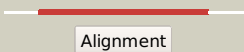

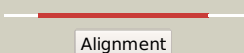
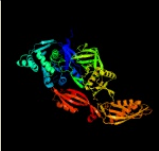
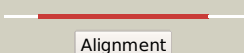

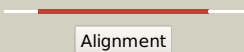


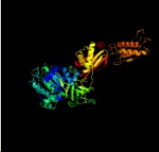


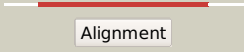

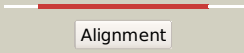



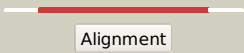

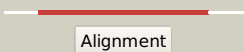






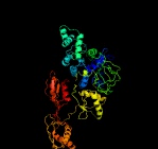





# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0120c\_(fusA2)\_145625\_147769  
 Date Tue Jul 23 14:50:16 BST 2019  
 Unique Job ID bef1b41d140271fc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ancK_</a>			100.0	22	<b>PDB header:</b> translation <b>Chain:</b> K: <b>PDB Molecule:</b> elongation factor tu gtp-binding domain-containing protein <b>PDBTitle:</b> mechanism of eif6 release from the nascent 60s ribosomal subunit
2	<a href="#">c2bm0A_</a>			100.0	34	<b>PDB header:</b> elongation factor <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
3	<a href="#">c2xexA_</a>			100.0	36	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of staphylococcus aureus elongation factor2 g
4	<a href="#">c5mqfB_</a>			100.0	21	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
5	<a href="#">c2rdo7_</a>			100.0	33	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdnpn) and rrf bound
6	<a href="#">c3j38z_</a>			100.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
7	<a href="#">c1zn0B_</a>			100.0	35	<b>PDB header:</b> translation/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdnpn) and rrf
8	<a href="#">c3jb9B_</a>			100.0	20	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> pre-mrna-splicing factor cwf10; <b>PDBTitle:</b> cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
9	<a href="#">c2dy1A_</a>			100.0	37	<b>PDB header:</b> signaling protein, translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of ef-g-2 from thermus thermophilus
10	<a href="#">c4fn5A_</a>			100.0	31	<b>PDB header:</b> translation/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g 1; <b>PDBTitle:</b> elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
11	<a href="#">c3jcrB_</a>			100.0	21	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> hsnu114; <b>PDBTitle:</b> 3d structure determination of the human*u4/u6.u5* trisnrnp complex

12	<a href="#">c5z58C_</a>	Alignment		100.0	21	<b>PDB header:</b> splicing <b>Chain:</b> C; <b>PDB Molecule:</b> 116 kda u5 small nuclear ribonucleoprotein component; <b>PDBTitle:</b> cryo-em structure of a human activated spliceosome (early back) at 4.92 angstrom.
13	<a href="#">c5ganC_</a>	Alignment		100.0	20	<b>PDB header:</b> transcription <b>Chain:</b> C; <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snRNP at 3.7 angstrom
14	<a href="#">c5lj3C_</a>	Alignment		100.0	21	<b>PDB header:</b> splicing <b>Chain:</b> C; <b>PDB Molecule:</b> pre-mrna-splicing factor snu114; <b>PDBTitle:</b> structure of the core of the yeast spliceosome immediately after 2 branching
15	<a href="#">c3b8hA_</a>	Alignment		100.0	21	<b>PDB header:</b> biosynthetic protein/transferase <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> structure of the eef2-exoa(e546a)-nad+ complex
16	<a href="#">c6notB_</a>	Alignment		100.0	30	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> crystal structure of a full length elongation factor g (ef-g) from Rickettsia prowazekii
17	<a href="#">c3j25A_</a>	Alignment		100.0	23	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> tetracycline resistance protein tetM; <b>PDBTitle:</b> structural basis for tetM-mediated tetracycline resistance
18	<a href="#">c5h7lB_</a>	Alignment		100.0	25	<b>PDB header:</b> translation/ribosomal protein <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor 2; <b>PDBTitle:</b> complex of elongation factor 2-50s ribosomal protein l12
19	<a href="#">c3degC_</a>	Alignment		100.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> C; <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmpPnp
20	<a href="#">c4zciA_</a>	Alignment		100.0	25	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> gtp-binding protein typA/bipA; <b>PDBTitle:</b> crystal structure of escherichia coli GTPase bipA/typA
21	<a href="#">c3vr1B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> crystal structure analysis of the translation factor rf3
22	<a href="#">c3tr5C_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> translation <b>Chain:</b> C; <b>PDB Molecule:</b> peptide chain release factor 3; <b>PDBTitle:</b> structure of a peptide chain release factor 3 (prfc) from Coxiella burnetii
23	<a href="#">c2ywfA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> crystal structure of gmpPnp-bound lepa from Aquifex aeolicus
24	<a href="#">c3cb4D_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> translation <b>Chain:</b> D; <b>PDB Molecule:</b> gtp-binding protein lepa; <b>PDBTitle:</b> the crystal structure of lepa
25	<a href="#">c4qjty_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> ribosome <b>Chain:</b> Y; <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of elongation factor 4 (ef4/lepa) bound to the 28S thermophilus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
26	<a href="#">c2h5eB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> peptide chain release factor rf-3; <b>PDBTitle:</b> crystal structure of e.coli polypeptide release factor rf3
27	<a href="#">c4zu9A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor selB; <b>PDBTitle:</b> crystal structure of bacterial selenocysteine-specific elongation factor ef-sec
28	<a href="#">c4byrP_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> ribosome <b>Chain:</b> P; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
						<b>PDB header:</b> protein synthesis

