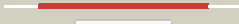



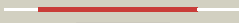




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1165_(typA)_1294173_1296059
Date	Wed Jul 31 22:05:25 BST 2019
Unique Job ID	fa38f573c46f9359

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4zciA_	 Alignment		100.0	48	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typA/bipA; PDBTitle: crystal structure of escherichia coli gtpase bipA/typA
2	c3j38z_	 Alignment		100.0	25	PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s25; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
3	c3jcrB_	 Alignment		100.0	25	PDB header: splicing Chain: B: PDB Molecule: hsnu114; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrrp complex
4	c5mqfB_	 Alignment		100.0	27	PDB header: splicing Chain: B: PDB Molecule: 116 kda u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
5	c3jb9B_	 Alignment		100.0	28	PDB header: rna binding protein/rna Chain: B: PDB Molecule: pre-mrna-splicing factor cwf10; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
6	c5z58C_	 Alignment		100.0	28	PDB header: splicing Chain: C: PDB Molecule: 116 kda u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
7	c3b8hA_	 Alignment		100.0	27	PDB header: biosynthetic protein/transferase Chain: A: PDB Molecule: elongation factor 2; PDBTitle: structure of the eef2-exoa(e546a)-nad+ complex
8	c5ganC_	 Alignment		100.0	21	PDB header: transcription Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrrp at2 3.7 angstrom
9	c5lj3C_	 Alignment		100.0	21	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
10	c3degC_	 Alignment		100.0	30	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
11	c3cb4D_	 Alignment		100.0	27	PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa

12	c5ancK_	Alignment		100.0	28	PDB header: translation Chain: K; PDB Molecule: elongation factor tu gtp-binding domain-containing protein PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
13	c2dy1A_	Alignment		100.0	25	PDB header: signaling protein, translation Chain: A; PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
14	c2ywfA_	Alignment		100.0	31	PDB header: translation Chain: A; PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
15	c3j25A_	Alignment		100.0	26	PDB header: translation Chain: A; PDB Molecule: tetracycline resistance protein tetm; PDBTitle: structural basis for tetm-mediated tetracycline resistance
16	c2rdo7_	Alignment		100.0	29	PDB header: ribosome Chain: 7; PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdnpn) and rrf bound
17	c4fn5A_	Alignment		100.0	32	PDB header: translation/antibiotic Chain: A; PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
18	c2bm0A_	Alignment		100.0	33	PDB header: elongation factor Chain: A; PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
19	c2xexA_	Alignment		100.0	31	PDB header: translation Chain: A; PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
20	c5h7IB_	Alignment		100.0	29	PDB header: translation/ribosomal protein Chain: B; PDB Molecule: elongation factor 2; PDBTitle: complex of elongation factor 2-50s ribosomal protein l12
21	c6notB_	Alignment	not modelled	100.0	33	PDB header: translation Chain: B; PDB Molecule: elongation factor g; PDBTitle: crystal structure of a full length elongation factor g (ef-g) from2 rickettsia prowazekii
22	c1zn0B_	Alignment	not modelled	100.0	33	PDB header: translation/biosynthetic protein/rna Chain: B; PDB Molecule: elongation factor g; PDBTitle: coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdnpn) and rrf
23	c4qjty_	Alignment	not modelled	100.0	31	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
24	c3vr1B_	Alignment	not modelled	100.0	23	PDB header: translation Chain: B; PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
25	c3e3xA_	Alignment	not modelled	100.0	46	PDB header: hydrolase Chain: A; PDB Molecule: bipa; PDBTitle: the c-terminal part of bipa protein from vibrio parahaemolyticus rimd2 2210633
26	c3tr5C_	Alignment	not modelled	100.0	22	PDB header: translation Chain: C; PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
27	c2h5eB_	Alignment	not modelled	100.0	25	PDB header: translation Chain: B; PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
28	c4byrP_	Alignment	not modelled	100.0	20	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 PDB header: ribosomal protein,hydrolase

29	c3izq1_	Alignment	not modelled	100.0	24	Chain: 1: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: structure of the dom34-hbs1-gdnpn complex bound to a translating2 ribosome
30	c1zunB_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylate transferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
31	c1mj1A_	Alignment	not modelled	100.0	25	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
32	c4nclB_	Alignment	not modelled	100.0	22	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	c1g7cA_	Alignment	not modelled	100.0	25	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: yeast eef1a:eef1ba in complex with gdnpn
34	c1wb1C_	Alignment	not modelled	100.0	20	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
35	c3p27A_	Alignment	not modelled	100.0	20	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
36	c4zu9A_	Alignment	not modelled	100.0	19	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
37	c3mmpC_	Alignment	not modelled	100.0	28	PDB header: transferase Chain: C: PDB Molecule: elongation factor tu 2, elongation factor ts; PDBTitle: structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
38	c1d2eA_	Alignment	not modelled	100.0	25	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
39	c4b3xA_	Alignment	not modelled	100.0	26	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
40	c3agiC_	Alignment	not modelled	100.0	28	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
41	c1skqB_	Alignment	not modelled	100.0	22	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
42	c5fg3A_	Alignment	not modelled	100.0	25	PDB header: translation Chain: A: PDB Molecule: probable translation initiation factor if-2; PDBTitle: crystal structure of gdp-bound aif5b from aeropyrum pernix
43	c1g7tA_	Alignment	not modelled	100.0	25	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if2/eif5b; PDBTitle: x-ray structure of translation initiation factor if2/eif5b2 complexed with gdnpn
44	c3j4jA_	Alignment	not modelled	100.0	27	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
45	c4zkeA_	Alignment	not modelled	100.0	19	PDB header: gtp binding protein Chain: A: PDB Molecule: superkiller protein 7; PDBTitle: crystal structure of the s. cerevisiae ski7 gtpase-like domain, bound2 to gtp.
46	c4crnP_	Alignment	not modelled	100.0	25	PDB header: translation Chain: P: PDB Molecule: erf3 in ribosome bound erf1-erf3-gdnpn complex; PDBTitle: cryo-em of a pretermination complex with erf1 and erf3
47	c3izyP_	Alignment	not modelled	100.0	28	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
48	c2bvnB_	Alignment	not modelled	100.0	27	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdnpn in complex with the antibiotic enacyloxin iia
49	c4byxV_	Alignment	not modelled	100.0	19	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
50	c3wbkB_	Alignment	not modelled	100.0	21	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
51	c3j2k7_	Alignment	not modelled	100.0	24	PDB header: ribosome/translation Chain: 7: PDB Molecule: eukaryotic polypeptide chain release factor 3; PDB Fragment: unp residues 147-584; PDBTitle: cryo-em structure of the mammalian erf1-erf3-associated termination2 complex
52	c5izmA_	Alignment	not modelled	100.0	24	PDB header: translation Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdnpn
						PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1-like

53	c3wyaA_	Alignment	not modelled	100.0	25	Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
54	c3agqA_	Alignment	not modelled	100.0	29	PDB header: translation,transferase Chain: A: PDB Molecule: elongation factor ts, elongation factor tu 1, linker, q PDBTitle: structure of viral polymerase form ii
55	c4kzD_	Alignment	not modelled	100.0	26	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)
56	c1zo1I_	Alignment	not modelled	100.0	28	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
57	c4upyB_	Alignment	not modelled	100.0	20	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
58	c2plfA_	Alignment	not modelled	100.0	21	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.
59	c5k0yS_	Alignment	not modelled	100.0	22	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
60	c3mcaA_	Alignment	not modelled	100.0	22	PDB header: translation regulation/hydrolase Chain: A: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
61	c1r5nA_	Alignment	not modelled	100.0	24	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor gtp- PDBTitle: crystal structure analysis of sup35 complexed with gdp
62	c2elfA_	Alignment	not modelled	100.0	16	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
63	c1kk3A_	Alignment	not modelled	100.0	26	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+
64	c4n3nA_	Alignment	not modelled	100.0	20	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
65	c3j81k_	Alignment	not modelled	100.0	23	PDB header: ribosome Chain: K: PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
66	c5izkB_	Alignment	not modelled	100.0	21	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
67	c1s0uA_	Alignment	not modelled	100.0	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: eif2gamma apo
68	c2hdnJ_	Alignment	not modelled	100.0	26	PDB header: translation Chain: J: PDB Molecule: elongation factor ef-tu; PDBTitle: trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution
69	d1n0ua2	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
70	d2dy1a2	Alignment	not modelled	100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	d2bv3a2	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
72	d1f60a3	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
73	d1zunb3	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	d2c78a3	Alignment	not modelled	99.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
75	d2bv3a1	Alignment	not modelled	99.9	35	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
76	d2dy1a5	Alignment	not modelled	99.9	24	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
77	d2bv3a5	Alignment	not modelled	99.9	29	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
78	d1n0ua5	Alignment	not modelled	99.9	20	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like

						Family:EF-G/eEF-2 domains III and V
79	d1n0ua1	Alignment	not modelled	99.9	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
80	d1d2ea3	Alignment	not modelled	99.9	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
81	d2dy1a1	Alignment	not modelled	99.9	23	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
82	d1r5ba3	Alignment	not modelled	99.8	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
83	d1jnya3	Alignment	not modelled	99.8	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
84	c5dn8A	Alignment	not modelled	99.8	24	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.
85	c1mkyA	Alignment	not modelled	99.8	26	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
86	d1s0ua3	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
87	d1efca3	Alignment	not modelled	99.7	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
88	c3j8gX	Alignment	not modelled	99.7	28	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
89	c2hjaA	Alignment	not modelled	99.7	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
90	c3qq5A	Alignment	not modelled	99.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hyd
91	c5hcnA	Alignment	not modelled	99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
92	c2e87A	Alignment	not modelled	99.7	23	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
93	c2qthA	Alignment	not modelled	99.7	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
94	d2dy1a4	Alignment	not modelled	99.7	22	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
95	d1kk1a3	Alignment	not modelled	99.6	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
96	c1jqsc	Alignment	not modelled	99.6	29	PDB header: ribosome Chain: C: PDB Molecule: elongation factor g; PDBTitle: fitting of I11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
97	d1g7sa4	Alignment	not modelled	99.6	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
98	c3k53B	Alignment	not modelled	99.6	22	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
99	c2gedB	Alignment	not modelled	99.6	24	PDB header: protein transport, signaling protein Chain: B: PDB Molecule: signal recognition particle receptor beta subunit; PDBTitle: signal recognition particle receptor beta-subunit in nucleotide-free2 dimerized form
100	d1wbl1a4	Alignment	not modelled	99.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
101	c3ievA	Alignment	not modelled	99.6	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
102	d1yrba1	Alignment	not modelled	99.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
103	c1xzqa	Alignment	not modelled	99.6	23	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
104	d2qn6a3	Alignment	not modelled	99.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins

105	c2qptA_	 Alignment	not modelled	99.6	20	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
106	c5ady6_	 Alignment	not modelled	99.5	22	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
107	c3a1vB_	 Alignment	not modelled	99.5	25	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
108	c4dheA_	 Alignment	not modelled	99.5	18	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
109	c1wf3A_	 Alignment	not modelled	99.5	32	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
110	c3gehA_	 Alignment	not modelled	99.5	23	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
111	c3ibyA_	 Alignment	not modelled	99.5	19	PDB header: transport protein Chain: A: PDB Molecule: ferrous iron transport protein b; PDBTitle: structure of cytosolic domain of l. pneumophila feob
112	c1egaB_	 Alignment	not modelled	99.5	24	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
113	d2bm0a4	 Alignment	not modelled	99.5	28	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
114	c2wsmB_	 Alignment	not modelled	99.5	19	PDB header: metal binding protein Chain: B: PDB Molecule: hydrogenase expression/formation protein (hypb); PDBTitle: crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus
115	c3md0A_	 Alignment	not modelled	99.5	26	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)
116	c3j65o_	 Alignment	not modelled	99.4	17	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.
117	d1n0ua4	 Alignment	not modelled	99.4	18	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: EF-G/eEF-2 domains III and V
118	c6cesA_	 Alignment	not modelled	99.4	20	PDB header: signaling protein Chain: A: PDB Molecule: ras-related gtp-binding protein a; PDBTitle: cryo-em structure of gator1-rag
119	c2qagC_	 Alignment	not modelled	99.4	16	PDB header: cell cycle, structural protein Chain: C: PDB Molecule: septin-7; PDBTitle: crystal structure of human septin trimer 2/6/7
120	c5ck3D_	 Alignment	not modelled	99.4	18	PDB header: signaling protein Chain: D: PDB Molecule: putative signal recognition particle protein; PDBTitle: signal recognition particle receptor srb-gtp/srx complex from2 chaetomium thermophilum