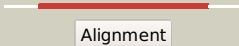


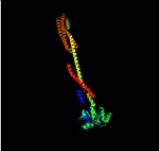
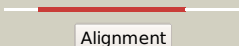
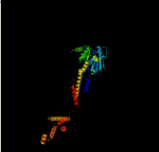
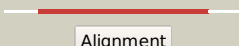
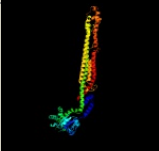
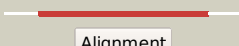

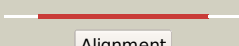

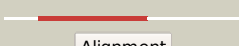




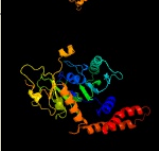











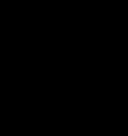



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0342\_(iniA)\_410838\_412760  
 Date Tue Jul 23 14:50:41 BST 2019  
 Unique Job ID 30fd623fef0c238e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2j69D_</a>	 Alignment		100.0	12	<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="#">c5owvA_</a>	 Alignment		100.0	14	<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
3	<a href="#">c5oxfB_</a>	 Alignment		100.0	16	<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="#">c4aurA_</a>	 Alignment		100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leoa; <b>PDBTitle:</b> leoa bacterial dynamin gtpase from etec
5	<a href="#">c5owvC_</a>	 Alignment		100.0	16	<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
6	<a href="#">c4bejB_</a>	 Alignment		100.0	10	<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)
7	<a href="#">c5gnuA_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin-1; <b>PDBTitle:</b> the structure of mini-mfn1 apo
8	<a href="#">c6ql4B_</a>	 Alignment		100.0	14	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative mitochondrial dynamin protein; <b>PDBTitle:</b> crystal structure of nucleotide-free mgm1
9	<a href="#">c2x2fD_</a>	 Alignment		100.0	14	<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
10	<a href="#">c4whjA_</a>	 Alignment		100.0	12	<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)
11	<a href="#">c5a3fD_</a>	 Alignment		100.0	12	<b>PDB header:</b> endocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> dynamin 3; <b>PDBTitle:</b> crystal structure of the dynamin tetramer

12	<a href="#">c4h1vA</a>	Alignment		100.0	15	<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
13	<a href="#">c6fgzA</a>	Alignment		100.0	12	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> dynamin; <b>PDBTitle:</b> cyanidioschyzon merolae dnm1 (cmdnm1)
14	<a href="#">d2akab1</a>	Alignment		100.0	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
15	<a href="#">c6djqa</a>	Alignment		100.0	14	<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-
16	<a href="#">c4p4sB</a>	Alignment		100.0	13	<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="#">c3zvrA</a>	Alignment		100.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> crystal structure of dynamin
18	<a href="#">c5mvfA</a>	Alignment		100.0	12	<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
19	<a href="#">d1jwyb</a>	Alignment		100.0	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
20	<a href="#">c3snhA</a>	Alignment		100.0	13	<b>PDB header:</b> endocytosis <b>Chain:</b> A; <b>PDB Molecule:</b> dynamin-1; <b>PDBTitle:</b> crystal structure of nucleotide-free human dynamin1
21	<a href="#">c4p4sA</a>	Alignment	not modelled	99.9	14	<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
22	<a href="#">c3t35A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> dynamin-related protein 1a, linker, dynamin-related protein <b>PDBTitle:</b> arabidopsis thaliana dynamin-related protein 1a in postfission state
23	<a href="#">c2qptA</a>	Alignment	not modelled	99.9	15	<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
24	<a href="#">d1tq4a</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
25	<a href="#">c1xzqa</a>	Alignment	not modelled	99.8	24	<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
26	<a href="#">c1f5nA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1; <b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp analogue,2 gmppnp.
27	<a href="#">c3j8gX</a>	Alignment	not modelled	99.7	21	<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
28	<a href="#">d1h65a</a>	Alianment	not modelled	99.7	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

