



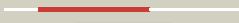
















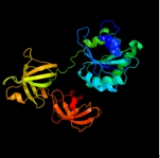




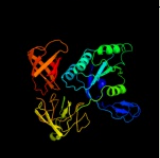
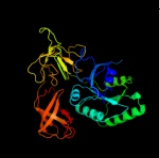
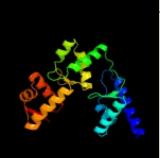
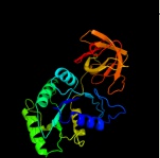
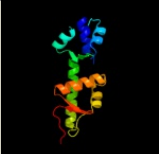


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3agqA_</a>	 Alignment		100.0	31	<b>PDB header:</b> translation,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor ts, elongation factor tu 1, linker, q <b>PDBTitle:</b> structure of viral polymerase form ii
2	<a href="#">c3mmpC_</a>	 Alignment		100.0	31	<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
3	<a href="#">c2elfA_</a>	 Alignment		100.0	22	<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-pyl2 from methanosarcina mazei
4	<a href="#">c2bvnB_</a>	 Alignment		100.0	31	<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 c enacyloxin iia
5	<a href="#">c1g7cA_</a>	 Alignment		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 gdpnp
6	<a href="#">c1kk3A_</a>	 Alignment		100.0	29	<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+
7	<a href="#">c1d2eA_</a>	 Alignment		100.0	30	<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
8	<a href="#">c3izq1_</a>	 Alignment		100.0	24	<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-gdpnp complex bound to a translating2 ribosome
9	<a href="#">c1mj1A_</a>	 Alignment		100.0	29	<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
10	<a href="#">c1skqB_</a>	 Alignment		100.0	30	<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 elongation2 factor 1-alpha in complex with magnesium and gdp
11	<a href="#">c1wb1C_</a>	 Alignment		100.0	28	<b>PDB header:</b> protein synthesis <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

12	<a href="#">c1zunB_</a>	Alignment		100.0	25	<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
13	<a href="#">c2hdnJ_</a>	Alignment		100.0	29	<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
14	<a href="#">c3mcaA_</a>	Alignment		100.0	27	<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
15	<a href="#">c3p27A_</a>	Alignment		100.0	22	<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 a translational gtpase (gdp form)
16	<a href="#">c1r5nA_</a>	Alignment		100.0	26	<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
17	<a href="#">c1s0uA_</a>	Alignment		100.0	25	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
18	<a href="#">c2plfA_</a>	Alignment		100.0	27	<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.
19	<a href="#">c2plyB_</a>	Alignment		100.0	24	<b>PDB header:</b> translation/rna <b>Chain:</b> B: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.
20	<a href="#">c2ywfa_</a>	Alignment		100.0	24	<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
21	<a href="#">c3degC_</a>	Alignment	not modelled	100.0	23	<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
22	<a href="#">c1zo1I_</a>	Alignment	not modelled	100.0	30	<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
23	<a href="#">c3izyP_</a>	Alignment	not modelled	100.0	28	<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
24	<a href="#">c1g7tA_</a>	Alignment	not modelled	100.0	29	<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 gdpnp
25	<a href="#">c2dy1A_</a>	Alignment	not modelled	100.0	27	<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
26	<a href="#">c3cb4D_</a>	Alignment	not modelled	100.0	20	<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
27	<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 coxiella2 burnetii
28	<a href="#">c2xexA_</a>	Alignment	not modelled	100.0	22	<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 <b>PDB header:</b> elongation factor

29	<a href="#">c2bm0A_</a>	Alignment	not modelled	100.0	24	<b>Chain:</b> A: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
30	<a href="#">c2rdo7_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdpnp) and rrf bound
31	<a href="#">c1zn0B_</a>	Alignment	not modelled	100.0	26	<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 (gdpnp) and rrf
32	<a href="#">c2h5eB_</a>	Alignment	not modelled	100.0	25	<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
33	<a href="#">c3b8hA_</a>	Alignment	not modelled	100.0	26	<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
34	<a href="#">c3e1yG_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> translation <b>Chain:</b> G: <b>PDB Molecule:</b> eukaryotic peptide chain release factor gtp-binding subunit <b>PDBTitle:</b> crystal structure of human erf1/erf3 complex
35	<a href="#">c2pjpA_</a>	Alignment	not modelled	100.0	100	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
36	<a href="#">c1wsuA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> translation/rna <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> c-terminal domain of elongation factor selb complexed with2 secis rna
37	<a href="#">c3e20A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic peptide chain release factor gtp-binding <b>PDBTitle:</b> crystal structure of s.pombe erf1/erf3 complex
38	<a href="#">d1f60a3</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
39	<a href="#">d2dy1a2</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
40	<a href="#">d1zunb3</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
41	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
42	<a href="#">c2e87A_</a>	Alignment	not modelled	99.9	22	<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
43	<a href="#">d1n0ua2</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
44	<a href="#">c1mkya_</a>	Alignment	not modelled	99.9	26	<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, a2 switch protein containing two gtpase domains
45	<a href="#">d2c78a3</a>	Alignment	not modelled	99.9	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
46	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.9	38	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
47	<a href="#">c2higA_</a>	Alignment	not modelled	99.9	17	<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 in2 complex with gdp
48	<a href="#">c3ievA_</a>	Alignment	not modelled	99.9	17	<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 mggpn and the 3' end of 16s2 rrna
49	<a href="#">d1kk1a1</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
50	<a href="#">d1jnya3</a>	Alignment	not modelled	99.9	27	<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="#">d1s0ua1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
52	<a href="#">c2qthA_</a>	Alignment	not modelled	99.9	19	<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 the2 hyperthermophilic archaeon sulfolobus solfataricus in3 complex with gdp
53	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.9	38	<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="#">d1r5ha3</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate

54	<a href="#">d1f0ua3</a>	Alignment	not modelled	99.9	27	hydrolases <b>Family:</b> G proteins
55	<a href="#">d1jnya1</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
56	<a href="#">c1xzqa</a>	Alignment	not modelled	99.9	21	<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
57	<a href="#">c1udxa</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> the gtp-binding protein obg; <b>PDBTitle:</b> crystal structure of the conserved protein tt1381 from thermus2 thermophilus hb8
58	<a href="#">c3qq5A</a>	Alignment	not modelled	99.9	20	<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
59	<a href="#">d1d2ea1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
60	<a href="#">d1zunb1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
61	<a href="#">c3gehA</a>	Alignment	not modelled	99.9	23	<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
62	<a href="#">d1f60a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
63	<a href="#">d1efca1</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
64	<a href="#">c1wf3A</a>	Alignment	not modelled	99.9	19	<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
65	<a href="#">d2c78a1</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
66	<a href="#">c2v9vA</a>	Alignment		99.9	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> selenocysteine-specific elongation factor; <b>PDBTitle:</b> crystal structure of moorella thermoacetica selb(377-511)
67	<a href="#">c1lnzA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> spo0b-associated gtp-binding protein; <b>PDBTitle:</b> structure of the obg gtp-binding protein
68	<a href="#">d1s0ua3</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
69	<a href="#">d2qn6a1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
70	<a href="#">c1egaB</a>	Alignment	not modelled	99.9	18	<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
71	<a href="#">d1yrba1</a>	Alignment	not modelled	99.8	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
72	<a href="#">c3k53B</a>	Alignment	not modelled	99.8	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
73	<a href="#">d1efca3</a>	Alignment	not modelled	99.8	42	<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="#">d2qn6a3</a>	Alignment	not modelled	99.8	32	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
75	<a href="#">d1wb1a1</a>	Alignment	not modelled	99.8	38	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
76	<a href="#">c3md0A</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> arginine/ornithine transport system atpase; <b>PDBTitle:</b> crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein)
77	<a href="#">d1r5ba1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
78	<a href="#">c3i8sC</a>	Alignment	not modelled	99.8	21	<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
79	<a href="#">c3ibyA</a>	Alignment	not modelled	99.8	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
80	<a href="#">d1wb1a4</a>	Alignment	not modelled	99.8	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
81	<a href="#">c3lx8A_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferrous iron uptake transporter protein b; <b>PDBTitle:</b> crystal structure of gdp-bound nfeob from s. thermophilus
82	<a href="#">c3a1vB_</a>	Alignment	not modelled	99.8	21	<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
83	<a href="#">d1svia_</a>	Alignment	not modelled	99.8	17	<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="#">c3r7wC_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> gtp-binding protein gtr1; <b>PDBTitle:</b> crystal structure of gtr1p-gtr2p complex
85	<a href="#">c3nxsA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> lao/ao transport system atpase; <b>PDBTitle:</b> crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
86	<a href="#">d1lvaa4</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
87	<a href="#">d1tq4a_</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
88	<a href="#">d1g7sa4</a>	Alignment	not modelled	99.8	34	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
89	<a href="#">c1t9hA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtpase engc; <b>PDBTitle:</b> the crystal structure of yloq, a circularly permuted gtpase.
90	<a href="#">d2p67a1</a>	Alignment	not modelled	99.8	17	<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
91	<a href="#">c2qptA_</a>	Alignment	not modelled	99.8	20	<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
92	<a href="#">c3pqcA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable gtp-binding protein engb; <b>PDBTitle:</b> crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp
93	<a href="#">c2wsmB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hybp); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hybp from2 archaeoglobus fulgidus
94	<a href="#">d1puia_</a>	Alignment	not modelled	99.7	16	<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="#">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
96	<a href="#">d1egaa1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
97	<a href="#">d1udxa2</a>	Alignment	not modelled	99.7	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
98	<a href="#">c2wwwB_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> methylmalonic aciduria type a protein, <b>PDBTitle:</b> crystal structure of methylmalonic acidemia type a protein
99	<a href="#">c2gedB_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> protein transport, signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor beta <b>PDBTitle:</b> signal recognition particle receptor beta-subunit in2 nucleotide-free dimerized form
100	<a href="#">d2qm8a1</a>	Alignment	not modelled	99.6	18	<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
101	<a href="#">d2v9va2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> C-terminal fragment of elongation factor SelB
102	<a href="#">c3t1tC_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gliding protein mglA; <b>PDBTitle:</b> mglA bound to gdp in p1 tetrameric arrangement
103	<a href="#">c2xtpA_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of nucleotide-free human gimap2, amino2 acid residues 1-260
104	<a href="#">c3lvrE_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> arf-gap with sh3 domain, ank repeat and ph domain- <b>PDBTitle:</b> the crystal structure of asap3 in complex with arf6 in transition2 state soaked with calcium



105	<a href="#">d1lnza2</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
106	<a href="#">d2fh5b1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
107	<a href="#">c2wjJB_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferrous iron transport protein b homolog; <b>PDBTitle:</b> structure and function of the feob g-domain from2 methanococcus jannaschii
108	<a href="#">d1wf3a1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
109	<a href="#">c2qa5A_</a>	Alignment	not modelled	99.6	10	<b>PDB header:</b> cell cycle, structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> sepin-2; <b>PDBTitle:</b> crystal structure of sept2 g-domain
110	<a href="#">c2hf9A_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> hydrolase, metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable hydrogenase nickel incorporation <b>PDBTitle:</b> crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
111	<a href="#">c2q3fB_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> ras-related gtp-binding protein d; <b>PDBTitle:</b> x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmpnp
112	<a href="#">d2cxa1</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
113	<a href="#">c3c5hA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> glucocorticoid receptor dna-binding factor 1; <b>PDBTitle:</b> crystal structure of the ras homolog domain of human grlf12 (p190rhogap)
114	<a href="#">c2dykB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> ribosome <b>Chain:</b> B: <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> crystal structure of n-terminal gtp-binding domain of enga from2 thermus thermophilus hb8
115	<a href="#">c3a1wA_</a>	Alignment	not modelled	99.6	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structue of the g domain of t. maritima feob iron2 transporter
116	<a href="#">c2qu8A_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleolar gtp-binding protein 1; <b>PDBTitle:</b> crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
117	<a href="#">c3pljC_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> gtpase imap family member 2; <b>PDBTitle:</b> crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
118	<a href="#">d1mkya2</a>	Alignment	not modelled	99.5	23	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
119	<a href="#">d1nrjb_</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
120	<a href="#">c2j3eA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> t7i23.11 protein; <b>PDBTitle:</b> dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159