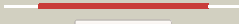



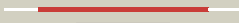




























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1112_(- )_1238260_1239333
Date	Wed Jul 31 22:05:19 BST 2019
Unique Job ID	7e4a0c3b3b8890bc

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ni3A_</a>	 Alignment		100.0	39	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ychf gtp-binding protein; <b>PDBTitle:</b> structure of the schizosaccharomyces pombe ychf gtpase
2	<a href="#">c5ee1A_</a>	 Alignment		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> obg-like atpase 1; <b>PDBTitle:</b> crystal structure of osychf1 at ph 7.85
3	<a href="#">c1jalA_</a>	 Alignment		100.0	52	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ychf protein; <b>PDBTitle:</b> ychf protein (hi0393)
4	<a href="#">c2dwqB_</a>	 Alignment		100.0	53	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> thermus thermophilus ychf gtp-binding protein
5	<a href="#">c2ohfA_</a>	 Alignment		100.0	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein 9; <b>PDBTitle:</b> crystal structure of human ola1 in complex with amppcp
6	<a href="#">c1wxqA_</a>	 Alignment		100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
7	<a href="#">c4a9aB_</a>	 Alignment		100.0	25	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome-interacting gtpase 1; <b>PDBTitle:</b> structure of rbg1 in complex with tma46 dfrp domain
8	<a href="#">d1ni3a1</a>	 Alignment		100.0	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
9	<a href="#">d1wxqa1</a>	 Alignment		100.0	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
10	<a href="#">d1jla1</a>	 Alignment		100.0	48	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
11	<a href="#">d1jla2</a>	 Alignment		100.0	62	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain

12	<a href="#">d1ni3a2</a>	Alignment		100.0	46	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
13	<a href="#">c1udxA</a>	Alignment		100.0	35	<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
14	<a href="#">c4csu9</a>	Alignment		100.0	37	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> gtpase obge/cgta; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with obge
15	<a href="#">c1lnzA</a>	Alignment		100.0	33	<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
16	<a href="#">c6em5b</a>	Alignment		100.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 60s ribosomal protein l3; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
17	<a href="#">c5ady6</a>	Alignment		99.9	27	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> gtpase hflx; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with hflx
18	<a href="#">c2e87A</a>	Alignment		99.9	27	<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
19	<a href="#">c5dn8A</a>	Alignment		99.9	35	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
20	<a href="#">c1xzqA</a>	Alignment		99.9	32	<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
21	<a href="#">c1wf3A</a>	Alignment	not modelled	99.9	31	<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
22	<a href="#">c3gehA</a>	Alignment	not modelled	99.9	28	<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
23	<a href="#">c3j65o</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l15; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
24	<a href="#">c1mkyA</a>	Alignment	not modelled	99.8	34	<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, a switch2 protein containing two gtpase domains
25	<a href="#">c3ievA</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> nucleotide binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein era; <b>PDBTitle:</b> crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
26	<a href="#">c3j8gX</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
27	<a href="#">c3k53B</a>	Alignment	not modelled	99.8	25	<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
28	<a href="#">c2qthA</a>	Alignment	not modelled	99.8	27	<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 the hyperthermophilic2 archaeon sulfobolus solfataricus in complex with gdp