						Family:G proteins
29	<a href="#">c2h9gA_</a>	Alignment	not modelled	99.7	19	<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
30	<a href="#">c1mkYA_</a>	Alignment	not modelled	99.7	20	<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="#">c5ady6_</a>	Alignment	not modelled	99.7	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
32	<a href="#">c3ievA_</a>	Alignment	not modelled	99.7	21	<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
33	<a href="#">c2j3eA_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t7i23.11 protein; <b>PDBTitle:</b> dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
34	<a href="#">c2e87A_</a>	Alignment	not modelled	99.7	20	<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
35	<a href="#">c3zjcC_</a>	Alignment	not modelled	99.7	18	<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
36	<a href="#">c3gehA_</a>	Alignment	not modelled	99.7	22	<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
37	<a href="#">c2qthA_</a>	Alignment	not modelled	99.6	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
38	<a href="#">c5k0yS_</a>	Alignment	not modelled	99.6	16	<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
39	<a href="#">d2dy1a2</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
40	<a href="#">c5dn8A_</a>	Alignment	not modelled	99.6	22	<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.
41	<a href="#">c2qagC_</a>	Alignment	not modelled	99.6	19	<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
42	<a href="#">c1kk3A_</a>	Alignment	not modelled	99.6	22	<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+
43	<a href="#">c3sopB_</a>	Alignment	not modelled	99.6	19	<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
44	<a href="#">c1egaB_</a>	Alignment	not modelled	99.6	20	<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
45	<a href="#">c1wf3A_</a>	Alignment	not modelled	99.6	25	<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
46	<a href="#">c3lx8A_</a>	Alignment	not modelled	99.6	18	<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
47	<a href="#">c4yqfA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> septin-9; <b>PDBTitle:</b> gtpase domain of human septin 9
48	<a href="#">c3t5dC_</a>	Alignment	not modelled	99.6	17	<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
49	<a href="#">c4b3xA_</a>	Alignment	not modelled	99.6	19	<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
50	<a href="#">c4zu9A_</a>	Alignment	not modelled	99.6	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
51	<a href="#">d2c78a3</a>	Alignment	not modelled	99.6	21	<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="#">c5irrB_</a>	Alignment	not modelled	99.6	20	<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
53	<a href="#">c2plfA_</a>	Alignment	not modelled	99.5	18	<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

					sulfolobus solfataricus in the nucleotide-free form.
54	<a href="#">c4kzD_</a>	Alignment	not modelled	99.5	19 <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)
55	<a href="#">c3i8sC_</a>	Alignment	not modelled	99.5	25 <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
56	<a href="#">c2xtpA_</a>	Alignment	not modelled	99.5	15 <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
57	<a href="#">c1udxA_</a>	Alignment	not modelled	99.5	29 <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
58	<a href="#">c3j81k_</a>	Alignment	not modelled	99.5	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
59	<a href="#">c2qagB_</a>	Alignment	not modelled	99.5	16 <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
60	<a href="#">c6em5b_</a>	Alignment	not modelled	99.5	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 the2 assembly pathway of nucleolar pre-60s ribosomes
61	<a href="#">c4csu9_</a>	Alignment	not modelled	99.5	19 <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
62	<a href="#">c1s0uA_</a>	Alignment	not modelled	99.5	20 <b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
63	<a href="#">c3j4jA_</a>	Alignment	not modelled	99.5	18 <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
64	<a href="#">d1f60a3</a>	Alignment	not modelled	99.5	15 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
65	<a href="#">c3a1vB_</a>	Alignment	not modelled	99.5	25 <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
66	<a href="#">c1d2eA_</a>	Alignment	not modelled	99.5	18 <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
67	<a href="#">c3md0A_</a>	Alignment	not modelled	99.5	14 <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)
68	<a href="#">c3p1jC_</a>	Alignment	not modelled	99.5	17 <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
69	<a href="#">c2qa5A_</a>	Alignment	not modelled	99.5	19 <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
70	<a href="#">c3ftqA_</a>	Alignment	not modelled	99.5	18 <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 and2 mg2+
71	<a href="#">c1mj1A_</a>	Alignment	not modelled	99.5	18 <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
72	<a href="#">c1wb1C_</a>	Alignment	not modelled	99.5	19 <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
73	<a href="#">c3j65o_</a>	Alignment	not modelled	99.5	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.
74	<a href="#">c2xtnA_</a>	Alignment	not modelled	99.4	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 gtp-bound human gimap2, amino acid2 residues 1-234
75	<a href="#">c2bvnB_</a>	Alignment	not modelled	99.4	22 <b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdppnp in complex with the antibiotic enacyloxin iia
76	<a href="#">c3qq5A_</a>	Alignment	not modelled	99.4	32 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [efe]-hydrogenase maturation protein hydf
77	<a href="#">c4dheA_</a>	Alignment	not modelled	99.4	21 <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
78	<a href="#">c3wbkB_</a>	Alignment	not modelled	99.4	23 <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

