Phyre^2

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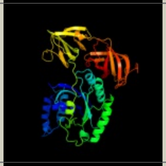
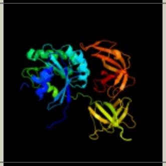
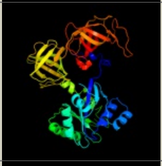
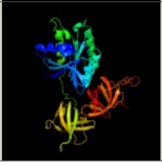
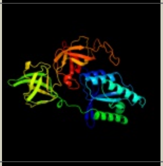
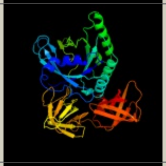
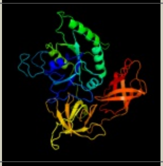
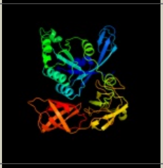
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3izq1_	Alignment		100.0	30	**PDB header:**ribosomal protein,hydrolase **Chain:** 1: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
2	c1g7cA_	Alignment		100.0	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp
3	c1zunB_	Alignment		100.0	57	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
4	c1skqB_	Alignment		100.0	30	**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
5	c3agqA_	Alignment		100.0	25	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
6	c3mmpC_	Alignment		100.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**elongation factor tu 2, elongation factor ts; **PDBTitle:** structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
7	c3p27A_	Alignment		100.0	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** crystal structure of a translational gtpase (gdp form)
8	c3mcaA_	Alignment		100.0	27	**PDB header:**translation regulation/hydrolase **Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
9	c1r5nA_	Alignment		100.0	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp- **PDBTitle:** crystal structure analysis of sup35 complexed with gdp
10	c1mj1A_	Alignment		100.0	23	**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
11	c1d2eA_	Alignment		100.0	24	**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

12	c2bvnB_	Alignment		100.0	24	**PDB header:**elongation factor **Chain:** B: **PDB Molecule:**elongation factor tu; **PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia
13	c2hdnJ_	Alignment		100.0	23	**PDB header:**translation **Chain:** J: **PDB Molecule:**elongation factor ef-tu; **PDBTitle:** trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
14	c2elfA_	Alignment		100.0	18	**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
15	c1kk3A_	Alignment		100.0	21	**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+
16	c2plfA_	Alignment		100.0	22	**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.
17	c1s0uA_	Alignment		100.0	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
18	c1wb1C_	Alignment		100.0	22	**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
19	c3degC_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
20	c2ywfA_	Alignment		100.0	26	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
21	c2dy1A_	Alignment	not modelled	100.0	20	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus
22	c1zo1I_	Alignment	not modelled	100.0	21	**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
23	c3cb4D_	Alignment	not modelled	100.0	23	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
24	c3e20A_	Alignment	not modelled	100.0	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding **PDBTitle:** crystal structure of s.pombe erf1/erf3 complex
25	c3tr5C_	Alignment	not modelled	100.0	22	**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
26	c3e1yG_	Alignment	not modelled	100.0	18	**PDB header:**translation **Chain:** G: **PDB Molecule:**eukaryotic peptide chain release factor gtp-binding subunit **PDBTitle:** crystal structure of human erf1/erf3 complex
27	c1g7tA_	Alignment	not modelled	100.0	19	**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
28	c2bm0A_	Alignment	not modelled	100.0	24	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
						PDB header:translation

29	c2xexA_	Alignment	not modelled	100.0	23	**Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
30	c3izyP_	Alignment	not modelled	100.0	24	**PDB header:**rna, ribosomal protein **Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial; **PDBTitle:** mammalian mitochondrial translation initiation factor 2
31	c1zn0B_	Alignment	not modelled	100.0	26	**PDB header:**translation/biosynthetic protein/rna **Chain:** B: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdpnp) and rrf
32	d1f60a3	Alignment	not modelled	100.0	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
33	c2rdo7_	Alignment	not modelled	100.0	20	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
34	c3b8hA_	Alignment	not modelled	100.0	23	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
35	c2h5eB_	Alignment	not modelled	100.0	25	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
36	d1zunb3	Alignment	not modelled	100.0	65	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
37	d1jnya3	Alignment	not modelled	100.0	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
38	d1r5ba3	Alignment	not modelled	100.0	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
39	d2c78a3	Alignment	not modelled	100.0	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
40	d1zunb2	Alignment	not modelled	100.0	39	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
41	d2dy1a2	Alignment	not modelled	99.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
42	d1d2ea3	Alignment	not modelled	99.9	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
43	d1n0ua2	Alignment	not modelled	99.9	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
44	d1f60a2	Alignment	not modelled	99.9	18	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
45	d1jnya2	Alignment	not modelled	99.9	16	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
46	c1mkyA_	Alignment	not modelled	99.9	26	**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
47	c2hjgA_	Alignment	not modelled	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
48	d2bv3a2	Alignment	not modelled	99.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
49	d1efca3	Alignment	not modelled	99.9	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
50	d1zunb1	Alignment	not modelled	99.9	60	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
51	d1jnya1	Alignment	not modelled	99.9	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
52	d1f60a1	Alignment	not modelled	99.9	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
53	c2e87A_	Alignment	not modelled	99.9	21	**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
54	d1kk1a1	Alignment	not modelled	99.9	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
55	d2c78a1	Alignment	not modelled	99.8	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors

56	d1d2ea1	Alignment	not modelled	99.8	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
57	c2qthA_	Alignment	not modelled	99.8	21	**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
58	d1efca1	Alignment	not modelled	99.8	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
59	d1s0ua1	Alignment	not modelled	99.8	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
60	d1r5ba1	Alignment	not modelled	99.8	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
61	d1kk1a3	Alignment	not modelled	99.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
62	d1s0ua3	Alignment	not modelled	99.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
63	d2qn6a3	Alignment	not modelled	99.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
64	d1wb1a1	Alignment	not modelled	99.8	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
65	c1xzqA_	Alignment	not modelled	99.8	26	**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
66	d1efca2	Alignment	not modelled	99.8	18	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
67	c3ievA_	Alignment	not modelled	99.8	22	**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
68	d1wb1a4	Alignment	not modelled	99.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
69	d2qn6a1	Alignment	not modelled	99.8	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
70	c3qq5A_	Alignment	not modelled	99.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
71	c3gehA_	Alignment	not modelled	99.8	29	**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
72	c1wf3A_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
73	d2c78a2	Alignment	not modelled	99.8	17	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
74	d1d2ea2	Alignment	not modelled	99.7	20	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
75	c1egaB_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
76	d1yrba1	Alignment	not modelled	99.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
77	c3md0A_	Alignment	not modelled	99.7	19	**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)
78	c2qptA_	Alignment	not modelled	99.7	21	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**eh domain-containing protein-2; **PDBTitle:** crystal structure of an ehd atpase involved in membrane remodelling
79	c1udxA_	Alignment	not modelled	99.7	18	**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
80	c3a1vB_	Alignment	not modelled	99.7	15	**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
81	d1svia_	Alignment	not modelled	99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family:G proteins
82	c1lnzA_	Alignment	not modelled	99.7	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein; **PDBTitle:** structure of the obg gtp-binding protein
83	c2wsmB_	Alignment	not modelled	99.7	11	**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
84	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
85	c3r7wC_	Alignment	not modelled	99.6	23	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**gtp-binding protein gtr1; **PDBTitle:** crystal structure of gtr1p-gtr2p complex
86	d1g7sa4	Alignment	not modelled	99.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
87	c3k53B_	Alignment	not modelled	99.6	18	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** crystal structure of nfeob from p. furiosus
88	c3i8sC_	Alignment	not modelled	99.6	23	**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
89	c3ibyA_	Alignment	not modelled	99.6	22	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** structure of cytosolic domain of l. pneumophila feob
90	c3nxsA_	Alignment	not modelled	99.6	21	**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
91	c2gedB_	Alignment	not modelled	99.6	27	**PDB header:**protein transport, signaling protein **Chain:** B: **PDB Molecule:**signal recognition particle receptor beta **PDBTitle:** signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
92	c3lx8A_	Alignment	not modelled	99.6	20	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron uptake transporter protein b; **PDBTitle:** crystal structure of gdp-bound nfeob from s. thermophilus
93	d1tq4a_	Alignment	not modelled	99.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
94	d1puia_	Alignment	not modelled	99.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
95	c3lvrE_	Alignment	not modelled	99.5	17	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**arf-gap with sh3 domain, ank repeat and ph domain- **PDBTitle:** the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium
96	c2j3eA_	Alignment	not modelled	99.5	15	**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
97	d2qm8a1	Alignment	not modelled	99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
98	d2p67a1	Alignment	not modelled	99.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
99	c2xtpA_	Alignment	not modelled	99.5	19	**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
100	c2qa5A_	Alignment	not modelled	99.5	19	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of sept2 g-domain
101	d1h65a_	Alignment	not modelled	99.5	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
102	c2hf9A_	Alignment	not modelled	99.5	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
103	c3pqcA_	Alignment	not modelled	99.4	21	**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
104	d1mkya2	Alignment	not modelled	99.4	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
105	c2j69D_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**bacterial dynamin-like protein; **PDBTitle:** bacterial dynamin-like protein bdlp
106	c2wwwB_	Alignment	not modelled	99.4	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**methylmalonic aciduria type a protein, **PDBTitle:** crystal structure of methylmalonic acidemia type a protein

107	c2xtnA_	Alignment	not modelled	99.4	17	**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
108	d1zcaa2	Alignment	not modelled	99.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
109	c3t1tC_	Alignment	not modelled	99.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**gliding protein mgla; **PDBTitle:** mgla bound to gdp in p1 tetrameric arrangement
110	c3t5dC_	Alignment	not modelled	99.4	17	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
111	d1g7sa2	Alignment	not modelled	99.4	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
112	d1egaa1	Alignment	not modelled	99.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
113	c3c5hA_	Alignment	not modelled	99.4	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**glucocorticoid receptor dna-binding factor 1; **PDBTitle:** crystal structure of the ras homolog domain of human grlf12 (p190rhogap)
114	d1jwyb_	Alignment	not modelled	99.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
115	c3p1jC_	Alignment	not modelled	99.4	15	**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
116	c3lxxA_	Alignment	not modelled	99.3	17	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 4; **PDBTitle:** crystal structure of human gtpase imap family member 4
117	d2fh5b1	Alignment	not modelled	99.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
118	c3o47A_	Alignment	not modelled	99.3	25	**PDB header:**hydrolase, hydrolase activator **Chain:** A: **PDB Molecule:**adp-ribosylation factor gtpase-activating protein 1, adp- **PDBTitle:** crystal structure of arfgap1-arf1 fusion protein
119	c2qu8A_	Alignment	not modelled	99.3	19	**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
120	c2dykB_	Alignment	not modelled	99.3	26	**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