29	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
30	<a href="#">c1egaB</a>	Alignment	not modelled	99.8	29	<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
31	<a href="#">c3i8sC</a>	Alignment	not modelled	99.8	32	<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
32	<a href="#">c3a1vB</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form
33	<a href="#">c3lx8A</a>	Alignment	not modelled	99.8	26	<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
34	<a href="#">c3ibyA</a>	Alignment	not modelled	99.8	32	<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
35	<a href="#">c2hjqA</a>	Alignment	not modelled	99.8	34	<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 in complex with2 gdp
36	<a href="#">c2j3eA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t7i23.11 protein; <b>PDBTitle:</b> dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
37	<a href="#">d1h65a</a>	Alignment	not modelled	99.7	20	<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="#">c4b3xA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> bacterial translation initiation factor if2 (1-363), apo form
39	<a href="#">c2ekiA</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> developmentally-regulated gtp-binding protein 1; <b>PDBTitle:</b> solution structures of the tgs domain of human2 developmentally-regulated gtp-binding protein 1
40	<a href="#">d2dy1a2</a>	Alignment	not modelled	99.7	25	<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="#">c3qq5A</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefe]-hydrogenase maturation protein hydF
42	<a href="#">d1lnza2</a>	Alignment	not modelled	99.7	33	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
43	<a href="#">c3j4jA</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map
44	<a href="#">c3md0A</a>	Alignment	not modelled	99.6	22	<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 system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
45	<a href="#">c4kzD</a>	Alignment	not modelled	99.6	28	<b>PDB header:</b> translation <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
46	<a href="#">c1kk3A</a>	Alignment	not modelled	99.6	22	<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+
47	<a href="#">c3w5iB</a>	Alignment	not modelled	99.6	26	<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 gallionella capsiferriformans
48	<a href="#">c3nxsA</a>	Alignment	not modelled	99.6	23	<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
49	<a href="#">c2xtpA</a>	Alignment	not modelled	99.6	15	<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
50	<a href="#">d1tq4a</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
51	<a href="#">c2wwwB</a>	Alignment	not modelled	99.6	16	<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
52	<a href="#">c5k0yS</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> translation <b>Chain:</b> S: <b>PDB Molecule:</b> eukaryotic initiation factor 2 gamma subunit (eif2-gamma); <b>PDBTitle:</b> 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
53	<a href="#">c3lxwA</a>	Alianment	not modelled	99.6	27	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase imap family member 1;

						<b>PDBTitle:</b> crystal structure of human gtpase imap family member 1
54	<a href="#">c3zjc_C</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 7; <b>PDBTitle:</b> crystal structure of gmppnp-bound human gimap7 I100q variant
55	<a href="#">c2qptA</a>	Alignment	not modelled	99.5	15	<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
56	<a href="#">c4dheA</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of a probable gtp-binding protein engb from2 burkholderia thailandensis
57	<a href="#">c5ymxB</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> signaling protein, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mutual gliding-motility protein mgla; <b>PDBTitle:</b> myxococcus xanthus mgla in gdp bound conformation
58	<a href="#">c4zu9A</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor selb; <b>PDBTitle:</b> crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
59	<a href="#">c4lpsA</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein hypb; <b>PDBTitle:</b> crystal structure of hypb from helicobacter pylori in complex with2 nickel
60	<a href="#">c3j81k</a>	Alignment	not modelled	99.5	15	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> es10; <b>PDBTitle:</b> cryoem structure of a partial yeast 48s preinitiation complex
61	<a href="#">c2bvnB</a>	Alignment	not modelled	99.5	23	<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 antibiotic enacyloxin iia
62	<a href="#">c4aurA</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> leoa; <b>PDBTitle:</b> leoa bacterial dynamin gtpase from etec
63	<a href="#">d2cxa1</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
64	<a href="#">c2xtnA</a>	Alignment	not modelled	99.5	15	<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
65	<a href="#">d1f60a3</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
66	<a href="#">c4wnrA</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich-repeat protein; <b>PDBTitle:</b> structure of methanosarcina barkeri roco2 roccordc bound to gdp
67	<a href="#">d2qm8a1</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> Nitrogenase iron protein-like
68	<a href="#">c1wb1C</a>	Alignment	not modelled	99.4	25	<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
69	<a href="#">d1udxa2</a>	Alignment	not modelled	99.4	42	<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="#">d1zunb3</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
71	<a href="#">d1wxqa2</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> G domain-linked domain
72	<a href="#">d1wf3a1</a>	Alignment	not modelled	99.4	31	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
73	<a href="#">c2qa5A</a>	Alignment	not modelled	99.4	30	<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
74	<a href="#">c2qu8A</a>	Alignment	not modelled	99.4	25	<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
75	<a href="#">d2p67a1</a>	Alignment	not modelled	99.4	23	<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
76	<a href="#">c3wyaA</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
77	<a href="#">c3izyP</a>	Alignment	not modelled	99.4	33	<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
78	<a href="#">c5oxfB</a>	Alignment	not modelled	99.4	21	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long range sensing and tethering of membranes
79	<a href="#">c4nclB</a>	Alignment	not modelled	99.4	17	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein; <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor

						eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
80	<a href="#">c3p1jC</a>	Alignment	not modelled	99.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
81	<a href="#">c2dy1A</a>	Alignment	not modelled	99.4	25	<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
82	<a href="#">c5mvfA</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> eh domain-containing protein 4; <b>PDBTitle:</b> active structure of ehd4 complexed with adp
83	<a href="#">c5izmA</a>	Alignment	not modelled	99.4	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdpnp
84	<a href="#">c2plfA</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form.
85	<a href="#">c5owvA</a>	Alignment	not modelled	99.4	27	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long-range sensing and tethering of membranes
86	<a href="#">c2ywfA</a>	Alignment	not modelled	99.4	16	<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
87	<a href="#">c3t1tC</a>	Alignment	not modelled	99.4	12	<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
88	<a href="#">c6bbqA</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytohesin-3,adp-ribosylation factor 6; <b>PDBTitle:</b> model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
89	<a href="#">c3degC</a>	Alignment	not modelled	99.4	20	<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
90	<a href="#">c3r7wC</a>	Alignment	not modelled	99.4	14	<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
91	<a href="#">d2c78a3</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
92	<a href="#">c6g15A</a>	Alignment	not modelled	99.3	34	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ribosome biogenesis gtpase a; <b>PDBTitle:</b> crystal structure of pppgpp bound rbga from s. aureus
93	<a href="#">d1svia</a>	Alignment	not modelled	99.3	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
94	<a href="#">c2wsmB</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hybp); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hybp from2 archaeoglobus fulgidus
95	<a href="#">c1zo1l</a>	Alignment	not modelled	99.3	29	<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
96	<a href="#">c5gnuA</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitofusin-1; <b>PDBTitle:</b> the structure of mini-mfn1 apo
97	<a href="#">c2wjJB</a>	Alignment	not modelled	99.3	32	<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
98	<a href="#">c5fg3A</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of gdp-bound aif5b from aeropyrum pernix
99	<a href="#">c2j69D</a>	Alignment	not modelled	99.3	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> bacterial dynamin-like protein; <b>PDBTitle:</b> bacterial dynamin-like protein bdlp
100	<a href="#">d1n0ua2</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
101	<a href="#">c6cesA</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ras-related gtp-binding protein a; <b>PDBTitle:</b> cryo-em structure of gator1-rag
102	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.3	25	<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="#">c1s0uA</a>	Alignment	not modelled	99.3	28	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
104	<a href="#">c3lxxA</a>	Alignment	not modelled	99.3	21	<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
						<b>PDB header:</b> hydrolase, hydrolase activator



105	<a href="#">c3o47A_</a>	Alignment	not modelled	99.3	23	<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
106	<a href="#">c1mj1A_</a>	Alignment	not modelled	99.3	20	<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
107	<a href="#">c5izkB_</a>	Alignment	not modelled	99.3	31	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdp
108	<a href="#">c3wbkB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
109	<a href="#">c3agjC_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> translation/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
110	<a href="#">c3ec1A_</a>	Alignment	not modelled	99.3	32	<b>PDB header:</b> hydrolase, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> yqeh gtpase; <b>PDBTitle:</b> structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
111	<a href="#">d1egaa1</a>	Alignment	not modelled	99.3	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
112	<a href="#">c1zunB_</a>	Alignment	not modelled	99.2	19	<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
113	<a href="#">c2dykB_</a>	Alignment	not modelled	99.2	33	<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
114	<a href="#">c3sopB_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> neuronal-specific septin-3; <b>PDBTitle:</b> crystal structure of human septin 3 gtpase domain
115	<a href="#">c1d2eA_</a>	Alignment	not modelled	99.2	21	<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
116	<a href="#">c1skqB_</a>	Alignment	not modelled	99.2	23	<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 elongation factor 1-2 alpha in complex with magnesium and gdp
117	<a href="#">c3p1jB_</a>	Alignment	not modelled	99.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
118	<a href="#">c2qagC_</a>	Alignment	not modelled	99.2	24	<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
119	<a href="#">c2bm0A_</a>	Alignment	not modelled	99.2	22	<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 resistant mutant2 t84a
120	<a href="#">c2qagA_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> septin-2; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7