

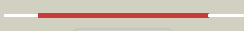


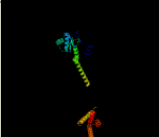





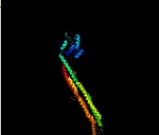





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0210 (-) _250120_251598
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	59ee5e4f22bb4ad4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2j69D_</a>	 Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> bacterial dynamin-like protein; <b>PDBTitle:</b> bacterial dynamin-like protein bdlp
2	<a href="#">c4aurA_</a>	 Alignment		99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leoa; <b>PDBTitle:</b> leoa bacterial dynamin gtpase from etec
3	<a href="#">c5oxfB_</a>	 Alignment		99.6	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long range sensing and tethering of membranes
4	<a href="#">c5owvA_</a>	 Alignment		99.6	11	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
5	<a href="#">c5gnuA_</a>	 Alignment		99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin-1; <b>PDBTitle:</b> the structure of mini-mfn1 apo
6	<a href="#">c5owvC_</a>	 Alignment		99.5	9	<b>PDB header:</b> lipid binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
7	<a href="#">c5mvfA_</a>	 Alignment		99.4	15	<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
8	<a href="#">d1tq4a_</a>	 Alignment		99.3	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
9	<a href="#">c4b3xA_</a>	 Alignment		99.2	16	<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
10	<a href="#">c2hjgA_</a>	 Alignment		99.2	22	<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
11	<a href="#">c4kzD_</a>	 Alignment		99.2	18	<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)

12	<a href="#">c3wbkB_</a>	Alignment		99.2	16	<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
13	<a href="#">c4upyB_</a>	Alignment		99.2	19	<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
14	<a href="#">c2x2fD_</a>	Alignment		99.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> dynamin 1 gtpase dimer, short axis form
15	<a href="#">c1mkyA_</a>	Alignment		99.2	21	<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
16	<a href="#">c4p4sB_</a>	Alignment		99.1	11	<b>PDB header:</b> antiviral protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> interferon-induced gtp-binding protein mx1; <b>PDBTitle:</b> gmppcp-bound stalkless-mxa
17	<a href="#">c3j8gX_</a>	Alignment		99.1	14	<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
18	<a href="#">c5fg3A_</a>	Alignment		99.1	21	<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
19	<a href="#">c5izmA_</a>	Alignment		99.1	18	<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
20	<a href="#">c1g7tA_</a>	Alignment		99.1	21	<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
21	<a href="#">c5dn8A_</a>	Alignment	not modelled	99.1	21	<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.
22	<a href="#">c4n3nA_</a>	Alignment	not modelled	99.1	21	<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
23	<a href="#">c3j4jA_</a>	Alignment	not modelled	99.1	19	<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
24	<a href="#">c5k0yS_</a>	Alignment	not modelled	99.0	13	<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
25	<a href="#">c1wb1C_</a>	Alignment	not modelled	99.0	15	<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
26	<a href="#">c1d2eA_</a>	Alignment	not modelled	98.9	20	<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
27	<a href="#">c6djgA_</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vps1 gtpase-bse; <b>PDBTitle:</b> vps1 gtpase-bse fusion complexed with gdp.alf4-
						<b>PDB header:</b> translation

28	<a href="#">c2plfA</a>	Alignment	not modelled	98.9	14	<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.
29	<a href="#">c5izkB</a>	Alignment	not modelled	98.9	19	<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
30	<a href="#">c3gehA</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mme; <b>PDBTitle:</b> crystal structure of mme from nostoc in complex with gdp, folinic2 acid and zn
31	<a href="#">c3j81k</a>	Alignment	not modelled	98.9	18	<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
32	<a href="#">c4nclB</a>	Alignment	not modelled	98.9	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
33	<a href="#">c4byxV</a>	Alignment	not modelled	98.9	18	<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
34	<a href="#">c2qptA</a>	Alignment	not modelled	98.8	19	<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
35	<a href="#">c4zu9A</a>	Alignment	not modelled	98.8	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
36	<a href="#">c4h1vA</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dynamin-1-like protein; <b>PDBTitle:</b> gmp-pnp bound dynamin-1-like protein gtpase-ged fusion
37	<a href="#">c4bejB</a>	Alignment	not modelled	98.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dynamin 1-like protein; <b>PDBTitle:</b> nucleotide-free dynamin 1-like protein (dnm1l, drp1, dlp1)
38	<a href="#">c2e87A</a>	Alignment	not modelled	98.8	15	<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
39	<a href="#">c1kk3A</a>	Alignment	not modelled	98.8	15	<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+
40	<a href="#">c2bvnB</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdnpn in complex with the antibiotic enacyloxin iia
41	<a href="#">c1xzqA</a>	Alignment	not modelled	98.8	19	<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
42	<a href="#">c5ady6</a>	Alignment	not modelled	98.8	22	<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
43	<a href="#">c2hdnJ</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> elongation factor ef-tu; <b>PDBTitle:</b> trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
44	<a href="#">c3izyP</a>	Alignment	not modelled	98.8	17	<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
45	<a href="#">c2qthA</a>	Alignment	not modelled	98.8	17	<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
46	<a href="#">d2dy1a2</a>	Alignment	not modelled	98.8	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
47	<a href="#">c3wyaA</a>	Alignment	not modelled	98.8	15	<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
48	<a href="#">c1zo1l</a>	Alignment	not modelled	98.8	21	<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
49	<a href="#">c3ievA</a>	Alignment	not modelled	98.7	22	<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 mggpn and the 3' end of 16s2 rrna
50	<a href="#">c2ywfA</a>	Alignment	not modelled	98.7	16	<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="#">d2c78a3</a>	Alignment	not modelled	98.7	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
52	<a href="#">c3cb4D</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> the crystal structure of lepa

53	<a href="#">c3j65o_</a>	Alignment	not modelled	98.7	16	<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 and 2 biogenesis factors.
54	<a href="#">d1jwyb_</a>	Alignment	not modelled	98.7	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
55	<a href="#">c1mj1A_</a>	Alignment	not modelled	98.7	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 13 a cryo-em map of the coli 70s ribosome
56	<a href="#">c3agqA_</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> translation,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor ts, elongation factor tu 1, linker, q <b>PDBTitle:</b> structure of viral polymerase form ii
57	<a href="#">c3degC_</a>	Alignment	not modelled	98.7	21	<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
58	<a href="#">c3agiC_</a>	Alignment	not modelled	98.6	21	<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
59	<a href="#">c3md0A_</a>	Alignment	not modelled	98.6	19	<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)
60	<a href="#">c1skqB_</a>	Alignment	not modelled	98.6	18	<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
61	<a href="#">c4byrP_</a>	Alignment	not modelled	98.6	17	<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
62	<a href="#">c3qq5A_</a>	Alignment	not modelled	98.6	23	<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
63	<a href="#">c6em5b_</a>	Alignment	not modelled	98.5	18	<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 the 2 assembly pathway of nucleolar pre-60s ribosomes
64	<a href="#">c4qjty_</a>	Alignment	not modelled	98.5	20	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of elongation factor 4 (ef4/lepa) bound to the 2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
65	<a href="#">d2akab1</a>	Alignment	not modelled	98.5	15	<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="#">c1egaB_</a>	Alignment	not modelled	98.5	24	<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
67	<a href="#">c2elfA_</a>	Alignment	not modelled	98.5	11	<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 2 methanosarcina mazei
68	<a href="#">d1svia_</a>	Alignment	not modelled	98.5	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="#">c4zciA_</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein tupa/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/tupa
70	<a href="#">c5ucvA_</a>	Alignment	not modelled	98.5	17	<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
71	<a href="#">c3mmpC_</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor tu 2, elongation factor ts; <b>PDBTitle:</b> structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
72	<a href="#">c4csu9_</a>	Alignment	not modelled	98.4	15	<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
73	<a href="#">c3vr1B_</a>	Alignment	not modelled	98.4	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
74	<a href="#">c3p27A_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> crystal structure of s. cerevisiae hbs1 protein (gdp-bound form), a2 translational gtpase involved in rna quality control pathways and 3 interacting with dom34/pelota
75	<a href="#">c1zunB_</a>	Alignment	not modelled	98.4	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
76	<a href="#">d1f60a3</a>	Alignment	not modelled	98.4	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
77	<a href="#">d1h65a_</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins

78	<a href="#">c1g7cA</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> yeast eef1a:eef1ba in complex with gdpnp
79	<a href="#">c3nxsA</a>	Alignment	not modelled	98.3	21	<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
80	<a href="#">d1puia</a>	Alignment	not modelled	98.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
81	<a href="#">c2qagC</a>	Alignment	not modelled	98.3	13	<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
82	<a href="#">c1wf3A</a>	Alignment	not modelled	98.3	23	<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
83	<a href="#">c1s0uA</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
84	<a href="#">c6h4dA</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> small ribosomal subunit biogenesis gtpase rsga; <b>PDBTitle:</b> crystal structure of rsga from pseudomonas aeruginosa
85	<a href="#">c2wsmB</a>	Alignment	not modelled	98.3	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hyhb); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hyhb from2 archaeoglobus fulgidus
86	<a href="#">c4dheA</a>	Alignment	not modelled	98.3	22	<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
87	<a href="#">c1udxA</a>	Alignment	not modelled	98.3	21	<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
88	<a href="#">c3geiB</a>	Alignment	not modelled	98.2	13	<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
89	<a href="#">c4whjA</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> antiviral protein, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced gtp-binding protein mx2; <b>PDBTitle:</b> myxovirus resistance protein 2 (mx2)
90	<a href="#">d1zunb3</a>	Alignment	not modelled	98.2	18	<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="#">d2bv3a2</a>	Alignment	not modelled	98.2	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
92	<a href="#">c6fgzA</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynamain; <b>PDBTitle:</b> cyanidioschyzon merolae dnm1 (cmdnm1)
93	<a href="#">d1u0la2</a>	Alignment	not modelled	98.2	20	<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="#">c4a2iV</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> ribosome/hydrolase <b>Chain:</b> V: <b>PDB Molecule:</b> putative ribosome biogenesis gtpase rsga; <b>PDBTitle:</b> cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
95	<a href="#">d2p67a1</a>	Alignment	not modelled	98.1	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
96	<a href="#">c3p1jC</a>	Alignment	not modelled	98.1	12	<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
97	<a href="#">c2h5eB</a>	Alignment	not modelled	98.1	15	<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
98	<a href="#">d1d2ea3</a>	Alignment	not modelled	98.1	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
99	<a href="#">c3j25A</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline resistance protein tetm; <b>PDBTitle:</b> structural basis for tetm-mediated tetracycline resistance
100	<a href="#">c3mcaA</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> translation regulation/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
101	<a href="#">c2qa5A</a>	Alignment	not modelled	98.1	20	<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
102	<a href="#">c3izq1</a>	Alignment	not modelled	98.1	11	<b>PDB header:</b> ribosomal protein,hydrolase <b>Chain:</b> 1: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
103	<a href="#">c2rcnA</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
						<b>PDB header:</b> signaling protein

104	<a href="#">c3t5dC_</a>	Alignment	not modelled	98.0	16	<b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of septin 7 in complex with gdp
105	<a href="#">c1ja1A_</a>	Alignment	not modelled	98.0	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yCHF protein; <b>PDBTitle:</b> yCHF protein (hi0393)
106	<a href="#">c2j3eA_</a>	Alignment	not modelled	98.0	21	<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
107	<a href="#">c2yv5A_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yjeq protein; <b>PDBTitle:</b> crystal structure of yjeq from aquifex aeolicus
108	<a href="#">d1t9ha2</a>	Alignment	not modelled	98.0	13	<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="#">c1t9hA_</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> the crystal structure of yloq, a circularly permuted gtpase.
110	<a href="#">c3t35A_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynamamin-related protein 1a, linker, dynamamin-related protein <b>PDBTitle:</b> arabidopsis thaliana dynamamin-related protein 1a in postfission state
111	<a href="#">d2qm8a1</a>	Alignment	not modelled	98.0	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
112	<a href="#">c4lpsA_</a>	Alignment	not modelled	98.0	14	<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 with 2 nickel
113	<a href="#">c6cesA_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related gtp-binding protein a; <b>PDBTitle:</b> cryo-em structure of gator1-rag
114	<a href="#">c4fn5A_</a>	Alignment	not modelled	98.0	17	<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
115	<a href="#">c5hcnA_</a>	Alignment	not modelled	98.0	18	<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
116	<a href="#">c4p4sA_</a>	Alignment	not modelled	98.0	10	<b>PDB header:</b> antiviral protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced gtp-binding protein mx1; <b>PDBTitle:</b> gmppcp-bound stalkless-mxa
117	<a href="#">c5irrB_</a>	Alignment	not modelled	98.0	25	<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
118	<a href="#">c3j2k7_</a>	Alignment	not modelled	97.9	13	<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
119	<a href="#">c4a9aB_</a>	Alignment	not modelled	97.9	23	<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
120	<a href="#">d1efca3</a>	Alignment	not modelled	97.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins