Phyre2

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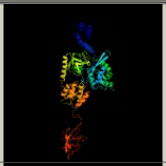
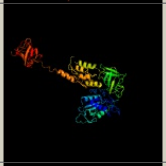
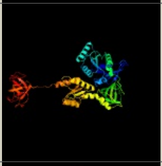
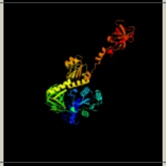
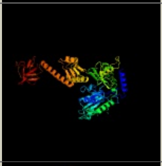
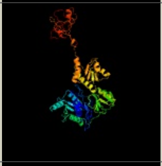
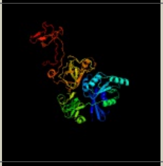
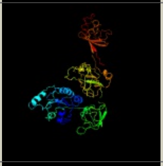
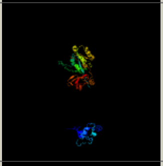
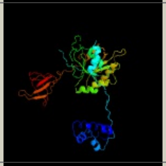
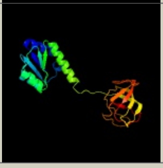
Description	RVBD2839c_(infB)_3145181_3147883
Date	Wed Aug 7 12:50:50 BST 2019
Unique Job ID	a3d6cb52721bc8f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3j4jA_	Alignment		100.0	42	**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
2	c1zo1I_	Alignment		100.0	53	**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
3	c3izyP_	Alignment		100.0	46	**PDB header:**rna, ribosomal protein **Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial; **PDBTitle:** mammalian mitochondrial translation initiation factor 2
4	c4n3nA_	Alignment		100.0	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
5	c3wbkB_	Alignment		100.0	28	**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
6	c1g7tA_	Alignment		100.0	29	**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
7	c5fg3A_	Alignment		100.0	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor if-2; **PDBTitle:** crystal structure of gdp-bound aif5b from aeropyrum pernix
8	c4upyB_	Alignment		100.0	27	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**eif5b; **PDBTitle:** mammalian 80s hcv-ires initiation complex with eif5b pre-like state
9	c4byxV_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** V: **PDB Molecule:**eukaryotic translation initiation factor 5b, probable **PDBTitle:** cryo-em reconstruction of the 80s-eif5b-met-itrnamet eukaryotic2 translation initiation complex
10	c4kjzD_	Alignment		100.0	40	**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)
11	c4nclB_	Alignment		100.0	30	**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

12	c4b3xA_	Alignment		100.0	45	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** bacterial translation initiation factor if2 (1-363), apo form
13	c5izmA_	Alignment		100.0	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** the crystal structure of human eefsec in complex with gdpnp
14	c5izkB_	Alignment		100.0	19	**PDB header:**translation **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** the crystal structure of human eefsec in complex with gdp
15	c1wb1C_	Alignment		100.0	21	**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
16	c4qjty_	Alignment		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
17	c4byrP_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**eukaryotic translation initiation factor 5b; **PDBTitle:** cryo-em reconstruction of the 80s-eif5b-met-itrnamet2 eukaryotic translation initiation complex
18	c3izq1_	Alignment		100.0	22	**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
19	c3agqA_	Alignment		100.0	25	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
20	c4n3gA_	Alignment		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 (870-1116) from chaetomium thermophilum, domains iii and iv
21	c2ywfA_	Alignment	not modelled	100.0	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
22	c3mmpC_	Alignment	not modelled	100.0	27	**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
23	c4zu9A_	Alignment	not modelled	100.0	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor selb; **PDBTitle:** crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
24	c4zciA_	Alignment	not modelled	100.0	27	**PDB header:**gtp-binding protein **Chain:** A: **PDB Molecule:**gtp-binding protein typa/bipa; **PDBTitle:** crystal structure of escherichia coli gtpase bipa/typa
25	c3degC_	Alignment	not modelled	100.0	27	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
26	c2xexA_	Alignment	not modelled	100.0	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
27	c1d2eA_	Alignment	not modelled	100.0	29	**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
28	c2dy1A_	Alignment	not modelled	100.0	31	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus

29	c2bm0A_	Alignment	not modelled	100.0	30	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
30	c3tr5C_	Alignment	not modelled	100.0	25	**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
31	c1zn0B_	Alignment	not modelled	100.0	32	**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 (gdpnp) and rrf
32	c3cb4D_	Alignment	not modelled	100.0	26	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
33	c4fn5A_	Alignment	not modelled	100.0	31	**PDB header:**translation/antibiotic **Chain:** A: **PDB Molecule:**elongation factor g 1; **PDBTitle:** elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
34	c1g7cA_	Alignment	not modelled	100.0	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp
35	c5k0yS_	Alignment	not modelled	100.0	24	**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
36	c1zunB_	Alignment	not modelled	100.0	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
37	c3j25A_	Alignment	not modelled	100.0	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**tetracycline resistance protein tetm; **PDBTitle:** structural basis for tetm-mediated tetracycline resistance
38	c1mj1A_	Alignment	not modelled	100.0	28	**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
39	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
40	c3agjC_	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	c3wyaA_	Alignment	not modelled	100.0	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
42	c3j38z_	Alignment	not modelled	100.0	25	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**40s ribosomal protein s25; **PDBTitle:** structure of the d. melanogaster 40s ribosomal proteins
43	c2h5eB_	Alignment	not modelled	100.0	26	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
44	c3mcaA_	Alignment	not modelled	100.0	24	**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
45	c3b8hA_	Alignment	not modelled	100.0	27	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
46	c2bvnB_	Alignment	not modelled	100.0	29	**PDB header:**elongation factor **Chain:** B: **PDB Molecule:**elongation factor tu; **PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
47	c1kk3A_	Alignment	not modelled	100.0	30	**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+
48	c4zkeA_	Alignment	not modelled	100.0	21	**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.
49	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
50	c3p27A_	Alignment	not modelled	100.0	21	**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
51	c2rdo7_	Alignment	not modelled	100.0	32	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
52	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-snrnp complex
53	c1skqB_	Alignment	not modelled	100.0	29	**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
						PDB header:translation/ribosomal protein

54	c5h7lB_	Alignment	not modelled	100.0	31	**Chain:** B: **PDB Molecule:**elongation factor 2; **PDBTitle:** complex of elongation factor 2-50s ribosomal protein l12
55	c2plfA_	Alignment	not modelled	100.0	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form.
56	c4crnP_	Alignment	not modelled	100.0	24	**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
57	c6notB_	Alignment	not modelled	100.0	27	**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
58	c5z58C_	Alignment	not modelled	100.0	27	**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.
59	c3jb9B_	Alignment	not modelled	100.0	27	**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	c3j81k_	Alignment	not modelled	100.0	19	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**es10; **PDBTitle:** cryoem structure of a partial yeast 48s preinitiation complex
61	c1r5nA_	Alignment	not modelled	100.0	23	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp- **PDBTitle:** crystal structure analysis of sup35 complexed with gdp
62	c5ganC_	Alignment	not modelled	100.0	28	**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
63	c5lj3C_	Alignment	not modelled	100.0	27	**PDB header:**splicing **Chain:** C: **PDB Molecule:**pre-mrna-splicing factor snu114; **PDBTitle:** structure of the core of the yeast spliceosome immediately after2 branching
64	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)
65	c1s0uA_	Alignment	not modelled	100.0	26	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
66	c3j2k7_	Alignment	not modelled	100.0	23	**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
67	c2hdnJ_	Alignment	not modelled	100.0	28	**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
68	c5anck_	Alignment	not modelled	100.0	37	**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
69	d1d1na_	Alignment	not modelled	100.0	57	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
70	c2nbgA_	Alignment	not modelled	100.0	50	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** structure of the geobacillus stearothermophilus if2 g3-subdomain
71	c2crvA_	Alignment	not modelled	100.0	31	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
72	c1z9bA_	Alignment	not modelled	100.0	40	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
73	d1g7sa3	Alignment	not modelled	100.0	21	**Fold:**Initiation factor IF2/eIF5b, domain 3 **Superfamily:**Initiation factor IF2/eIF5b, domain 3 **Family:**Initiation factor IF2/eIF5b, domain 3
74	d1f60a3	Alignment	not modelled	99.9	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
75	c2e87A_	Alignment	not modelled	99.9	26	**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
76	d2bv3a2	Alignment	not modelled	99.9	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
77	d1n0ua2	Alignment	not modelled	99.9	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
78	d2dy1a2	Alignment	not modelled	99.9	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
						Fold:P-loop containing nucleoside triphosphate hydrolases

79	d1zunb3	Alignment	not modelled	99.9	29	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
80	c2lkcA_	Alignment	not modelled	99.9	66	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** free b.st if2-g2
81	c1mkyA_	Alignment	not modelled	99.9	21	**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
82	c3j8gX_	Alignment	not modelled	99.9	20	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**gtpase der; **PDBTitle:** electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
83	c5dn8A_	Alignment	not modelled	99.9	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.
84	d1r5ba3	Alignment	not modelled	99.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
85	d1yrba1	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
86	d1g7sa4	Alignment	not modelled	99.9	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
87	c2qthA_	Alignment	not modelled	99.9	27	**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
88	c2hjgA_	Alignment	not modelled	99.9	17	**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
89	c3j65o_	Alignment	not modelled	99.9	13	**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.
90	c3ievA_	Alignment	not modelled	99.8	26	**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
91	c5ady6_	Alignment	not modelled	99.8	25	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**gtpase hflx; **PDBTitle:** cryo-em structures of the 50s ribosome subunit bound with hflx
92	c5wwnA_	Alignment	not modelled	99.8	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ribosome biogenesis protein tsr1; **PDBTitle:** crystal structure of tsr1
93	d1jnya3	Alignment	not modelled	99.8	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
94	d1d2ea3	Alignment	not modelled	99.8	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
95	d2c78a3	Alignment	not modelled	99.8	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
96	c1wf3A_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
97	c1egaB_	Alignment	not modelled	99.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (gtp-binding protein era); **PDBTitle:** crystal structure of a widely conserved gtpase era
98	c3md0A_	Alignment	not modelled	99.8	18	**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)
99	c3gehA_	Alignment	not modelled	99.8	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
100	d1wb1a4	Alignment	not modelled	99.8	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
101	c3qq5A_	Alignment	not modelled	99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
102	d1g7sa1	Alignment	not modelled	99.8	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
103	c4dheA_	Alignment	not modelled	99.8	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
104	c3k53B_	Alignment	not modelled	99.8	19	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** crystal structure of nfeob from p. furiosus
						Fold:P-loop containing nucleoside triphosphate hydrolases

105	d1kk1a3	Alignment	not modelled	99.8	29	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
106	c2wsmB_	Alignment	not modelled	99.8	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
107	c5jcpB_	Alignment	not modelled	99.8	25	**PDB header:**signaling protein,hydrolase **Chain:** B: **PDB Molecule:**arf-gap with rho-gap domain, ank repeat and ph domain- **PDBTitle:** rhogap domain of arap3 in complex with rhoa in the transition state
108	c3a1vB_	Alignment	not modelled	99.8	22	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**iron(ii) transport protein b; **PDBTitle:** crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form
109	c5hcnA_	Alignment	not modelled	99.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gpn-loop gtpase 1; **PDBTitle:** gpn-loop gtpase npa3 in complex with gmppcp
110	c1xzqA_	Alignment	not modelled	99.8	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
111	d1efca3	Alignment	not modelled	99.7	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
112	c4csu9_	Alignment	not modelled	99.7	20	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**gtpase obge/cgta; **PDBTitle:** cryo-em structures of the 50s ribosome subunit bound with obge
113	c2gedB_	Alignment	not modelled	99.7	22	**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
114	d2qn6a3	Alignment	not modelled	99.7	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
115	d1s0ua3	Alignment	not modelled	99.7	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
116	c5c2kA_	Alignment	not modelled	99.7	23	**PDB header:**hydrolase activator **Chain:** A: **PDB Molecule:**transforming protein rhoa,rac gtpase-activating protein 1; **PDBTitle:** crystal structure of the fusion protein linked by rhoa and the gap2 domain of mgcracgap
117	d1svia_	Alignment	not modelled	99.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
118	c1lnzA_	Alignment	not modelled	99.7	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**spo0b-associated gtp-binding protein; **PDBTitle:** structure of the obg gtp-binding protein
119	c4wnrA_	Alignment	not modelled	99.7	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**leucine-rich-repeat protein; **PDBTitle:** structure of methanosarcina barkeri roco2 roccordc bound to gdp
120	c5ucvA_	Alignment	not modelled	99.7	15	**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