




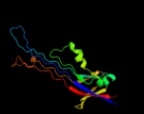






















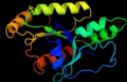




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1udxA_</a>	 Alignment		100.0	41	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> the gtp-binding protein obg; <b>PDBTitle:</b> crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8
2	<a href="#">c1lnzA_</a>	 Alignment		100.0	48	<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
3	<a href="#">d1lnza1</a>	 Alignment		100.0	52	<b>Fold:</b> Obg-fold <b>Superfamily:</b> Obg GTP-binding protein N-terminal domain <b>Family:</b> Obg GTP-binding protein N-terminal domain
4	<a href="#">d1udxa1</a>	 Alignment		100.0	49	<b>Fold:</b> Obg-fold <b>Superfamily:</b> Obg GTP-binding protein N-terminal domain <b>Family:</b> Obg GTP-binding protein N-terminal domain
5	<a href="#">c2e87A_</a>	 Alignment		100.0	25	<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
6	<a href="#">c3ievA_</a>	 Alignment		100.0	23	<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
7	<a href="#">c1ni3A_</a>	 Alignment		100.0	31	<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
8	<a href="#">c1wf3A_</a>	 Alignment		100.0	22	<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
9	<a href="#">c1legaB_</a>	 Alignment		100.0	19	<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
10	<a href="#">c1jalA_</a>	 Alignment		100.0	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ychf protein; <b>PDBTitle:</b> ychf protein (hi0393)
11	<a href="#">c1xzqA_</a>	 Alignment		99.9	21	<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

12	<a href="#">d1ni3a1</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> G proteins
13	<a href="#">c1mkyA</a>	Alignment		99.9	19	<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, a2 switch protein containing two gtpase domains
14	<a href="#">c2qthA</a>	Alignment		99.9	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 the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp
15	<a href="#">c2dwqB</a>	Alignment		99.9	32	<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
16	<a href="#">c3k53B</a>	Alignment		99.9	22	<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
17	<a href="#">c3gehA</a>	Alignment		99.9	23	<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
18	<a href="#">d1lnza2</a>	Alignment		99.9	45	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
19	<a href="#">d1jala1</a>	Alignment		99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
20	<a href="#">c3a1vB</a>	Alignment		99.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structue of the cytosolic domain of t. maritima feob2 iron transporter in apo form
21	<a href="#">c2hjga</a>	Alignment	not modelled	99.9	23	<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 in2 complex with gdp
22	<a href="#">c2ohfA</a>	Alignment	not modelled	99.9	29	<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
23	<a href="#">c3lx8A</a>	Alignment	not modelled	99.9	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
24	<a href="#">c3ibyA</a>	Alignment	not modelled	99.9	15	<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
25	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
26	<a href="#">c3i8sC</a>	Alignment	not modelled	99.9	13	<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
27	<a href="#">d1wxqa1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
28	<a href="#">c3md0A</a>	Alignment	not modelled	99.9	18	<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 system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like

						gtpase superfamily protein) <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+
29	<a href="#">c1kk3A_</a>	Alignment	not modelled	99.9	22	<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
30	<a href="#">c1wb1C_</a>	Alignment	not modelled	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
31	<a href="#">c2wwwB_</a>	Alignment	not modelled	99.9	20	<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
32	<a href="#">c3nxsA_</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
33	<a href="#">d1udxa2</a>	Alignment	not modelled	99.9	39	<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 hyd
34	<a href="#">c3qq5A_</a>	Alignment	not modelled	99.9	22	<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
35	<a href="#">c3izyP_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
36	<a href="#">c1wxqA_</a>	Alignment	not modelled	99.8	31	<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
37	<a href="#">d2p67a1</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
38	<a href="#">d2dy1a2</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> Nitrogenase iron protein-like
39	<a href="#">d2qm8a1</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
40	<a href="#">c2xtpA_</a>	Alignment	not modelled	99.8	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
41	<a href="#">c3degC_</a>	Alignment	not modelled	99.8	19	<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 gmpnp
42	<a href="#">c2qu8A_</a>	Alignment	not modelled	99.8	23	<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
43	<a href="#">c2plfA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form.
44	<a href="#">c3t1tC_</a>	Alignment	not modelled	99.8	19	<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
45	<a href="#">c2ywfA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> crystal structure of gmpnp-bound lepa from aquifex aeolicus
46	<a href="#">d1svia_</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
47	<a href="#">d1egaa1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
48	<a href="#">c1zo1l_</a>	Alignment	not modelled	99.8	19	<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="#">c3r7wC_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein gtr1; <b>PDBTitle:</b> crystal structure of gtr1p-gtr2p complex
50	<a href="#">d2cxa1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
51	<a href="#">c1g7tA_</a>	Alignment	not modelled	99.8	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
52	<a href="#">d1tq4a_</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
53	<a href="#">c2bvnB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia

54	<a href="#">d1wfa1</a>	Alignment	not modelled	99.8	20	<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="#">c3o47A</a>	Alignment	not modelled	99.8	20	<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
56	<a href="#">c2wsmB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hybp); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hybp from2 archaeoglobus fulgidus
57	<a href="#">c3lxaA</a>	Alignment	not modelled	99.8	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
58	<a href="#">d1kk1a3</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
59	<a href="#">d1puia</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
60	<a href="#">d1h65a</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
61	<a href="#">c2wjJB</a>	Alignment	not modelled	99.7	23	<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
62	<a href="#">c2xtnA</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 gtp-bound human gimap2, amino acid2 residues 1-234
63	<a href="#">c2j3eA</a>	Alignment	not modelled	99.7	20	<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 attoc33 and pstoc159
64	<a href="#">c3pqcA</a>	Alignment	not modelled	99.7	18	<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
65	<a href="#">d1zunb3</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
66	<a href="#">c3lxxA</a>	Alignment	not modelled	99.7	18	<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
67	<a href="#">d1yrba1</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> Nitrogenase iron protein-like
68	<a href="#">c3p1jC</a>	Alignment	not modelled	99.7	14	<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="#">d1d2ea3</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
70	<a href="#">d1wb1a4</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
71	<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 from2 thermus thermophilus hb8
72	<a href="#">c2qptA</a>	Alignment	not modelled	99.7	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
73	<a href="#">c1d2eA</a>	Alignment	not modelled	99.7	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
74	<a href="#">d2c78a3</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
75	<a href="#">c3a1wA</a>	Alignment	not modelled	99.7	20	<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
76	<a href="#">c2hf9A</a>	Alignment	not modelled	99.7	16	<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 hybp from methanocaldococcus2 jannaschii in the triphosphate form
77	<a href="#">c3lvrE</a>	Alignment	not modelled	99.7	19	<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
78	<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-pyl2 from methanosarcina mazei

79	<a href="#">d1f60a3</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
80	<a href="#">d1jnya3</a>	Alignment	not modelled	99.7	12	<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="#">d2fh5b1</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
82	<a href="#">d2gj8a1</a>	Alignment	not modelled	99.7	23	<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="#">c2q3fB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ras-related gtp-binding protein d; <b>PDBTitle:</b> x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmppnp
84	<a href="#">c1skqB_</a>	Alignment	not modelled	99.7	14	<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 elongation2 factor 1-alpha in complex with magnesium and gdp
85	<a href="#">c3p1jB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <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
86	<a href="#">c1mj1A_</a>	Alignment	not modelled	99.7	17	<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
87	<a href="#">d1mkya1</a>	Alignment	not modelled	99.6	20	<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="#">c2wkqA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> transferase, cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> nph1-1, ras-related c3 botulinum toxin substrate <b>PDBTitle:</b> structure of a photoactivatable rac1 containing the lov22 c450a mutant
89	<a href="#">d2qn6a3</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
90	<a href="#">c1s0uA_</a>	Alignment	not modelled	99.6	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
91	<a href="#">c2dy1A_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> signaling protein, translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of ef-g-2 from thermus thermophilus
92	<a href="#">d1nrjb_</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
93	<a href="#">d1s0ua3</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
94	<a href="#">c1zunB_</a>	Alignment	not modelled	99.6	22	<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
95	<a href="#">d1mkya2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
96	<a href="#">c2qagC_</a>	Alignment	not modelled	99.6	16	<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
97	<a href="#">c2qa5A_</a>	Alignment	not modelled	99.6	23	<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
98	<a href="#">c2h5eB_</a>	Alignment	not modelled	99.6	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
99	<a href="#">d1r5ba3</a>	Alignment	not modelled	99.6	20	<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="#">c3c5hA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucocorticoid receptor dna-binding factor 1; <b>PDBTitle:</b> crystal structure of the ras homolog domain of human grlf12 (p190rhogap)
101	<a href="#">c3p27A_</a>	Alignment	not modelled	99.6	21	<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 a translational gtpase (gdp form)
102	<a href="#">d1efca3</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
103	<a href="#">d1g7sa4</a>	Alignment	not modelled	99.6	18	<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="#">c2h57A_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> adp-ribosylation factor-like protein 6;

					<b>PDBTitle:</b> crystal structure of human adp-ribosylation factor-like 6
105	<a href="#">d1zca2</a>	Alignment	not modelled	99.5	16 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
106	<a href="#">c3geiB</a>	Alignment	not modelled	99.5	18 <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
107	<a href="#">d2bcgy1</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
108	<a href="#">d1n0ua2</a>	Alignment	not modelled	99.5	14 <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="#">c2bm0A</a>	Alignment	not modelled	99.5	21 <b>PDB header:</b> elongation factor <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
110	<a href="#">d1x3sa1</a>	Alignment	not modelled	99.5	14 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
111	<a href="#">d1fzqa</a>	Alignment	not modelled	99.5	24 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
112	<a href="#">c2rexD</a>	Alignment	not modelled	99.5	12 <b>PDB header:</b> signaling protein/lipoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> rho-related gtp-binding protein rho6; <b>PDBTitle:</b> crystal structure of the effector domain of plxnbl bound with rnd12 gtpase
113	<a href="#">d1shza2</a>	Alignment	not modelled	99.5	20 <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="#">d2g3ya1</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
115	<a href="#">c2g3yA</a>	Alignment	not modelled	99.5	15 <b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein gem; <b>PDBTitle:</b> crystal structure of the human small gtpase gem
116	<a href="#">c2oi1A</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related protein rab-25; <b>PDBTitle:</b> crystal structure of human rab25 in complex with gdp
117	<a href="#">c2xexA</a>	Alignment	not modelled	99.5	20 <b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of staphylococcus aureus elongation factor2 g
118	<a href="#">d1zj6a1</a>	Alignment	not modelled	99.5	16 <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="#">c3cbqA</a>	Alignment	not modelled	99.5	18 <b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein rem 2; <b>PDBTitle:</b> crystal structure of the human rem2 gtpase with bound gdp
120	<a href="#">d1vg8a</a>	Alignment	not modelled	99.5	17 <b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins