
























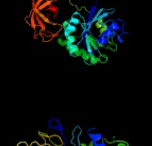
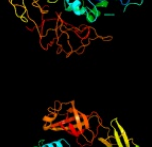
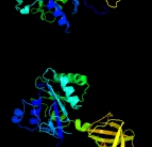


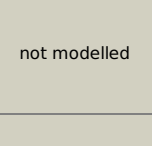


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0685_(tuf_784824_786014)
 Date Fri Jul 26 01:50:25 BST 2019
 Unique Job ID e41676c5f62b5858

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3agqA_	Alignment 		100.0	74	PDB header: translation,transferase Chain: A: PDB Molecule: elongation factor ts, elongation factor tu 1, linker, q PDBTitle: structure of viral polymerase form ii
2	c3mmpC_	Alignment 		100.0	74	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
3	c1mj1A_	Alignment 		100.0	68	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
4	c2bvnB_	Alignment 		100.0	76	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
5	c1d2eA_	Alignment 		100.0	57	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
6	c1g7cA_	Alignment 		100.0	34	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: yeast eef1a:eef1ba in complex with gdpnp
7	c3agiC_	Alignment 		100.0	37	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
8	c3izq1_	Alignment 		100.0	25	PDB header: ribosomal protein,hydrolase Chain: 1: PDB Molecule: elongation factor 1 alpha-like protein; PDBTitle: structure of the dom34-hbs1-gdpnp complex bound to a translating2 ribosome
9	c4crnP_	Alignment 		100.0	27	PDB header: translation Chain: P: PDB Molecule: erf3 in ribosome bound erf1-erf3-gdpnp complex; PDBTitle: cryo-em of a pretermination complex with erf1 and erf3
10	c1skqB_	Alignment 		100.0	33	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
11	c2hdnJ_	Alignment 		100.0	76	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

12	c3wyaA	Alignment		100.0	38 PDB header: translation Chain: A; PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
13	c3p27A	Alignment		100.0	23 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
14	c4zkeA	Alignment		100.0	16 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.
15	c1zunB	Alignment		100.0	25 PDB header: transferase Chain: B; PDB Molecule: sulfate adenylate transferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
16	c3j2k7	Alignment		100.0	27 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
17	c3mcaA	Alignment		100.0	26 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
18	c1r5nA	Alignment		100.0	27 PDB header: translation Chain: A; PDB Molecule: eukaryotic peptide chain release factor gtp- PDBTitle: crystal structure analysis of sup35 complexed with gdp
19	c1kk3A	Alignment		100.0	32 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+
20	c2elfA	Alignment		100.0	20 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
21	c5k0yS	Alignment	not modelled	100.0	27 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
22	c1s0uA	Alignment	not modelled	100.0	31 PDB header: translation Chain: A; PDB Molecule: translation initiation factor 2 gamma subunit; PDBTitle: eif2gamma apo
23	c4zu9A	Alignment	not modelled	100.0	29 PDB header: translation Chain: A; PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
24	c3j81k	Alignment	not modelled	100.0	25 PDB header: ribosome Chain: K; PDB Molecule: es10; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
25	c2plfA	Alignment	not modelled	100.0	27 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.
26	c1wb1C	Alignment	not modelled	100.0	29 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
27	c5izmA	Alignment	not modelled	100.0	23 PDB header: translation Chain: A; PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdpnp
					PDB header: translation

28	c5izkB_	Alignment	not modelled	100.0	23	Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
29	c4zciA_	Alignment	not modelled	100.0	30	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
30	c3degC_	Alignment	not modelled	100.0	24	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
31	c2ywfA_	Alignment	not modelled	100.0	25	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
32	c2dy1A_	Alignment	not modelled	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
33	c4b3xA_	Alignment	not modelled	100.0	24	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
34	c3j25A_	Alignment	not modelled	100.0	25	PDB header: translation Chain: A: PDB Molecule: tetracycline resistance protein tetm; PDBTitle: structural basis for tetm-mediated tetracycline resistance
35	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
36	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
37	c4kzD_	Alignment	not modelled	100.0	25	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)
38	c3wbkB_	Alignment	not modelled	100.0	20	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
39	c4qjty_	Alignment	not modelled	100.0	25	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
40	c1zo1l_	Alignment	not modelled	100.0	27	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
41	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
42	c1g7tA_	Alignment	not modelled	100.0	22	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
43	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
44	c3vr1B_	Alignment	not modelled	100.0	26	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
45	c4upyB_	Alignment	not modelled	100.0	22	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
46	c4ncIB_	Alignment	not modelled	100.0	21	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
47	c4fn5A_	Alignment	not modelled	100.0	28	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyri2 b
48	c3izyP_	Alignment	not modelled	100.0	27	PDB header: rna, ribosomal protein Chain: P: PDB Molecule: translation initiation factor if-2, mitochondrial; PDBTitle: mammalian mitochondrial translation initiation factor 2
49	c3cb4D_	Alignment	not modelled	100.0	21	PDB header: translation Chain: D: PDB Molecule: gtp-binding protein lepa; PDBTitle: the crystal structure of lepa
50	c3jcrB_	Alignment	not modelled	100.0	26	PDB header: splicing Chain: B: PDB Molecule: hsnu114; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrp complex
51	c2bm0A_	Alignment	not modelled	100.0	29	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
52	c4byxV_	Alignment	not modelled	100.0	20	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 PDB header: translation