29	<a href="#">c1wb1C_</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> C; <b>PDB Molecule:</b> translation elongation factor selb; <b>PDBTitle:</b> crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp
30	<a href="#">c4nc1B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein; <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
31	<a href="#">c3izq1_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ribosomal protein,hydrolase <b>Chain:</b> 1; <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1-gdnpn complex bound to a translating2 ribosome
32	<a href="#">c1g7tA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if2/eif5b; <b>PDBTitle:</b> x-ray structure of translation initiation factor if2/eif5b2 complexed with gdnpn
33	<a href="#">c5fg3A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> probable translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of gdp-bound aif5b from aeropyrum pernix
34	<a href="#">c4b3xA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> bacterial translation initiation factor if2 (1-363), apo form
35	<a href="#">c4byxV_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ribosome <b>Chain:</b> V; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b, probable <b>PDBTitle:</b> cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
36	<a href="#">c3wbkB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b; <b>PDBTitle:</b> crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
37	<a href="#">c1zunB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> sulfate adenylate transferase, subunit <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
38	<a href="#">c1mj1A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> ribosome <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> 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	<a href="#">c4upyB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> B; <b>PDB Molecule:</b> eif5b; <b>PDBTitle:</b> mammalian 80s hcv-ires initiation complex with eif5b pre-like state
40	<a href="#">c1g7cA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> yeast eef1a:eef1ba in complex with gdnpn
41	<a href="#">c1d2eA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> rna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor tu (ef-tu); <b>PDBTitle:</b> crystal structure of mitochondrial ef-tu in complex with gdp
42	<a href="#">d2dy1a2</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
43	<a href="#">c3p27A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> crystal structure of s. cerevisiae hbs1 protein (gdp-bound form), a2 translational gtpase involved in rna quality control pathways and3 interacting with dom34/pelota
44	<a href="#">c3j4jA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map
45	<a href="#">c3izyP_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> rna, ribosomal protein <b>Chain:</b> P; <b>PDB Molecule:</b> translation initiation factor if-2, mitochondrial; <b>PDBTitle:</b> mammalian mitochondrial translation initiation factor 2
46	<a href="#">c3agiC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> translation/hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
47	<a href="#">c3mmpC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> elongation factor tu 2, elongation factor ts; <b>PDBTitle:</b> structure of the qb replicase, an rna-dependent rna polymerase2 consisting of viral and host proteins
48	<a href="#">c1zo1l_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> translation/rna <b>Chain:</b> I; <b>PDB Molecule:</b> translation initiation factor 2; <b>PDBTitle:</b> if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
49	<a href="#">c1skqB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> the crystal structure of sulfobolus solfataricus elongation factor 1-2 alpha in complex with magnesium and gdp
50	<a href="#">d1n0ua2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
51	<a href="#">c4n3nA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5b-like protein, <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form
52	<a href="#">c4kjdD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> translation <b>Chain:</b> D; <b>PDB Molecule:</b> translation initiation factor if-2; <b>PDBTitle:</b> crystal structure of thermus thermophilus if2, apo and gdp-bound forms2 (2-474)
53	<a href="#">d2bv3a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases

							<b>Family:</b> G proteins
54	<a href="#">c2bvnB</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia	
55	<a href="#">c3j2k7</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> ribosome/translation <b>Chain:</b> 7: <b>PDB Molecule:</b> eukaryotic polypeptide chain release factor 3; <b>PDB Fragment:</b> unp residues 147-584; <b>PDBTitle:</b> cryo-em structure of the mammalian erf1-erf3-associated termination2 complex	
56	<a href="#">c5k0yS</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> translation <b>Chain:</b> S: <b>PDB Molecule:</b> eukaryotic initiation factor 2 gamma subunit (eif2-gamma); <b>PDBTitle:</b> 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	
57	<a href="#">c4crnP</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> translation <b>Chain:</b> P: <b>PDB Molecule:</b> erf3 in ribosome bound erf1-erf3-gdpnp complex; <b>PDBTitle:</b> cryo-em of a pretermination complex with erf1 and erf3	
58	<a href="#">c2plfA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> the structure of aif2gamma subunit from the archaeon2 sulfobolus solfataricus in the nucleotide-free form.	
59	<a href="#">c5izmA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdpnp	
60	<a href="#">c4zkeA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> gtp binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> superkiller protein 7; <b>PDBTitle:</b> crystal structure of the s. cerevisiae ski7 gtpase-like domain, bound2 to gtp.	
61	<a href="#">c3wyaA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii	
62	<a href="#">c3agqA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> translation,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor ts, elongation factor tu 1, linker, q <b>PDBTitle:</b> structure of viral polymerase form ii	
63	<a href="#">c2elfA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> protein translation elongation factor 1a; <b>PDBTitle:</b> crystal structure of the selb-like elongation factor ef-pyl from2 methanosarcina mazei	
64	<a href="#">c3mcaA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> translation regulation/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor 1 alpha-like protein; <b>PDBTitle:</b> structure of the dom34-hbs1 complex and implications for its role in2 no-go decay	
65	<a href="#">c1r5nA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptide chain release factor gtp- <b>PDBTitle:</b> crystal structure analysis of sup35 complexed with gdp	
66	<a href="#">c1kk3A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eif2gamma; <b>PDBTitle:</b> structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+	
67	<a href="#">c3j81k</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> es10; <b>PDBTitle:</b> cryoem structure of a partial yeast 48s preinitiation complex	
68	<a href="#">c5izkB</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> the crystal structure of human eefsec in complex with gdp	
69	<a href="#">c1s0uA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo	
70	<a href="#">c2hdnJ</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> translation <b>Chain:</b> J: <b>PDB Molecule:</b> elongation factor ef-tu; <b>PDBTitle:</b> trypsin-modified elongation factor tu in complex with2 tetracycline at 2.8 angstrom resolution	
71	<a href="#">d2bv3a3</a>	Alignment	not modelled	100.0	49	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components	
72	<a href="#">c3e3xA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bipa; <b>PDBTitle:</b> the c-terminal part of bipa protein from vibrio parahaemolyticus rimd2 2210633	
73	<a href="#">d1f60a3</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins	
74	<a href="#">d2dy1a3</a>	Alignment	not modelled	99.9	40	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components	
75	<a href="#">d1n0ua1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors	
76	<a href="#">d1n0ua3</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components	
77	<a href="#">d2dy1a5</a>	Alignment	not modelled	99.9	43	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V	
78	<a href="#">d2bv3a5</a>	Alignment	not modelled	99.9	40	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like	

						<b>Family:</b> EF-G/eEF-2 domains III and V
79	<a href="#">d1n0ua5</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
80	<a href="#">c5dn8A</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
81	<a href="#">d2bv3a1</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
82	<a href="#">d2c78a3</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
83	<a href="#">d1zunb3</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
84	<a href="#">c1mkyA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein enga; <b>PDBTitle:</b> structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains
85	<a href="#">d2dy1a4</a>	Alignment	not modelled	99.9	36	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
86	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
87	<a href="#">d1n0ua4</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
88	<a href="#">d2bm0a4</a>	Alignment	not modelled	99.8	39	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> EF-G/eEF-2 domains III and V
89	<a href="#">c3j8gX</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> ribosome <b>Chain:</b> X: <b>PDB Molecule:</b> gtpase der; <b>PDBTitle:</b> electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
90	<a href="#">d1jnva3</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
91	<a href="#">c2hjaA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein enga; <b>PDBTitle:</b> the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp
92	<a href="#">d2dy1a1</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
93	<a href="#">d1r5ba3</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
94	<a href="#">d1s0ua3</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
95	<a href="#">c2e87A</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1320; <b>PDBTitle:</b> crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp
96	<a href="#">c2qthA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfobolus solfataricus in complex with gdp
97	<a href="#">d1yrba1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
98	<a href="#">c3ibyA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of cytosolic domain of l. pneumophila feob
99	<a href="#">c3qq5A</a>	Alignment	not modelled	99.7	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefe]-hydrogenase maturation protein hydF
100	<a href="#">d1efca3</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
101	<a href="#">d1g7sa4</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
102	<a href="#">c5hcnA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gpn-loop gtpase 1; <b>PDBTitle:</b> gpn-loop gtpase npa3 in complex with gmppcp
103	<a href="#">c1egaB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gtp-binding protein era); <b>PDBTitle:</b> crystal structure of a widely conserved gtpase era
104	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
105	<a href="#">c3k53B</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b;

						<b>PDBTitle:</b> crystal structure of nfeob from p. furiosus
106	<a href="#">c3ievA_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> nucleotide binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein era; <b>PDBTitle:</b> crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
107	<a href="#">c1xzqA_</a>	Alignment	not modelled	99.7	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna modification gtpase trme; <b>PDBTitle:</b> structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
108	<a href="#">c3i8sC_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> ferrous iron transport protein b; <b>PDBTitle:</b> structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
109	<a href="#">c3a1vB_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structue of the cytosolic domain of t. maritima feob2 iron transporter in apo form
110	<a href="#">c2qptA_</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> eh domain-containing protein-2; <b>PDBTitle:</b> crystal structure of an ehd atpase involved in membrane remodelling
111	<a href="#">d1wblA4</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
112	<a href="#">c2qagC_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> septin-7; <b>PDBTitle:</b> crystal structure of human septin trimer 2/6/7
113	<a href="#">c1wF3A_</a>	Alignment	not modelled	99.7	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of gtp-binding protein tt1341 from thermus2 thermophilus hb8
114	<a href="#">c3j65o_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l15; <b>PDBTitle:</b> arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
115	<a href="#">c2gedB_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> protein transport, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor beta subunit; <b>PDBTitle:</b> signal recognition particle receptor beta-subunit in nucleotide-free2 dimerized form
116	<a href="#">c5ady6_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> ribosome <b>Chain:</b> 6: <b>PDB Molecule:</b> gtpase hflx; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with hflx
117	<a href="#">c3gehA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
118	<a href="#">c4dheA_</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of a probable gtp-binding protein engb from2 burkholderia thailandensis
119	<a href="#">c1jqsc_</a>	Alignment	not modelled	99.6	44	<b>PDB header:</b> ribosome <b>Chain:</b> C: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> fitting of l11 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
120	<a href="#">c6em5b_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> 60s ribosomal protein l3; <b>PDBTitle:</b> state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes