

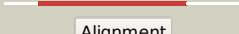
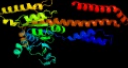
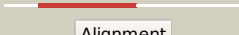


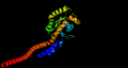
























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0343_(iniC)_412757_414238
Date	Tue Jul 23 14:50:41 BST 2019
Unique Job ID	80a1b186fa40fa6f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oxfB_	 Alignment		100.0	16	PDB header: lipid binding protein Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long range sensing and tethering of membranes
2	c2j69D_	 Alignment		100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: bacterial dynamin-like protein; PDBTitle: bacterial dynamin-like protein bdlp
3	c5owvA_	 Alignment		100.0	19	PDB header: lipid binding protein Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
4	c4aurA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: leoa; PDBTitle: leoa bacterial dynamin gtpase from etec
5	c5gnuA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: mitofusin-1; PDBTitle: the structure of mini-mfn1 apo
6	c5owvC_	 Alignment		100.0	21	PDB header: lipid binding protein Chain: C: PDB Molecule: gtp-binding protein; PDBTitle: an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
7	c2x2fD_	 Alignment		99.9	14	PDB header: hydrolase Chain: D: PDB Molecule: dynamin-1; PDBTitle: dynamin 1 gtpase dimer, short axis form
8	c4h1vA_	 Alignment		99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: dynamin-1-like protein; PDBTitle: gmp-pnp bound dynamin-1-like protein gtpase-ged fusion
9	d2akab1	 Alignment		99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
10	c4p4sB_	 Alignment		99.9	12	PDB header: antiviral protein/hydrolase Chain: B: PDB Molecule: interferon-induced gtp-binding protein mx1; PDBTitle: gmppcp-bound stalkless-mxa
11	c5mvfA_	 Alignment		99.9	15	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein 4; PDBTitle: active structure of ehd4 complexed with adp

12	c6djqa_	Alignment		99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: vps1 gtpase-bse; PDBTitle: vps1 gtpase-bse fusion complexed with gdp.alf4-
13	d1jwyb_	Alignment		99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
14	c4bejb_	Alignment		99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: dynamin 1-like protein; PDBTitle: nucleotide-free dynamin 1-like protein (dnm1l, drp1, dlp1)
15	c5a3fd_	Alignment		99.9	15	PDB header: endocytosis Chain: D: PDB Molecule: dynamin 3; PDBTitle: crystal structure of the dynamin tetramer
16	c3t35a_	Alignment		99.9	17	PDB header: motor protein Chain: A: PDB Molecule: dynamin-related protein 1a, linker, dynamin-related protein PDBTitle: arabidopsis thaliana dynamin-related protein 1a in postfission state
17	c4whja_	Alignment		99.9	15	PDB header: antiviral protein, hydrolase Chain: A: PDB Molecule: interferon-induced gtp-binding protein mx2; PDBTitle: myxovirus resistance protein 2 (mx2)
18	c6ql4b_	Alignment		99.9	17	PDB header: motor protein Chain: B: PDB Molecule: putative mitochondrial dynamin protein; PDBTitle: crystal structure of nucleotide-free mgm1
19	c2qpta_	Alignment		99.9	21	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
20	c4p4sa_	Alignment		99.9	16	PDB header: antiviral protein/hydrolase Chain: A: PDB Molecule: interferon-induced gtp-binding protein mx1; PDBTitle: gmppcp-bound stalkless-mxa
21	c6fgza_	Alignment	not modelled	99.9	16	PDB header: lipid binding protein Chain: A: PDB Molecule: dynamin; PDBTitle: cyanidioschyzon merolae dnm1 (cmdnm1)
22	c3zvrA_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: A: PDB Molecule: dynamin-1; PDBTitle: crystal structure of dynamin
23	c3snhA_	Alignment	not modelled	99.9	16	PDB header: endocytosis Chain: A: PDB Molecule: dynamin-1; PDBTitle: crystal structure of nucleotide-free human dynamin1
24	d1tq4a_	Alignment	not modelled	99.8	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
25	d1h65a_	Alignment	not modelled	99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
26	c2j3ea_	Alignment	not modelled	99.7	15	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
27	c5ady6_	Alignment	not modelled	99.6	17	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hfx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hfx
28	c3zjcC_	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 I100q variant
29	c3ievA_	Alignment	not modelled	99.6	18	PDB header: nucleotide binding protein/rna Chain: A: PDB Molecule: gtp-binding protein era;

29	c1eva_	Alignment	not modelled	99.6	10	PDBTitle: crystal structure of era in complex with mgnp and the 3' end of 16s2 rrna PDB header: hydrolase
30	c1xzqA_	Alignment	not modelled	99.6	27	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
31	c3sopB_	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: B: PDB Molecule: neuronal-specific septin-3; PDBTitle: crystal structure of human septin 3 gtpase domain
32	c2qthA_	Alignment	not modelled	99.6	18	PDB header: nucleotide binding protein Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfolobus solfataricus in complex with gdp
33	c2qagC_	Alignment	not modelled	99.6	18	PDB header: cell cycle, structural protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of human septin trimer 2/6/7
34	c3j8gX_	Alignment	not modelled	99.5	17	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
35	c4yqfA_	Alignment	not modelled	99.5	18	PDB header: hydrolase Chain: A: PDB Molecule: septin-9; PDBTitle: gtpase domain of human septin 9
36	d2dy1a2	Alignment	not modelled	99.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
37	c3md0A_	Alignment	not modelled	99.5	20	PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
38	d2p67a1	Alignment	not modelled	99.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
39	c3t5dC_	Alignment	not modelled	99.5	25	PDB header: signaling protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of septin 7 in complex with gdp
40	c2e87A_	Alignment	not modelled	99.5	17	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
41	c2hjaA_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein enga; PDBTitle: the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp
42	c3a1vB_	Alignment	not modelled	99.5	21	PDB header: transport protein Chain: B: PDB Molecule: iron(ii) transport protein b; PDBTitle: crystal structure of the cytosolic domain of t. maritima feob2 iron transporter in apo form
43	c1mkyA_	Alignment	not modelled	99.5	17	PDB header: ligand binding protein Chain: A: PDB Molecule: probable gtp-binding protein enga; PDBTitle: structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains
44	c2xtpA_	Alignment	not modelled	99.5	17	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
45	c3gehA_	Alignment	not modelled	99.5	27	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folicin2 acid and zn
46	c4b3xA_	Alignment	not modelled	99.5	18	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
47	c5k0yS_	Alignment	not modelled	99.5	13	PDB header: translation Chain: S: PDB Molecule: eukaryotic initiation factor 2 gamma subunit (eif2-gamma); PDBTitle: m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face
48	c5dn8A_	Alignment	not modelled	99.5	30	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
49	c3lx8A_	Alignment	not modelled	99.5	23	PDB header: metal transport Chain: A: PDB Molecule: ferrous iron uptake transporter protein b; PDBTitle: crystal structure of gdp-bound nfeob from s. thermophilus
50	c3i8sC_	Alignment	not modelled	99.5	21	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
51	d2qm8a1	Alignment	not modelled	99.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
52	c1wf3A_	Alignment	not modelled	99.5	26	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
53	c5irrB_	Alignment	not modelled	99.5	17	PDB header: hydrolase Chain: B: PDB Molecule: septin-like protein; PDBTitle: crystal structure of septin gtpase domain from chlamydomonas2 reinhardtii
54	c3j4jA_	Alignment	not modelled	99.4	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: model of full-length t. thermophilus translation initiation

						factor 22 refined against its cryo-em density from a 30s initiation complex map
55	c3nxsA	Alignment	not modelled	99.4	18	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
56	c2qa5A	Alignment	not modelled	99.4	20	PDB header: cell cycle, structural protein Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of sept2 g-domain
57	c2qagB	Alignment	not modelled	99.4	20	PDB header: cell cycle, structural protein Chain: B: PDB Molecule: septin-6; PDBTitle: crystal structure of human septin trimer 2/6/7
58	c1egaB	Alignment	not modelled	99.4	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
59	c6em5b	Alignment	not modelled	99.4	17	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein l3; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
60	c1kk3A	Alignment	not modelled	99.4	14	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+
61	c3ibyA	Alignment	not modelled	99.4	21	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob
62	c2xtnA	Alignment	not modelled	99.4	16	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
63	c4kjzD	Alignment	not modelled	99.4	17	PDB header: translation Chain: D: PDB Molecule: translation initiation factor if-2; PDBTitle: crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
64	c3j65o	Alignment	not modelled	99.4	13	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l15; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
65	d2c78a3	Alignment	not modelled	99.4	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
66	c2plfA	Alignment	not modelled	99.3	18	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form.
67	c3p1jC	Alignment	not modelled	99.3	26	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
68	c3ftqA	Alignment	not modelled	99.3	22	PDB header: cell cycle Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of septin 2 in complex with gppnhp and2 mg2+
69	c3k53B	Alignment	not modelled	99.3	24	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
70	d1ni3a1	Alignment	not modelled	99.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	c1mj1A	Alignment	not modelled	99.3	17	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
72	c3lxA	Alignment	not modelled	99.3	22	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 1; PDBTitle: crystal structure of human gtpase imap family member 1
73	d1f60a3	Alignment	not modelled	99.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	c1udxA	Alignment	not modelled	99.3	22	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
75	c1d2eA	Alignment	not modelled	99.3	16	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
76	c2wwwB	Alignment	not modelled	99.3	15	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
77	c4zu9A	Alignment	not modelled	99.3	18	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
78	c3qq5A	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydf
79	c3j81k	Alignment	not modelled	99.3	14	PDB header: ribosome Chain: K: PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
						Fold: P-loop containing nucleoside triphosphate hydrolases

80	d2bv3a2	Alignment	not modelled	99.3	18	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
81	c4dheA	Alignment	not modelled	99.3	19	PDB header: cell cycle Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a probable gtp-binding protein engb from 2 burkholderia thailandensis
82	c3izyP	Alignment	not modelled	99.3	19	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
83	c2bvnB	Alignment	not modelled	99.3	18	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdppnp in complex with the antibiotic enacyloxin iia
84	c1s0uA	Alignment	not modelled	99.3	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: eif2gamma apo
85	c1zo1I	Alignment	not modelled	99.3	18	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
86	c2qagA	Alignment	not modelled	99.3	23	PDB header: cell cycle, structural protein Chain: A: PDB Molecule: septin-2; PDBTitle: crystal structure of human septin trimer 2/6/7
87	c4csu9	Alignment	not modelled	99.3	18	PDB header: ribosome Chain: 9: PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
88	c5fg3A	Alignment	not modelled	99.3	18	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
89	c1lnzA	Alignment	not modelled	99.2	19	PDB header: cell cycle Chain: A: PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein
90	c3degC	Alignment	not modelled	99.2	15	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
91	c5ar1A	Alignment	not modelled	99.2	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 11; PDBTitle: crystal structure of cdc11 from saccharomyces cerevisiae
92	c3lxxA	Alignment	not modelled	99.2	25	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4
93	d1jala1	Alignment	not modelled	99.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
94	c1wb1C	Alignment	not modelled	99.2	18	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
95	c3w5iB	Alignment	not modelled	99.2	24	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferiformans
96	c2ywfA	Alignment	not modelled	99.2	17	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
97	c1q7tA	Alignment	not modelled	99.2	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if2/eif5b; PDBTitle: x-ray structure of translation initiation factor if2/eif5b2 complexed with gdppnp
98	c3wbkB	Alignment	not modelled	99.2	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
99	c4upyB	Alignment	not modelled	99.2	18	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
100	d1d2ea3	Alignment	not modelled	99.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
101	c4a9aB	Alignment	not modelled	99.2	20	PDB header: translation Chain: B: PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
102	c1ni3A	Alignment	not modelled	99.2	25	PDB header: hydrolase Chain: A: PDB Molecule: yehf gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe yehf gtpase
103	c5izmA	Alignment	not modelled	99.2	13	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdppnp
104	c4nc1B	Alignment	not modelled	99.1	14	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b-like protein; PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
105	c3wyaA	Alignment	not modelled	99.1	19	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
						Fold: P-loop containing nucleoside triphosphate hydrolases

106	d1zunb3	Alignment	not modelled	99.1	18	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
107	c2h5eB	Alignment	not modelled	99.1	17	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
108	c3pqcA	Alignment	not modelled	99.1	19	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
109	c1skqB	Alignment	not modelled	99.1	21	PDB header: translation Chain: B: PDB Molecule: elongation factor 1-alpha; PDBTitle: the crystal structure of sulfolobus solfataricus elongation factor 1-2 alpha in complex with magnesium and gdp
110	c3q5eG	Alignment	not modelled	99.1	15	PDB header: hydrolase Chain: G: PDB Molecule: atlastin-1; PDBTitle: crystal structure of human atlastin-1 (residues 1-447) bound to gdp,2 crystal form 2
111	c3agjC	Alignment	not modelled	99.1	17	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
112	c1zunB	Alignment	not modelled	99.1	20	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylate transferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
113	c2dy1A	Alignment	not modelled	99.0	18	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
114	c4zciA	Alignment	not modelled	99.0	23	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein tyba/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/tyba
115	d1s0ua3	Alignment	not modelled	99.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
116	c4qjty	Alignment	not modelled	99.0	22	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
117	c4lpsA	Alignment	not modelled	99.0	13	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein hypb; PDBTitle: crystal structure of hypb from helicobacter pylori in complex with2 nickel
118	c5izkB	Alignment	not modelled	99.0	18	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
119	c2bm0A	Alignment	not modelled	99.0	18	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
120	c6cesA	Alignment	not modelled	99.0	12	PDB header: signaling protein Chain: A: PDB Molecule: ras-related gtp-binding protein a; PDBTitle: cryo-em structure of gator1-rag