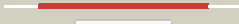



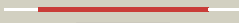














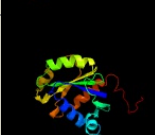


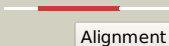

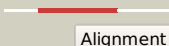







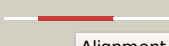
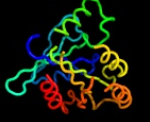








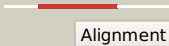

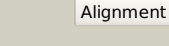
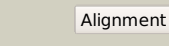
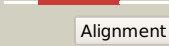



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1713_(engA)_1940295_1941686
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	29c4777945741f2b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j8gX_	 Alignment		100.0	36	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
2	c5dn8A_	 Alignment		100.0	38	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.
3	c2higA_	 Alignment		100.0	40	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
4	c1mkyA_	 Alignment		100.0	33	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
5	c5ady6_	 Alignment		100.0	22	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
6	c2e87A_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1320; PDBTitle: crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp
7	c1w3A_	 Alignment		100.0	34	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
8	c1xzqA_	 Alignment		100.0	32	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
9	c6em5b_	 Alignment		100.0	19	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
10	c3gehA_	 Alignment		100.0	32	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
11	c1egaB_	 Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era

12	c1udxA	 Alignment		100.0	21	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
13	c3ievA	 Alignment		100.0	30	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
14	d2dy1a2	 Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
15	d2bv3a2	 Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
16	c4b3xA	 Alignment		100.0	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
17	c3j65o	 Alignment		100.0	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.
18	c4csu9	 Alignment		100.0	24	PDB header: ribosome Chain: 9: PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
19	c4kjd	 Alignment		100.0	27	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)
20	c1lnzA	 Alignment		100.0	23	PDB header: cell cycle Chain: A: PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein
21	c2qthA	 Alignment	not modelled	100.0	23	PDB header: nucleotide binding protein Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfobolus solfataricus in complex with gdp
22	c3j4jA	 Alignment	not modelled	100.0	26	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
23	c3k53B	 Alignment	not modelled	99.9	23	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
24	c3a1vB	 Alignment	not modelled	99.9	24	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
25	c4a9aB	 Alignment	not modelled	99.9	27	PDB header: translation Chain: B: PDB Molecule: ribosome-interacting gtpase 1; PDBTitle: structure of rbg1 in complex with tma46 dfrp domain
26	c3lx8A	 Alignment	not modelled	99.9	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
27	c3i8sC	 Alignment	not modelled	99.9	22	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
28	c3ibyA	 Alignment	not modelled	99.9	25	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob

29	c1zo1l_	Alignment	not modelled	99.9	29	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
30	c3izyP_	Alignment	not modelled	99.9	22	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
31	c5fg3A_	Alignment	not modelled	99.9	26	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
32	c4nc1B_	Alignment	not modelled	99.9	24	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
33	c4upyB_	Alignment	not modelled	99.9	20	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
34	d1mkya3	Alignment	not modelled	99.9	29	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
35	c1wb1C_	Alignment	not modelled	99.9	19	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
36	c3wbkB_	Alignment	not modelled	99.9	24	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
37	c5ee1A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: obg-like atpase 1; PDBTitle: crystal structure of osychf1 at ph 7.85
38	c1g7tA_	Alignment	not modelled	99.9	28	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
39	d1h65a_	Alignment	not modelled	99.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
40	c3degC_	Alignment	not modelled	99.9	21	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
41	c3qq5A_	Alignment	not modelled	99.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
42	d1ni3a1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
43	c1kk3A_	Alignment	not modelled	99.9	24	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+
44	c4qity_	Alignment	not modelled	99.9	21	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
45	c5c1sB_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: small gtpase ehrabx3; PDBTitle: crystal structure of the gdp-bound fast hydrolyzing mutant (v71a/k73q)2 of ehrabx3 from entamoeba histolytica
46	c5izmA_	Alignment	not modelled	99.9	15	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdpnp
47	c2ywfA_	Alignment	not modelled	99.9	20	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
48	c1ni3A_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: yehf gtp-binding protein; PDBTitle: structure of the schizosaccharomyces pombe yehf gtpase
49	c3md0A_	Alignment	not modelled	99.9	24	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)
50	c3nxsA_	Alignment	not modelled	99.9	24	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
51	c3w5iB_	Alignment	not modelled	99.9	20	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from gallionella capsiferriformans
52	c4zu9A_	Alignment	not modelled	99.9	23	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
						PDB header: translation Chain: S: PDB Molecule: eukaryotic initiation factor 2 gamma

53	c5k0yS_	Alignment	not modelled	99.9	18	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
54	c4n3nA_	Alignment	not modelled	99.9	27	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5b-like protein, PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form
55	c2j3eA_	Alignment	not modelled	99.9	17	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
56	d2qm8a1	Alignment	not modelled	99.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
57	d2p67a1	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
58	c2wwwB_	Alignment	not modelled	99.9	21	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
59	d1tq4a_	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
60	c2qptA_	Alignment	not modelled	99.9	20	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
61	c4dheA_	Alignment	not modelled	99.9	19	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
62	c2plfA_	Alignment	not modelled	99.9	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.
63	c1jlaA_	Alignment	not modelled	99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ychf protein; PDBTitle: ychf protein (hi0393)
64	d1jla1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
65	c2dwqB_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: B: PDB Molecule: gtp-binding protein; PDBTitle: thermus thermophilus ychf gtp-binding protein
66	d1wf3a1	Alignment	not modelled	99.9	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
67	c4byrP_	Alignment	not modelled	99.9	28	PDB header: ribosome Chain: P: PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
68	c4fn5A_	Alignment	not modelled	99.9	18	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyri2 b
69	c2ohfA_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein 9; PDBTitle: crystal structure of human ola1 in complex with amppcp
70	d1f60a3	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	c4byxV_	Alignment	not modelled	99.9	27	PDB header: ribosome Chain: V: PDB Molecule: eukaryotic translation initiation factor 5b, probable PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
72	d1egaa1	Alignment	not modelled	99.9	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
73	d1svia_	Alignment	not modelled	99.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	c3j81k_	Alignment	not modelled	99.9	18	PDB header: ribosome Chain: K: PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
75	d1zunb3	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
76	c2rdo7_	Alignment	not modelled	99.9	18	PDB header: ribosome Chain: 7: PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdpnp) and rrf bound
77	c3zjcC_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: gtpase imap family member 7; PDBTitle: crystal structure of gmppnp-bound human gimap7 I100q variant
78	c2xtpA_	Alignment	not modelled	99.9	16	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

79	d1puja_	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
80	c4wnrA_	Alignment	not modelled	99.8	20	PDB header: signaling protein Chain: A: PDB Molecule: leucine-rich-repeat protein; PDBTitle: structure of methanosarcina barkeri roco2 roccordc bound to gdp
81	c2bvnB_	Alignment	not modelled	99.8	17	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
82	c2wjJB_	Alignment	not modelled	99.8	26	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
83	c3vr1B_	Alignment	not modelled	99.8	22	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
84	c1d2eA_	Alignment	not modelled	99.8	17	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
85	c3agjC_	Alignment	not modelled	99.8	26	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
86	c4zciA_	Alignment	not modelled	99.8	22	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
87	c6bbqA_	Alignment	not modelled	99.8	18	PDB header: lipid binding protein Chain: A: PDB Molecule: cytohesin-3,adp-ribosylation factor 6; PDBTitle: model for extended volume of truncated monomeric cytohesin-3 (grp1;2 amino acids 63-399) e161a arf6 q67l fusion protein
88	c3ec1A_	Alignment	not modelled	99.8	24	PDB header: hydrolase, signaling protein Chain: A: PDB Molecule: yqeh gtpase; PDBTitle: structure of yqeh gtpase from geobacillus stearothermophilus2 (an atnoa1 / atnoa1 ortholog)
89	c3wyaA_	Alignment	not modelled	99.8	19	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
90	c5izkB_	Alignment	not modelled	99.8	26	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
91	c2xtnA_	Alignment	not modelled	99.8	20	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
92	c2dykB_	Alignment	not modelled	99.8	40	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
93	c1mj1A_	Alignment	not modelled	99.8	21	PDB header: ribosome Chain: A: PDB Molecule: elongation factor tu; PDBTitle: fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
94	c6g15A_	Alignment	not modelled	99.8	20	PDB header: rna binding protein Chain: A: PDB Molecule: ribosome biogenesis gtpase a; PDBTitle: crystal structure of pppgpp bound rbgA from s. aureus
95	c3pqcA_	Alignment	not modelled	99.8	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
96	c1zunB_	Alignment	not modelled	99.8	23	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylate transferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
97	d1lnza2	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
98	c4lpsA_	Alignment	not modelled	99.8	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
99	c2dy1A_	Alignment	not modelled	99.8	26	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
100	c3j25A_	Alignment	not modelled	99.8	22	PDB header: translation Chain: A: PDB Molecule: tetracycline resistance protein tetm; PDBTitle: structural basis for tetm-mediated tetracycline resistance
101	c2xexA_	Alignment	not modelled	99.8	18	PDB header: translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
102	c2bm0A_	Alignment	not modelled	99.8	21	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
103	d1r5ba3	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
104	d2c78a3	Alianment	not modelled	99.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: G proteins
105	c2elfA_	Alignment	not modelled	99.8	18	PDB header: translation Chain: A: PDB Molecule: protein translation elongation factor 1a; PDBTitle: crystal structure of the selb-like elongation factor ef-pyl from2 methanosarcina mazei
106	d1n0ua2	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
107	d1wxqa1	Alignment	not modelled	99.8	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
108	c2h5eB_	Alignment	not modelled	99.8	23	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
109	c3lxaA_	Alignment	not modelled	99.8	21	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 1; PDBTitle: crystal structure of human gtpase imap family member 1
110	c2lkcA_	Alignment	not modelled	99.8	28	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: free b.st if2-g2
111	c3cb4D_	Alignment	not modelled	99.8	22	PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa
112	c5ucvA_	Alignment	not modelled	99.8	17	PDB header: cell cycle Chain: A: PDB Molecule: probable gtp-binding protein engb; PDBTitle: crystal structure of a ribosome biogenesis gtp-binding protein (ysxc)2 from neisseria gonorrhoeae with bound gdp
113	d1d2ea3	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
114	c3lxxA_	Alignment	not modelled	99.8	23	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4
115	c3p27A_	Alignment	not modelled	99.8	25	PDB header: signaling protein Chain: A: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: crystal structure of s. cerevisiae hbs1 protein (gdp-bound form), a2 translational gtpase involved in rna quality control pathways and3 interacting with dom34/pelota
116	c2qagC_	Alignment	not modelled	99.8	15	PDB header: cell cycle, structural protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of human septin trimer 2/6/7
117	d2gj8a1	Alignment	not modelled	99.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
118	c5hcnA_	Alignment	not modelled	99.8	20	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
119	c1skqB_	Alignment	not modelled	99.8	19	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
120	d1kk1a3	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins