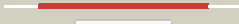



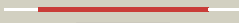


















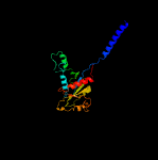


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1496_(-)_1686890_1687894
Date	Fri Aug 2 13:30:08 BST 2019
Unique Job ID	500fb8e81a6f98bf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2qm8a1</a>	 Alignment		100.0	56	<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
2	<a href="#">c3md0A</a>	 Alignment		100.0	99	<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 system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
3	<a href="#">c3nxsA</a>	 Alignment		100.0	79	<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
4	<a href="#">d2p67a1</a>	 Alignment		100.0	40	<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
5	<a href="#">c2wwwB</a>	 Alignment		100.0	46	<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
6	<a href="#">c4xc8B</a>	 Alignment		100.0	27	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> isobutyryl-coa mutase fused; <b>PDBTitle:</b> isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
7	<a href="#">c1xzqA</a>	 Alignment		100.0	20	<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
8	<a href="#">c3gehA</a>	 Alignment		100.0	21	<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
9	<a href="#">c2e87A</a>	 Alignment		99.9	18	<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
10	<a href="#">c2hf9A</a>	 Alignment		99.9	18	<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
11	<a href="#">c5ady6</a>	 Alignment		99.9	21	<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

12	<a href="#">c6em5b_</a>	Alignment		99.9	23	<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
13	<a href="#">c5dn8A_</a>	Alignment		99.9	30	<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.
14	<a href="#">c4lpsA_</a>	Alignment		99.9	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein hyhb; <b>PDBTitle:</b> crystal structure of hyhb from helicobacter pylori in complex with2 nickel
15	<a href="#">c1egaB_</a>	Alignment		99.9	20	<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
16	<a href="#">c3ievA_</a>	Alignment		99.9	21	<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
17	<a href="#">c1wf3A_</a>	Alignment		99.9	24	<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
18	<a href="#">c4b3xA_</a>	Alignment		99.9	21	<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
19	<a href="#">c2qthA_</a>	Alignment		99.9	20	<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 sulfolobus solfataricus in complex with gdp
20	<a href="#">c5xktA_</a>	Alignment		99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease accessory protein ureg; <b>PDBTitle:</b> klebsiella pneumoniae ureg in complex with gmppnp and nickel
21	<a href="#">c3j65o_</a>	Alignment	not modelled	99.9	21	<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.
22	<a href="#">c4kjd_</a>	Alignment	not modelled	99.9	25	<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)
23	<a href="#">c2wsmB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase expression/formation protein (hyhb); <b>PDBTitle:</b> crystal structure of hydrogenase maturation factor hyhb from2 archaeoglobus fulgidus
24	<a href="#">c3j8gX_</a>	Alignment	not modelled	99.9	21	<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
25	<a href="#">c3j4jA_</a>	Alignment	not modelled	99.9	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
26	<a href="#">c4csu9_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> gtpase obge/cgta; <b>PDBTitle:</b> cryo-em structures of the 50s ribosome subunit bound with obge
27	<a href="#">c1udxA_</a>	Alignment	not modelled	99.9	23	<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
28	<a href="#">c2hinA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein enga;

28	<a href="#">c2mgA</a>	Alignment	not modelled	99.9	19	<b>PDBTitle:</b> the crystal structure of the b. subtilis yphc gtpase in complex with2 gdp
29	<a href="#">c5hcnA</a>	Alignment	not modelled	99.9	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
30	<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, a switch2 protein containing two gtpase domains
31	<a href="#">c4hi0F</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> urease accessory protein ureg; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease accessory protein2 uref/h/g complex
32	<a href="#">c4upyB</a>	Alignment	not modelled	99.9	16	<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
33	<a href="#">c1lnzA</a>	Alignment	not modelled	99.9	23	<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
34	<a href="#">c5fg3A</a>	Alignment	not modelled	99.9	15	<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
35	<a href="#">c1g7tA</a>	Alignment	not modelled	99.8	21	<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
36	<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
37	<a href="#">c4nclB</a>	Alignment	not modelled	99.8	15	<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
38	<a href="#">c3wbkB</a>	Alignment	not modelled	99.8	16	<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
39	<a href="#">c3izyP</a>	Alignment	not modelled	99.8	18	<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
40	<a href="#">c5izmA</a>	Alignment	not modelled	99.8	21	<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
41	<a href="#">c4dheA</a>	Alignment	not modelled	99.8	16	<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
42	<a href="#">c1wb1C</a>	Alignment	not modelled	99.8	20	<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
43	<a href="#">c1kk3A</a>	Alignment	not modelled	99.8	16	<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+
44	<a href="#">c5k0yS</a>	Alignment	not modelled	99.8	12	<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
45	<a href="#">c3dm5A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
46	<a href="#">c4zu9A</a>	Alignment	not modelled	99.8	22	<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 elongation2 factor ef-sec
47	<a href="#">c3ibyA</a>	Alignment	not modelled	99.8	16	<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
48	<a href="#">c2plfA</a>	Alignment	not modelled	99.8	18	<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 sulfolobus solfataricus in the nucleotide-free form.
49	<a href="#">c1zo1l</a>	Alignment	not modelled	99.8	24	<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
50	<a href="#">c1zu4A</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ftsyt; <b>PDBTitle:</b> crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
51	<a href="#">c2ywfA</a>	Alignment	not modelled	99.8	22	<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
52	<a href="#">c4a9aB</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> translation <b>Chain:</b> B: <b>PDB Molecule:</b> ribosome-interacting gtpase 1; <b>PDBTitle:</b> structure of rbg1 in complex with tma46 dfrp domain

53	<a href="#">c5izkB</a>	Alignment	not modelled	99.8	21	<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
54	<a href="#">c3k53B</a>	Alignment	not modelled	99.8	21	<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
55	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
56	<a href="#">c3a1vB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> iron(ii) transport protein b; <b>PDBTitle:</b> crystal structure of the cytosolic domain of t. maritima feob2 iron transporter in apo form
57	<a href="#">c6cy1B</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
58	<a href="#">c2yhsA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy
59	<a href="#">c2j37W</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
60	<a href="#">c3j81k</a>	Alignment	not modelled	99.8	15	<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
61	<a href="#">c3lx8A</a>	Alignment	not modelled	99.8	18	<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
62	<a href="#">c2iy3A</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
63	<a href="#">c4byxV</a>	Alignment	not modelled	99.8	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
64	<a href="#">c4n3nA</a>	Alignment	not modelled	99.8	17	<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
65	<a href="#">c2qy9A</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
66	<a href="#">c2q9cA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of ftsy:gmpnp with mgcl complex
67	<a href="#">c5l3rC</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
68	<a href="#">c3i8sC</a>	Alignment	not modelled	99.8	20	<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
69	<a href="#">d1tq4a</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
70	<a href="#">c1vmaA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
71	<a href="#">c3geiB</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> trna modification gtpase mnme; <b>PDBTitle:</b> crystal structure of mnme from chlorobium tepidum in complex2 with gcp
72	<a href="#">c3dmdA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle receptor; <b>PDBTitle:</b> structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
73	<a href="#">c3degC</a>	Alignment	not modelled	99.8	21	<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 gmpnp
74	<a href="#">c4qjty</a>	Alignment	not modelled	99.8	20	<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 the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
75	<a href="#">c2j7pA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
76	<a href="#">c5l3sF</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
77	<a href="#">d1nija1</a>	Alignment	not modelled	99.7	22	<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

78	<a href="#">c4byrP</a>	Alignment	not modelled	99.7	14	<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-itramet2 eukaryotic translation initiation complex
79	<a href="#">c5gafi</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein l10; <b>PDBTitle:</b> rnc in complex with srp
80	<a href="#">c2v3cC</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
81	<a href="#">c3b9qA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpfts from arabidopsis thaliana
82	<a href="#">c2og2A</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
83	<a href="#">d1ni3a1</a>	Alignment	not modelled	99.7	21	<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="#">d2dy1a2</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
85	<a href="#">c1qzwC</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
86	<a href="#">d1svia</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
87	<a href="#">d1h65a</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
88	<a href="#">c3agjC</a>	Alignment	not modelled	99.7	18	<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
89	<a href="#">c2xtpA</a>	Alignment	not modelled	99.7	15	<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
90	<a href="#">c4zciA</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein tyba/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/tyba
91	<a href="#">c3w5iB</a>	Alignment	not modelled	99.7	18	<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 gallionella capsiferriformans
92	<a href="#">c3qq5A</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> small gtp-binding protein; <b>PDBTitle:</b> crystal structure of the [fefc]-hydrogenase maturation protein hydF
93	<a href="#">c2bvnB</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> elongation factor <b>Chain:</b> B: <b>PDB Molecule:</b> elongation factor tu; <b>PDBTitle:</b> e. coli ef-tu:gdnp in complex with the antibiotic enacyloxin iia
94	<a href="#">c2j289</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
95	<a href="#">d1zunb3</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
96	<a href="#">c5ucvA</a>	Alignment	not modelled	99.7	18	<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 ribosome biogenesis gtp-binding protein (ysxc)2 from neisseria gonorrhoeae with bound gdp
97	<a href="#">c1nijA</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
98	<a href="#">c3pqcA</a>	Alignment	not modelled	99.7	20	<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
99	<a href="#">c2j3eA</a>	Alignment	not modelled	99.7	16	<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 atoc33 and pstoc159
100	<a href="#">c4ak9A</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cpfts; y; <b>PDBTitle:</b> structure of chloroplast ftsy from physcomitrella patens
101	<a href="#">c5j3qB</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> signal recognition particle receptor subunit alpha; <b>PDBTitle:</b> structure of the gtpase heterodimer of human srp54 and sralpha
102	<a href="#">d1f60a3</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
103	<a href="#">c1d2eA</a>	Alignment	not modelled	99.7	20	<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
104	<a href="#">c2elfA_</a>	Alignment	not modelled	99.7	15	<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
105	<a href="#">d1kk1a3</a>	Alignment	not modelled	99.7	18	<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="#">c2qptA_</a>	Alignment	not modelled	99.7	18	<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
107	<a href="#">d1d2ea3</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
108	<a href="#">c5oxfB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> gtp-binding protein; <b>PDBTitle:</b> an oligomerised bacterial dynamin pair provides a mechanism for the2 long range sensing and tethering of membranes
109	<a href="#">c3wyaA_</a>	Alignment	not modelled	99.7	20	<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
110	<a href="#">c1skqB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor 1-alpha; <b>PDBTitle:</b> the crystal structure of sulfolobus solfataricus elongation factor 1-2 alpha in complex with magnesium and gdp
111	<a href="#">c2cnwF_</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> signal recognition <b>Chain:</b> F; <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> gdpalf4 complex of the srp gtpases ffh and ftsy
112	<a href="#">d2c78a3</a>	Alignment	not modelled	99.7	18	<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="#">d1g7sa4</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
114	<a href="#">c3zjcC_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> gtpase imap family member 7; <b>PDBTitle:</b> crystal structure of gmppnp-bound human gimap7 I100q variant
115	<a href="#">c3vr1B_</a>	Alignment	not modelled	99.6	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
116	<a href="#">d1egaa1</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
117	<a href="#">c5ee1A_</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> obg-like atpase 1; <b>PDBTitle:</b> crystal structure of ozychf1 at ph 7.85
118	<a href="#">c5ymxB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> signaling protein, hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> mutual gliding-motility protein mgla; <b>PDBTitle:</b> myxococcus xanthus mgla in gdp bound conformation
119	<a href="#">c1mj1A_</a>	Alignment	not modelled	99.6	21	<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
120	<a href="#">c2qu8A_</a>	Alignment	not modelled	99.6	17	<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