53	c2xexA	Alignment	not modelled	100.0	28	Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
54	c3j38z	Alignment	not modelled	100.0	26	PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s25; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
55	c4n3nA	Alignment	not modelled	100.0	23	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
56	c2rdo7	Alignment	not modelled	100.0	28	PDB header: ribosome Chain: 7: PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdnpn) and rrf bound
57	c5mqfB	Alignment	not modelled	100.0	26	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)
58	c3b8hA	Alignment	not modelled	100.0	24	PDB header: biosynthetic protein/transferase Chain: A: PDB Molecule: elongation factor 2; PDBTitle: structure of the eef2-exoa(e546a)-nad+ complex
59	c3jb9B	Alignment	not modelled	100.0	25	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
60	c1zn0B	Alignment	not modelled	100.0	30	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
61	c3e1yG	Alignment	not modelled	100.0	21	PDB header: translation Chain: G: PDB Molecule: eukaryotic peptide chain release factor gtp-binding subunit PDBTitle: crystal structure of human erf1/erf3 complex
62	c5z58C	Alignment	not modelled	100.0	24	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.
63	c5ganC	Alignment	not modelled	100.0	20	PDB header: transcription Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
64	c3e20A	Alignment	not modelled	100.0	27	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor gtp-binding PDBTitle: crystal structure of s.pombe erf1/erf3 complex
65	c5lj3C	Alignment	not modelled	100.0	17	PDB header: splicing Chain: C: PDB Molecule: pre-mrna-splicing factor snu114; PDBTitle: structure of the core of the yeast spliceosome immediately after2 branching
66	c5ancK	Alignment	not modelled	100.0	32	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
67	c2h5eB	Alignment	not modelled	100.0	27	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
68	c5h7lB	Alignment	not modelled	100.0	27	PDB header: translation/ribosomal protein Chain: B: PDB Molecule: elongation factor 2; PDBTitle: complex of elongation factor 2-50s ribosomal protein l12
69	c6notB	Alignment	not modelled	100.0	26	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
70	d1f60a3	Alignment	not modelled	100.0	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
71	d2c78a3	Alignment	not modelled	100.0	70	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
72	d1zunb3	Alignment	not modelled	100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
73	d1d2ea3	Alignment	not modelled	100.0	64	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
74	d2dy1a2	Alignment	not modelled	100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
75	d1jnya3	Alignment	not modelled	100.0	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
76	d1efca3	Alignment	not modelled	100.0	74	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
77	d1r5ba3	Alignment	not modelled	99.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
78	d1n0ua2	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins

79	c1mkyA	Alignment	not modelled	99.9	25	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
80	c3j8gX	Alignment	not modelled	99.9	22	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
81	d2bv3a2	Alignment	not modelled	99.9	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
82	c2hjqA	Alignment	not modelled	99.9	22	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
83	c5dn8A	Alignment	not modelled	99.9	21	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.
84	d1s0ua3	Alignment	not modelled	99.9	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
85	c2e87A	Alignment	not modelled	99.9	21	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
86	d2c78a1	Alignment	not modelled	99.9	74	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
87	c2qthA	Alignment	not modelled	99.9	24	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
88	c1xzqA	Alignment	not modelled	99.9	20	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
89	c3ievA	Alignment	not modelled	99.9	19	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
90	d1kk1a3	Alignment	not modelled	99.9	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
91	d1jnya1	Alignment	not modelled	99.9	37	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
92	d2qn6a3	Alignment	not modelled	99.9	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
93	d1kk1a1	Alignment	not modelled	99.9	30	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
94	d1efca2	Alignment	not modelled	99.9	76	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
95	d1f60a1	Alignment	not modelled	99.9	41	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
96	c5ady6	Alignment	not modelled	99.9	20	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
97	d1d2ea1	Alignment	not modelled	99.9	55	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
98	c3gehA	Alignment	not modelled	99.9	19	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
99	d1efca1	Alignment	not modelled	99.9	75	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
100	c1egaB	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
101	c1wf3A	Alignment	not modelled	99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
102	d2c78a2	Alignment	not modelled	99.8	75	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
103	d1d2ea2	Alignment	not modelled	99.8	41	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
104	d1s0ua1	Alignment	not modelled	99.8	31	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
105	c3j65o	Alignment	not modelled	99.8	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.
106	c1udxA	Alignment	not modelled	99.8	24	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
107	d1wb1a4	Alignment	not modelled	99.8	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
108	c1lnzA	Alignment	not modelled	99.8	19	PDB header: cell cycle Chain: A: PDB Molecule: spo0b-associated gtp-binding protein; PDBTitle: structure of the obg gtp-binding protein
109	c4csu9	Alignment	not modelled	99.8	20	PDB header: ribosome Chain: 9: PDB Molecule: gtpase obge/cgta; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with obge
110	d1zunb1	Alignment	not modelled	99.8	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
111	c6em5b	Alignment	not modelled	99.8	15	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
112	c3qq5A	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydF
113	c5oxfB	Alignment	not modelled	99.8	22	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
114	d1f60a2	Alignment	not modelled	99.8	19	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
115	d1wb1a1	Alignment	not modelled	99.8	34	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
116	d1r5ba1	Alignment	not modelled	99.8	29	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
117	c2qptA	Alignment	not modelled	99.8	18	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
118	c4dheA	Alignment	not modelled	99.8	17	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
119	d2qn6a1	Alignment	not modelled	99.8	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
120	d1jnya2	Alignment	not modelled	99.8	28	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain Family: EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain