from 23S subunit of thermus thermophilus hb8
96	<a href="#">c2lkA_</a>	Alignment	not modelled	99.7	15	<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
97	<a href="#">c3a1wA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structure of the g domain of t. maritima feob iron2 transporter
98	<a href="#">c5kutB_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mitochondrial rho gtpase 2; <b>PDBTitle:</b> hmiro2 c-terminal gtpase domain, gdp-bound
99	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
100	<a href="#">d1puia_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
101	<a href="#">d1r5ba3</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
102	<a href="#">c2elfA_</a>	Alignment	not modelled	99.7	13	<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 from 23S subunit of methanosarcina mazei
103	<a href="#">d1g7sa4</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> G proteins
104	<a href="#">d1tq4a_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

105	<a href="#">d1ksxa_</a>	Alignment	not modelled	99.7	12	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
106	<a href="#">c3lvrE_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> protein transport <b>Chain:</b> E; <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain- <b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
107	<a href="#">d1xzpa2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
108	<a href="#">d1udxa2</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> G proteins
109	<a href="#">c1d2eA_</a>	Alignment	not modelled	99.7	17	<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
110	<a href="#">c2xtpA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> immune system <b>Chain:</b> A; <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of nucleotide-free human gimap2, amino2 acid residues 1-260
111	<a href="#">c1zunB_</a>	Alignment	not modelled	99.7	17	<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
112	<a href="#">d1jnva3</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
113	<a href="#">d1mkya2</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> G proteins
114	<a href="#">c1skqB_</a>	Alignment	not modelled	99.6	16	<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
115	<a href="#">c4zciA_</a>	Alignment	not modelled	99.6	27	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> gtp-binding protein tyra/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/tyra
116	<a href="#">c3w5iB_</a>	Alignment	not modelled	99.6	18	<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 gallionella capsiferriformans
117	<a href="#">c2wkqA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase, cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> nph1-1, ras-related c3 botulinum toxin substrate 1; <b>PDBTitle:</b> structure of a photoactivatable rac1 containing the lov2 c450a mutant
118	<a href="#">d1zj6a1</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
119	<a href="#">c4v0iB_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> arf-like small gtpase; <b>PDBTitle:</b> crystal structure of the crarl6dn in the gtp bound form
120	<a href="#">c3agiC_</a>	Alignment	not modelled	99.6	18	<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