79	<a href="#">c1lnzA_</a>	Alignment	not modelled	99.4	21	<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
80	<a href="#">c2ywfA_</a>	Alignment	not modelled	99.4	20	<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
81	<a href="#">c5fg3A_</a>	Alignment	not modelled	99.4	22	<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
82	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.4	14	<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="#">d2bv3a2</a>	Alignment	not modelled	99.4	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
84	<a href="#">d2qm8a1</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
85	<a href="#">c3lxxA_</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase imap family member 4; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 4
86	<a href="#">c3degC_</a>	Alignment	not modelled	99.4	20	<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
87	<a href="#">c3wyaA_</a>	Alignment	not modelled	99.4	20	<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
88	<a href="#">c5izmA_</a>	Alignment	not modelled	99.4	22	<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
89	<a href="#">c3ibyA_</a>	Alignment	not modelled	99.4	18	<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
90	<a href="#">c3k53B_</a>	Alignment	not modelled	99.4	20	<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
91	<a href="#">c4a9aB_</a>	Alignment	not modelled	99.4	20	<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
92	<a href="#">d2p67a1</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
93	<a href="#">c2wwwB_</a>	Alignment	not modelled	99.4	13	<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
94	<a href="#">c5ar1A_</a>	Alignment	not modelled	99.4	24	<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
95	<a href="#">c3lxaA_</a>	Alignment	not modelled	99.3	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
96	<a href="#">c3pqcA_</a>	Alignment	not modelled	99.3	20	<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
97	<a href="#">c4upyB_</a>	Alignment	not modelled	99.3	16	<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
98	<a href="#">d1zunb3</a>	Alignment	not modelled	99.3	18	<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="#">c3w5iB_</a>	Alignment	not modelled	99.3	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 gallionella capsiferriformans
100	<a href="#">c3nxsA_</a>	Alignment	not modelled	99.3	12	<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="#">c1ni3A_</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> yehf gtp-binding protein; <b>PDBTitle:</b> structure of the schizosaccharomyces pombe yehf gtpase
102	<a href="#">d1svia_</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
103	<a href="#">c2qagA_</a>	Alignment	not modelled	99.3	17	<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
104	<a href="#">c1g7tA_</a>	Alignment	not modelled	99.3	23	<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
105	<a href="#">c4lpsA_</a>	Alignment	not modelled	99.3	15	<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 hybp from helicobacter pylori in complex with2 nickel
106	<a href="#">c4n3nA_</a>	Alignment	not modelled	99.3	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
107	<a href="#">d1n0ua2</a>	Alignment	not modelled	99.3	22	<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="#">c3x1dA_</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> atlastin; <b>PDBTitle:</b> crystal structure of atlastin from drosophila melanogaster
109	<a href="#">d1puia_</a>	Alignment	not modelled	99.3	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
110	<a href="#">c4nclB_</a>	Alignment	not modelled	99.3	22	<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
111	<a href="#">c4zciA_</a>	Alignment	not modelled	99.3	22	<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
112	<a href="#">c1skqB_</a>	Alignment	not modelled	99.3	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
113	<a href="#">c5izkB_</a>	Alignment	not modelled	99.3	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
114	<a href="#">c1zunB_</a>	Alignment	not modelled	99.3	16	<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
115	<a href="#">c2ohfA_</a>	Alignment	not modelled	99.3	24	<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
116	<a href="#">d1ni3a1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
117	<a href="#">c2h5eB_</a>	Alignment	not modelled	99.2	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
118	<a href="#">c1jalA_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> ychf protein; <b>PDBTitle:</b> ychf protein (hi0393)
119	<a href="#">c3p27A_</a>	Alignment	not modelled	99.2	14	<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 and3 interacting with dom34/pelota
120	<a href="#">c3agjC_</a>	Alignment	not modelled	99.2	17	<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