Phyre^2

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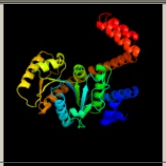
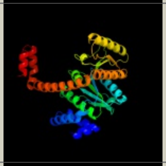
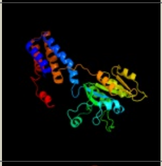
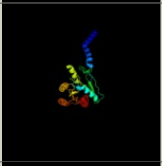
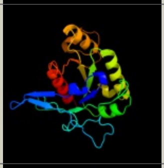
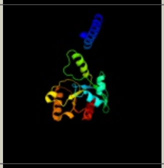
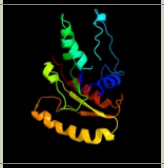
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qm8a1	Alignment		100.0	46	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
2	d2p67a1	Alignment		100.0	97	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
3	c3nxsA_	Alignment		100.0	42	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lao/ao transport system atpase; **PDBTitle:** crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
4	c3md0A_	Alignment		100.0	41	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**arginine/ornithine transport system atpase; **PDBTitle:** crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein)
5	c2wwwB_	Alignment		100.0	39	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**methylmalonic aciduria type a protein, **PDBTitle:** crystal structure of methylmalonic acidemia type a protein
6	c1xzqA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable trna modification gtpase trme; **PDBTitle:** structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
7	c3gehA_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
8	c2e87A_	Alignment		99.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1320; **PDBTitle:** crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp
9	c2hf9A_	Alignment		99.9	19	**PDB header:**hydrolase, metal binding protein **Chain:** A: **PDB Molecule:**probable hydrogenase nickel incorporation **PDBTitle:** crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
10	c1egaB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
11	c3ievA_	Alignment		99.9	17	**PDB header:**nucleotide binding protein/rna **Chain:** A: **PDB Molecule:**gtp-binding protein era; **PDBTitle:** crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna

12	c1wf3A_	Alignment		99.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
13	c1udxA_	Alignment		99.9	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**the gtp-binding protein obg; **PDBTitle:** crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8
14	c2qthA_	Alignment		99.9	16	**PDB header:**nucleotide binding protein **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of a gtp-binding protein from the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp
15	c2hjgA_	Alignment		99.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein enga; **PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
16	c1lnzA_	Alignment		99.9	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein; **PDBTitle:** structure of the obg gtp-binding protein
17	c1mkyA_	Alignment		99.9	24	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**probable gtp-binding protein enga; **PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains
18	c2wsmB_	Alignment		99.9	19	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**hydrogenase expression/formation protein (hypb); **PDBTitle:** crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus
19	d1yrba1	Alignment		99.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
20	c1kk3A_	Alignment		99.8	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**eif2gamma; **PDBTitle:** structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+
21	c1g7tA_	Alignment	not modelled	99.8	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if2/eif5b; **PDBTitle:** x-ray structure of translation initiation factor if2/eif5b2 complexed with gdpnp
22	c3ibyA_	Alignment	not modelled	99.8	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** structure of cytosolic domain of l. pneumophila feob
23	d2bv3a2	Alignment	not modelled	99.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
24	c1wb1C_	Alignment	not modelled	99.8	17	**PDB header:**protein synthesis **Chain:** C: **PDB Molecule:**translation elongation factor selb; **PDBTitle:** crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp
25	c3k53B_	Alignment	not modelled	99.8	18	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** crystal structure of nfeob from p. furiosus
26	c3izyP_	Alignment	not modelled	99.8	17	**PDB header:**rna, ribosomal protein **Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial; **PDBTitle:** mammalian mitochondrial translation initiation factor 2
27	c3geiB_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
28	c2plfA_	Alignment	not modelled	99.8	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form.

29	c3a1vB_	Alignment	not modelled	99.8	19	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**iron(ii) transport protein b; **PDBTitle:** crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form
30	c3dm5A_	Alignment	not modelled	99.8	18	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
31	d1tq4a_	Alignment	not modelled	99.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
32	c3lx8A_	Alignment	not modelled	99.8	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron uptake transporter protein b; **PDBTitle:** crystal structure of gdp-bound nfeob from s. thermophilus
33	c1zu4A_	Alignment	not modelled	99.8	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
34	d2dy1a2	Alignment	not modelled	99.8	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
35	c1zo1I_	Alignment	not modelled	99.8	19	**PDB header:**translation/rna **Chain:** I: **PDB Molecule:**translation initiation factor 2; **PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
36	c2ywfA_	Alignment	not modelled	99.8	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
37	c2yhsA_	Alignment	not modelled	99.8	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
38	c3i8sC_	Alignment	not modelled	99.8	20	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
39	d1svia_	Alignment	not modelled	99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
40	c3qq5A_	Alignment	not modelled	99.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
41	c2qy9A_	Alignment	not modelled	99.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
42	c1vmaA_	Alignment	not modelled	99.7	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
43	c3degC_	Alignment	not modelled	99.7	18	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
44	d1kk1a3	Alignment	not modelled	99.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
45	d1ni3a1	Alignment	not modelled	99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
46	d1h65a_	Alignment	not modelled	99.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
47	c3pqcA_	Alignment	not modelled	99.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtp-binding protein engb; **PDBTitle:** crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp
48	c2j3eA_	Alignment	not modelled	99.7	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t7i23.11 protein; **PDBTitle:** dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
49	c3b9qA_	Alignment	not modelled	99.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
50	c2j37W_	Alignment	not modelled	99.7	16	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
51	d1f60a3	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
52	c2iy3A_	Alignment	not modelled	99.7	14	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome
53	c3dmdA_	Alignment	not modelled	99.7	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus

54	d1zunb3	Alignment	not modelled	99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
55	c2bvnB_	Alignment	not modelled	99.7	18	**PDB header:**elongation factor **Chain:** B: **PDB Molecule:**elongation factor tu; **PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia
56	c2og2A_	Alignment	not modelled	99.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
57	c2xtpA_	Alignment	not modelled	99.7	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of nucleotide-free human gimap2, amino2 acid residues 1-260
58	d2c78a3	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
59	c2j7pA_	Alignment	not modelled	99.7	15	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
60	c2v3cC_	Alignment	not modelled	99.7	20	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
61	c2qu8A_	Alignment	not modelled	99.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nucleolar gtp-binding protein 1; **PDBTitle:** crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
62	d1d2ea3	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
63	c2elfA_	Alignment	not modelled	99.7	16	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
64	d1g7sa4	Alignment	not modelled	99.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
65	d1egaa1	Alignment	not modelled	99.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
66	c2ohfA_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein 9; **PDBTitle:** crystal structure of human ola1 in complex with amppcp
67	c1d2eA_	Alignment	not modelled	99.6	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**elongation factor tu (ef-tu); **PDBTitle:** crystal structure of mitochondrial ef-tu in complex with gdp
68	c1qzwC_	Alignment	not modelled	99.6	16	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
69	d1jnya3	Alignment	not modelled	99.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
70	d2cxxa1	Alignment	not modelled	99.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
71	c1skqB_	Alignment	not modelled	99.6	20	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** the crystal structure of sulfolobus solfataricus elongation2 factor 1-alpha in complex with magnesium and gdp
72	d1puia_	Alignment	not modelled	99.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
73	d2qn6a3	Alignment	not modelled	99.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
74	c1jalA_	Alignment	not modelled	99.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ychf protein; **PDBTitle:** ychf protein (hi0393)
75	c2dwqB_	Alignment	not modelled	99.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gtp-binding protein; **PDBTitle:** thermus thermophilus ychf gtp-binding protein
76	c2qptA_	Alignment	not modelled	99.6	16	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**eh domain-containing protein-2; **PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling
77	d1r5ba3	Alignment	not modelled	99.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
78	c2j69D_	Alignment	not modelled	99.6	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
79	d1nija1	Alignment	not modelled	99.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
80	c2cnwF_	Alignment	not modelled	99.6	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
81	d1efca3	Alignment	not modelled	99.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
82	c2j289_	Alignment	not modelled	99.6	18	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
83	c1mj1A_	Alignment	not modelled	99.6	21	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**elongation factor tu; **PDBTitle:** fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
84	d1wb1a4	Alignment	not modelled	99.6	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
85	c1zunB_	Alignment	not modelled	99.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
86	d1wf3a1	Alignment	not modelled	99.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
87	c2qagC_	Alignment	not modelled	99.6	15	**PDB header:**cell cycle, structural protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of human septin trimer 2/6/7
88	c1ni3A_	Alignment	not modelled	99.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ychf gtp-binding protein; **PDBTitle:** structure of the schizosaccharomyces pombe ychf gtpase
89	c3lxwA_	Alignment	not modelled	99.6	14	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
90	c3a1wA_	Alignment	not modelled	99.6	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron(ii) transport protein b; **PDBTitle:** crystal structue of the g domain of t. maritima feob iron2 iransporter
91	d2gj8a1	Alignment	not modelled	99.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
92	c2dy1A_	Alignment	not modelled	99.6	18	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus
93	d1udxa2	Alignment	not modelled	99.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
94	c2xtnA_	Alignment	not modelled	99.6	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of gtp-bound human gimap2, amino acid2 residues 1-234
95	c2wjjB_	Alignment	not modelled	99.6	23	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b homolog; **PDBTitle:** structure and function of the feob g-domain from2 methanococcus jannaschii
96	c2h5eB_	Alignment	not modelled	99.6	22	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
97	d1mkya2	Alignment	not modelled	99.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
98	d1s0ua3	Alignment	not modelled	99.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
99	c2xexA_	Alignment	not modelled	99.6	22	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
100	c2qa5A_	Alignment	not modelled	99.5	16	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of sept2 g-domain
101	d1lnza2	Alignment	not modelled	99.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
102	c3p1jC_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
103	c3p1jB_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
104	c2dykB_	Alignment	not modelled	99.5	19	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of n-terminal gtp-binding domain of enga from2 thermus thermophilus hb8
105	c3lxxA_	Alignment	not modelled	99.5	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 4; **PDBTitle:** crystal structure of human gtpase imap family member 4
						Fold:P-loop containing nucleoside triphosphate hydrolases

106	d1jala1	Alignment	not modelled	99.5	17	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
107	c3t1tC_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**gliding protein mgla; **PDBTitle:** mgla bound to gdp in p1 tetrameric arrangement
108	d1nrjb_	Alignment	not modelled	99.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
109	c1g7cA_	Alignment	not modelled	99.5	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp
110	c2bm0A_	Alignment	not modelled	99.5	24	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
111	c1r5nA_	Alignment	not modelled	99.5	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp- **PDBTitle:** crystal structure analysis of sup35 complexed with gdp
112	c1nijA_	Alignment	not modelled	99.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein
113	d1jwyb_	Alignment	not modelled	99.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
114	d1n0ua2	Alignment	not modelled	99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
115	c3p27A_	Alignment	not modelled	99.5	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** crystal structure of a translational gtpase (gdp form)
116	d2fh5b1	Alignment	not modelled	99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
117	d1xzpa2	Alignment	not modelled	99.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
118	d1mkya1	Alignment	not modelled	99.5	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
119	c3t5dC_	Alignment	not modelled	99.5	16	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
120	c3tr5C_	Alignment	not modelled	99.5	19	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii