

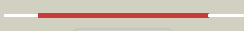




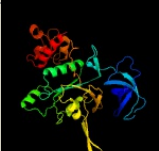





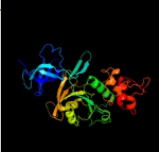



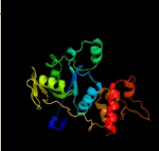



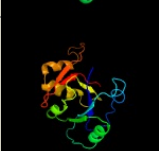


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3228 (-) _3604723_3605715
Date	Thu Aug 8 16:20:43 BST 2019
Unique Job ID	d1f86899a21ffe92

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5uz4Z_	 Alignment		100.0	27	PDB header: ribosome/hydrolase Chain: Z: PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
2	c2rcnA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
3	c6h4dA_	 Alignment		100.0	32	PDB header: rna binding protein Chain: A: PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: crystal structure of rsga from pseudomonas aeruginosa
4	c1u0lB_	 Alignment		100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
5	c4a2lV_	 Alignment		100.0	29	PDB header: ribosome/hydrolase Chain: V: PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
6	c1t9hA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
7	c2yv5A_	 Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
8	d1u0la2	 Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
9	d1t9ha2	 Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
10	c3cnlA_	 Alignment		99.9	21	PDB header: signaling protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of gnp-bound ylqf from t. maritima
11	c6g15A_	 Alignment		99.9	25	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome biogenesis gtpase a; PDBTitle: crystal structure of pppppp bound rbga from s. aureus

12	c3ec1A_	Alignment		99.9	28	PDB header: hydrolase, signaling protein Chain: A; PDB Molecule: yqeh gtpase; PDBTitle: structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnos1 / atnoa1 ortholog)
13	c3h2yA_	Alignment		99.8	24	PDB header: hydrolase Chain: A; PDB Molecule: gtpase family protein; PDBTitle: crystal structure of yqeh gtpase from bacillus anthracis with dgdp2 bound
14	d1puja_	Alignment		99.8	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
15	c3j8gX_	Alignment		99.7	27	PDB header: ribosome Chain: X; PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
16	c5dn8A_	Alignment		99.6	28	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.
17	c2higA_	Alignment		99.6	26	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
18	c1mkyA_	Alignment		99.6	20	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
19	c2j3eA_	Alignment		99.3	26	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
20	d1h65a_	Alignment		99.3	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
21	c3ibyA_	Alignment	not modelled	99.2	28	PDB header: transport protein Chain: A; PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob
22	c3zjcC_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: C; PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 I100q variant
23	c4aurA_	Alignment	not modelled	99.2	15	PDB header: hydrolase Chain: A; PDB Molecule: leoa; PDBTitle: leoa bacterial dynamin gtpase from etec
24	c3ix8A_	Alignment	not modelled	99.2	25	PDB header: metal transport Chain: A; PDB Molecule: ferrous iron uptake transporter protein b; PDBTitle: crystal structure of gdp-bound nfeob from s. thermophilus
25	c3i8sC_	Alignment	not modelled	99.2	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
26	c4yqfA_	Alignment	not modelled	99.2	20	PDB header: hydrolase Chain: A; PDB Molecule: septin-9; PDBTitle: gtpase domain of human septin 9
27	c1xzqA_	Alignment	not modelled	99.2	29	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
28	c2x2fD_	Alignment	not modelled	99.2	17	PDB header: hydrolase Chain: D; PDB Molecule: dynamin-1; PDBTitle: dynamin 1 gtpase dimer, short axis form
						Fold: OB-fold

29	d1t9ha1	Alignment	not modelled	99.1	16	Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
30	d1tq4a	Alignment	not modelled	99.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
31	c3k53B	Alignment	not modelled	99.1	31	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
32	c3ievA	Alignment	not modelled	99.1	29	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
33	c1egaB	Alignment	not modelled	99.1	23	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
34	c3a1vB	Alignment	not modelled	99.1	27	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
35	c2xtpA	Alignment	not modelled	99.1	20	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
36	d1u0la1	Alignment	not modelled	99.1	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
37	c6em5b	Alignment	not modelled	99.1	25	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
38	c5ady6	Alignment	not modelled	99.0	24	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hfx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hfx
39	c2e87A	Alignment	not modelled	99.0	24	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
40	c3sopB	Alignment	not modelled	99.0	26	PDB header: hydrolase Chain: B: PDB Molecule: neuronal-specific septin-3; PDBTitle: crystal structure of human septin 3 gtpase domain
41	c3w5iB	Alignment	not modelled	99.0	34	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferriformans
42	c2xtnA	Alignment	not modelled	99.0	19	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
43	c3lxaA	Alignment	not modelled	99.0	30	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 1; PDBTitle: crystal structure of human gtpase imap family member 1
44	c4dheA	Alignment	not modelled	99.0	21	PDB header: cell cycle Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a probable gtp-binding protein engb from2 burkholderia thailandensis
45	c5owvC	Alignment	not modelled	99.0	22	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
46	c1wf3A	Alignment	not modelled	99.0	25	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
47	d2bv3a2	Alignment	not modelled	99.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
48	c2qagC	Alignment	not modelled	98.9	24	PDB header: cell cycle, structural protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of human septin trimer 2/6/7
49	c3t5dC	Alignment	not modelled	98.9	24	PDB header: signaling protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of septin 7 in complex with gdp
50	c2qagB	Alignment	not modelled	98.9	21	PDB header: cell cycle, structural protein Chain: B: PDB Molecule: septin-6; PDBTitle: crystal structure of human septin trimer 2/6/7
51	c5oxfB	Alignment	not modelled	98.9	25	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
52	c5gnuA	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: A: PDB Molecule: mitofusin-1; PDBTitle: the structure of mini-mfn1 apo
53	c4lpsA	Alignment	not modelled	98.9	18	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
54	c6djqa	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: A: PDB Molecule: vps1 gtpase-bse; PDBTitle: vps1 gtpase-bse fusion complexed with gdp.alf4-
55	c5irrB	Alignment	not modelled	98.9	21	PDB header: hydrolase Chain: B: PDB Molecule: septin-like protein;

55	c3ttB_	Alignment	not modelled	98.9	41	PDBTitle: crystal structure of septin gtpase domain from chlamydomonas2 reinhardtii PDB header: antiviral protein/hydrolase Chain: B; PDB Molecule: interferon-induced gtp-binding protein mx1; PDBTitle: gmppcp-bound stalkless-mxa
56	c4p4sB_	Alignment	not modelled	98.9	24	PDB header: endocytosis Chain: A; PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
57	c2qptA_	Alignment	not modelled	98.8	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
58	d1jwyb_	Alignment	not modelled	98.8	22	PDB header: endocytosis Chain: A; PDB Molecule: eh domain-containing protein 4; PDBTitle: active structure of ehd4 complexed with adp
59	c5mvfA_	Alignment	not modelled	98.8	24	PDB header: cell cycle Chain: A; PDB Molecule: septin-2; PDBTitle: crystal structure of septin 2 in complex with gppnhp and2 mg2+
60	c3ftqA_	Alignment	not modelled	98.8	33	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
61	c3p1jC_	Alignment	not modelled	98.8	32	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
62	c5owvA_	Alignment	not modelled	98.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
63	d2dy1a2	Alignment	not modelled	98.8	28	PDB header: cell cycle, structural protein Chain: A; PDB Molecule: septin-2; PDBTitle: crystal structure of human septin trimer 2/6/7
64	c2qaqA_	Alignment	not modelled	98.8	38	PDB header: immune system Chain: A; PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4
65	c3lxxA_	Alignment	not modelled	98.8	28	PDB header: cell cycle, structural protein Chain: A; PDB Molecule: septin-2; PDBTitle: crystal structure of sept2 g-domain
66	c2qa5A_	Alignment	not modelled	98.8	31	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
67	c1udxA_	Alignment	not modelled	98.8	19	PDB header: hydrolase Chain: D; PDB Molecule: bacterial dynamin-like protein; PDBTitle: bacterial dynamin-like protein bdlp
68	c2j69D_	Alignment	not modelled	98.8	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
69	d1jala1	Alignment	not modelled	98.8	21	PDB header: hydrolase Chain: A; PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfolobus solfataricus in complex with gdp
70	c3pqcA_	Alignment	not modelled	98.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	d1ni3a1	Alignment	not modelled	98.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
72	d1egaa1	Alignment	not modelled	98.7	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
73	d2akab1	Alignment	not modelled	98.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	c2qthA_	Alignment	not modelled	98.7	19	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
75	c3j65o_	Alignment	not modelled	98.7	21	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.
76	c2ohfA_	Alignment	not modelled	98.7	24	PDB header: hydrolase Chain: A; PDB Molecule: gtp-binding protein 9; PDBTitle: crystal structure of human ola1 in complex with amppcp
77	c3gehA_	Alignment	not modelled	98.7	27	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
78	c2wwwB_	Alignment	not modelled	98.7	15	PDB header: transport protein Chain: B; PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
79	c5ar1A_	Alignment	not modelled	98.7	30	PDB header: cell cycle Chain: A; PDB Molecule: cell division control protein 11; PDBTitle: crystal structure of cdc11 from saccharomyces cerevisiae
80	c4h1vA_	Alignment	not modelled	98.7	20	PDB header: hydrolase Chain: A; PDB Molecule: dynamin-1-like protein; PDBTitle: gmp-pnp bound dynamin-1-like protein gtpase-ged fusion
						PDB header: motor protein Chain: A; PDB Molecule: dynamin-related protein 1a, linker,

81	c3t35A_	Alignment	not modelled	98.7	21	dynammin-related protein PDBTitle: arabidopsis thaliana dynammin-related protein 1a in postfission state
82	d1d2ea3	Alignment	not modelled	98.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
83	c3qq5A_	Alignment	not modelled	98.6	40	PDB header: oxidoreductase Chain: A; PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
84	d1zunb3	Alignment	not modelled	98.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
85	c3p1jB_	Alignment	not modelled	98.6	27	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
86	d1lnza2	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
87	d1wfa1	Alignment	not modelled	98.5	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
88	c4a9aB_	Alignment	not modelled	98.5	26	PDB header: translation Chain: B; PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
89	c2wjib_	Alignment	not modelled	98.5	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
90	c5k0yS_	Alignment	not modelled	98.5	15	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
91	c4csu9_	Alignment	not modelled	98.5	22	PDB header: ribosome Chain: 9; PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
92	d1wbl1a4	Alignment	not modelled	98.5	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
93	d2qj8a1	Alignment	not modelled	98.5	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
94	d1wxqa1	Alignment	not modelled	98.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
95	c3geiB_	Alignment	not modelled	98.4	24	PDB header: hydrolase Chain: B; PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
96	c2q3fb_	Alignment	not modelled	98.4	16	PDB header: protein binding Chain: B; PDB Molecule: ras-related gtp-binding protein d; PDBTitle: x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmppnp
97	c1lnza_	Alignment	not modelled	98.4	23	PDB header: cell cycle Chain: A; PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein
98	c1kk3A_	Alignment	not modelled	98.4	15	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+
99	d2qm8a1	Alignment	not modelled	98.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c3nxaA_	Alignment	not modelled	98.4	23	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
101	d1r5ba3	Alignment	not modelled	98.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
102	d1kk1a3	Alignment	not modelled	98.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
103	c1ni3A_	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: A; PDB Molecule: ychof gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe ychof gtpase
104	d2p67a1	Alignment	not modelled	98.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
105	c3j81k_	Alignment	not modelled	98.4	18	PDB header: ribosome Chain: K; PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
106	c2plfa_	Alignment	not modelled	98.4	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.

107	d2cxa1	Alignment	not modelled	98.3	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
108	c2qu8A	Alignment	not modelled	98.3	18	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
109	c3md0A	Alignment	not modelled	98.3	21	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)
110	c2lkA	Alignment	not modelled	98.3	19	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: free b.st if2-g2
111	d1svia	Alignment	not modelled	98.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
112	c5ee1A	Alignment	not modelled	98.3	24	PDB header: hydrolase Chain: A: PDB Molecule: obg-like atpase 1; PDBTitle: crystal structure of oychf1 at ph 7.85
113	d1f60a3	Alignment	not modelled	98.3	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
114	d2c78a3	Alignment	not modelled	98.3	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
115	d1nrjb	Alignment	not modelled	98.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
116	c4kzD	Alignment	not modelled	98.3	23	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)
117	d1udxa2	Alignment	not modelled	98.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
118	c3r7wC	Alignment	not modelled	98.3	22	PDB header: protein transport Chain: C: PDB Molecule: gtp-binding protein gtr1; PDBTitle: crystal structure of gtr1p-gtr2p complex
119	c3vr1B	Alignment	not modelled	98.3	25	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
120	c1s0uA	Alignment	not modelled	98.3	16	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: eif2gamma apo