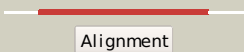

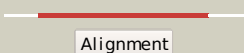

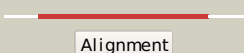

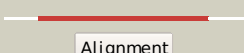



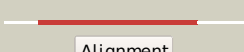

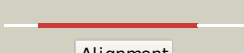

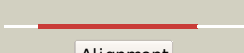












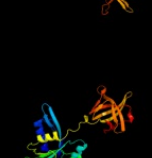
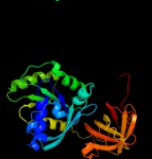
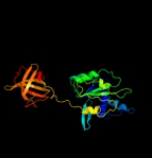
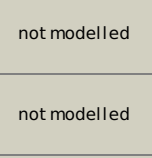
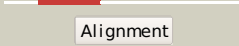

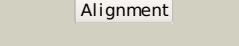

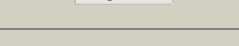

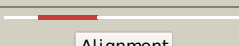
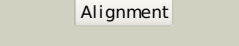


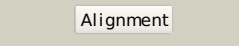


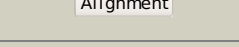
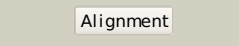





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3degC_</a>	 Alignment		100.0	100	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
2	<a href="#">c3cb4D_</a>	 Alignment		100.0	99	<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
3	<a href="#">c2ywfA_</a>	 Alignment		100.0	52	<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
4	<a href="#">c3b8hA_</a>	 Alignment		100.0	27	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
5	<a href="#">c2dy1A_</a>	 Alignment		100.0	26	<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
6	<a href="#">c2bm0A_</a>	 Alignment		100.0	33	<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
7	<a href="#">c2xexA_</a>	 Alignment		100.0	29	<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
8	<a href="#">c1zn0B_</a>	 Alignment		100.0	34	<b>PDB header:</b> translation/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf
9	<a href="#">c2rdo7_</a>	 Alignment		100.0	28	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdpnp) and rrf bound
10	<a href="#">c3tr5C_</a>	 Alignment		100.0	26	<b>PDB header:</b> translation <b>Chain:</b> C: <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
11	<a href="#">c2h5eB_</a>	 Alignment		100.0	26	<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

12	<a href="#">c1wb1C_</a>	Alignment		100.0	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
13	<a href="#">c3izq1_</a>	Alignment		100.0	21	<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
14	<a href="#">c1mj1A_</a>	Alignment		100.0	23	<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
15	<a href="#">c1g7cA_</a>	Alignment		100.0	27	<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
16	<a href="#">c1zunB_</a>	Alignment		100.0	23	<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
17	<a href="#">c1d2eA_</a>	Alignment		100.0	26	<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
18	<a href="#">c3mmpC_</a>	Alignment		100.0	26	<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
19	<a href="#">c3p27A_</a>	Alignment		100.0	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 a translational gtpase (gdp form)
20	<a href="#">c1skqB_</a>	Alignment		100.0	25	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
21	<a href="#">c1g7tA_</a>	Alignment	not modelled	100.0	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
22	<a href="#">c2bvnB_</a>	Alignment	not modelled	100.0	26	<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
23	<a href="#">c3agqA_</a>	Alignment	not modelled	100.0	27	<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
24	<a href="#">c1zo1I_</a>	Alignment	not modelled	100.0	28	<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
25	<a href="#">c3izyP_</a>	Alignment	not modelled	100.0	27	<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
26	<a href="#">c2plfA_</a>	Alignment	not modelled	100.0	21	<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.
27	<a href="#">c3mcaA_</a>	Alignment	not modelled	100.0	25	<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
28	<a href="#">c2elfA_</a>	Alignment	not modelled	100.0	16	<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
29	<a href="#">c1kk3A</a>	Alignment	not modelled	100.0	23	<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+
30	<a href="#">c1r5nA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptid chain release factor gtp- <b>PDBTitle:</b> crystal structure analysis of sup35 complexed with gdp
31	<a href="#">c1s0uA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
32	<a href="#">c2hdnJ</a>	Alignment	not modelled	100.0	25	<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
33	<a href="#">d2dy1a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
34	<a href="#">c3e3xA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bipa; <b>PDBTitle:</b> the c-terminal part of bipa protein from vibrio parahaemolyticus rimd2 2210633
35	<a href="#">d1n0ua2</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
36	<a href="#">d2bv3a2</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
37	<a href="#">d1f60a3</a>	Alignment	not modelled	100.0	30	<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="#">d1zunb3</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
39	<a href="#">c1mkYA</a>	Alignment	not modelled	99.9	22	<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
40	<a href="#">d2c78a3</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
41	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.9	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
42	<a href="#">c2hjgA</a>	Alignment	not modelled	99.9	21	<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
43	<a href="#">c2e87A</a>	Alignment	not modelled	99.9	23	<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
44	<a href="#">d1jnya3</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
45	<a href="#">d2dy1a5</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
46	<a href="#">d2bv3a5</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
47	<a href="#">d1s0ua3</a>	Alignment	not modelled	99.9	20	<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="#">d1n0ua5</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
49	<a href="#">c2qthA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of a gtp-binding protein from the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp
50	<a href="#">c3qq5A</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefc]-hydrogenase maturation protein hydf
51	<a href="#">c3ievA</a>	Alignment	not modelled	99.9	20	<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 rna
52	<a href="#">d1r5ba3</a>	Alignment	not modelled	99.9	25	<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="#">c1egaB</a>	Alignment	not modelled	99.8	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
						<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases

54	<a href="#">d1wbl1a4</a>	Alignment	not modelled	99.8	33	<b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
55	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
56	<a href="#">d1efca3</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> G proteins
57	<a href="#">c1xzqA</a>	Alignment	not modelled	99.8	23	<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
58	<a href="#">c1wf3A</a>	Alignment	not modelled	99.8	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
59	<a href="#">d2bv3a1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
60	<a href="#">c3gehA</a>	Alignment	not modelled	99.8	17	<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
61	<a href="#">c1udxA</a>	Alignment	not modelled	99.8	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
62	<a href="#">d2dy1a1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
63	<a href="#">c3k53B</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> crystal structure of nfeob from p. furiosus
64	<a href="#">d2qn6a3</a>	Alignment	not modelled	99.8	21	<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="#">c1lnzA</a>	Alignment	not modelled	99.8	20	<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
66	<a href="#">c3a1vB</a>	Alignment	not modelled	99.8	20	<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
67	<a href="#">d2dy1a4</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
68	<a href="#">c2wsmB</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hyphb); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hyphb from2 archaeoglobus fulgidus
69	<a href="#">d1svia</a>	Alignment	not modelled	99.8	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
70	<a href="#">c3c5hA</a>	Alignment	not modelled	99.8	21	<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)
71	<a href="#">d1n0ua4</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
72	<a href="#">d2bm0a4</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
73	<a href="#">d1g7sa4</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
74	<a href="#">c3ibyA</a>	Alignment	not modelled	99.7	17	<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
75	<a href="#">c3i8sC</a>	Alignment	not modelled	99.7	18	<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
76	<a href="#">c3lvrE</a>	Alignment	not modelled	99.7	20	<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
77	<a href="#">d1yrba1</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> Nitrogenase iron protein-like
78	<a href="#">c3t1tC</a>	Alignment	not modelled	99.7	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
79	<a href="#">d1legaa1</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

80	<a href="#">c3md0A</a>	 Alignment	not modelled	99.7	20	<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)
81	<a href="#">c1jqcC</a>	 Alignment	not modelled	99.7	26	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
82	<a href="#">c3lx8A</a>	 Alignment	not modelled	99.7	21	<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
83	<a href="#">c3r7wC</a>	 Alignment	not modelled	99.7	18	<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
84	<a href="#">d1tg4a</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
85	<a href="#">c2qptA</a>	 Alignment	not modelled	99.7	16	<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
86	<a href="#">c2gedB</a>	 Alignment	not modelled	99.7	25	<b>PDB header:</b> protein transport, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor beta <b>PDBTitle:</b> signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
87	<a href="#">c3pqcA</a>	 Alignment	not modelled	99.7	17	<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
88	<a href="#">c2hf9A</a>	 Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrogenase nickel incorporation <b>PDBTitle:</b> crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
89	<a href="#">c2qagC</a>	 Alignment	not modelled	99.7	20	<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
90	<a href="#">c3nxsA</a>	 Alignment	not modelled	99.6	22	<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
91	<a href="#">c3o47A</a>	 Alignment	not modelled	99.6	18	<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
92	<a href="#">d2fh5b1</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
93	<a href="#">c2wkqA</a>	 Alignment	not modelled	99.6	18	<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
94	<a href="#">c2dykB</a>	 Alignment	not modelled	99.6	24	<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
95	<a href="#">d1puia</a>	 Alignment	not modelled	99.6	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
96	<a href="#">c2xtpA</a>	 Alignment	not modelled	99.6	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
97	<a href="#">d1n0ua1</a>	 Alignment	not modelled	99.6	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
98	<a href="#">d2p67a1</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> Nitrogenase iron protein-like
99	<a href="#">d1zca2</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
100	<a href="#">c2wjJB</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b homolog; <b>PDBTitle:</b> structure and function of the feob g-domain from2 methanococcus jannaschii
101	<a href="#">c2qu8A</a>	Alignment	not modelled	99.6	19	<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
102	<a href="#">d1udxa2</a>	Alignment	not modelled	99.6	22	<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="#">d1nrjb</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
104	<a href="#">d2gm8a1</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate



104	<a href="#">d2qmba1</a>	Alignment	not modelled	99.5	20	hydrolases <b>Family:</b> Nitrogenase iron protein-like
105	<a href="#">d1svsa1</a>	Alignment	not modelled	99.5	19	<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="#">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
107	<a href="#">c2wwwB</a>	Alignment	not modelled	99.5	14	<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
108	<a href="#">d1wf3a1</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
109	<a href="#">d1mkyA2</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
110	<a href="#">c2q3fB</a>	Alignment	not modelled	99.5	13	<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 gmpnp
111	<a href="#">c3lxxA</a>	Alignment	not modelled	99.5	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
112	<a href="#">c3a1wA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structue of the g domain of t. maritima feob iron2 transporter
113	<a href="#">c2xtnA</a>	Alignment	not modelled	99.5	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
114	<a href="#">d1lnza2</a>	Alignment	not modelled	99.5	19	<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="#">c3dpuA</a>	Alignment	not modelled	99.5	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> rab family protein; <b>PDBTitle:</b> roccor domain tandem of rab family protein (roco)
116	<a href="#">d2a17a1</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
117	<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 plxnb1 bound with rnd12 gtpase
118	<a href="#">c1jalA</a>	Alignment	not modelled	99.5	19	<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="#">d1fzqa</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
120	<a href="#">d1tada2</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins