





























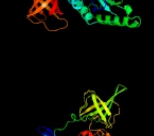


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1286_(cysN)_1438913_1440757
Date	Wed Jul 31 22:05:38 BST 2019
Unique Job ID	041d00995919a682

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3izq1_</a>	 Alignment		100.0	28	<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
2	<a href="#">c3agiC_</a>	 Alignment		100.0	32	<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
3	<a href="#">c1g7cA_</a>	 Alignment		100.0	29	<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
4	<a href="#">c4crnP_</a>	 Alignment		100.0	28	<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
5	<a href="#">c4zkeA_</a>	 Alignment		100.0	20	<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.
6	<a href="#">c1skqB_</a>	 Alignment		100.0	32	<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
7	<a href="#">c3j2k7_</a>	 Alignment		100.0	26	<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
8	<a href="#">c3aggA_</a>	 Alignment		100.0	22	<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
9	<a href="#">c1zunB_</a>	 Alignment		100.0	52	<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
10	<a href="#">c3wyaA_</a>	 Alignment		100.0	33	<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
11	<a href="#">c3mmpC_</a>	 Alignment		100.0	24	<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

12	<a href="#">c3p27A_</a>	Alignment		100.0	28	<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
13	<a href="#">c1r5nA_</a>	Alignment		100.0	30	<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
14	<a href="#">c3mcaA_</a>	Alignment		100.0	25	<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="#">c1d2eA_</a>	Alignment		100.0	24	<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
16	<a href="#">c1mj1A_</a>	Alignment		100.0	25	<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
17	<a href="#">c2bvnB_</a>	Alignment		100.0	24	<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
18	<a href="#">c2elfA_</a>	Alignment		100.0	17	<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
19	<a href="#">c1kk3A_</a>	Alignment		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+
20	<a href="#">c2hdnJ_</a>	Alignment		100.0	21	<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
21	<a href="#">c5k0yS_</a>	Alignment	not modelled	100.0	16	<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
22	<a href="#">c4zu9A_</a>	Alignment	not modelled	100.0	26	<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
23	<a href="#">c3j81k_</a>	Alignment	not modelled	100.0	18	<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
24	<a href="#">c5izmA_</a>	Alignment	not modelled	100.0	19	<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
25	<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 sulfolobus solfataricus in the nucleotide-free form.
26	<a href="#">c1s0uA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor 2 gamma subunit; <b>PDBTitle:</b> eif2gamma apo
27	<a href="#">c1wb1C_</a>	Alignment	not modelled	100.0	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
28	<a href="#">c5izkB_</a>	Alignment	not modelled	100.0	18	<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
29	<a href="#">c4zciA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> gtp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> gtp-binding protein tya/bipa; <b>PDBTitle:</b> crystal structure of escherichia coli gtpase bipa/tya
30	<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
31	<a href="#">c2ywfA_</a>	Alignment	not modelled	100.0	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
32	<a href="#">c3e1yG_</a>	Alignment	not modelled	100.0	21	<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
33	<a href="#">c2dy1A_</a>	Alignment	not modelled	100.0	23	<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
34	<a href="#">c3e20A_</a>	Alignment	not modelled	100.0	23	<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
35	<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
36	<a href="#">c3j4jA_</a>	Alignment	not modelled	100.0	27	<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
37	<a href="#">c4byrP_</a>	Alignment	not modelled	100.0	22	<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
38	<a href="#">c1zo1_</a>	Alignment	not modelled	100.0	22	<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
39	<a href="#">c3j25A_</a>	Alignment	not modelled	100.0	26	<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
40	<a href="#">c4qjty_</a>	Alignment	not modelled	100.0	21	<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
41	<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
42	<a href="#">c4kzD_</a>	Alignment	not modelled	100.0	28	<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)
43	<a href="#">c3wbkB_</a>	Alignment	not modelled	100.0	22	<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
44	<a href="#">c1xnjB_</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> aps complex of human paps synthetase 1
45	<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
46	<a href="#">c4upyB_</a>	Alignment	not modelled	100.0	20	<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
47	<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
48	<a href="#">c4fn5A_</a>	Alignment	not modelled	100.0	22	<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
49	<a href="#">c3tr5C_</a>	Alignment	not modelled	100.0	22	<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
50	<a href="#">c4nclB_</a>	Alignment	not modelled	100.0	21	<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
51	<a href="#">c1g7tA_</a>	Alignment	not modelled	100.0	23	<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
52	<a href="#">d1f60a3</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
53	<a href="#">c2bm0A_</a>	Alignment	not modelled	100.0	24	<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

54	<a href="#">c2xexA</a>	Alignment	not modelled	100.0	23	<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
55	<a href="#">c3izyP</a>	Alignment	not modelled	100.0	25	<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
56	<a href="#">c3jcrB</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> splicing <b>Chain:</b> B: <b>PDB Molecule:</b> hsnu114; <b>PDBTitle:</b> 3d structure determination of the human* <u>4/u6.u5*</u> tri-snrnp complex
57	<a href="#">c3j38z</a>	Alignment	not modelled	100.0	22	<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
58	<a href="#">c4byxV</a>	Alignment	not modelled	100.0	23	<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
59	<a href="#">c1zn0B</a>	Alignment	not modelled	100.0	24	<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
60	<a href="#">c4n3nA</a>	Alignment	not modelled	100.0	24	<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
61	<a href="#">c2rdo7</a>	Alignment	not modelled	100.0	20	<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
62	<a href="#">c3b8hA</a>	Alignment	not modelled	100.0	22	<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
63	<a href="#">c5mqfB</a>	Alignment	not modelled	100.0	23	<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)
64	<a href="#">c5ganC</a>	Alignment	not modelled	100.0	22	<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 at2 3.7 angstrom
65	<a href="#">c5lj3C</a>	Alignment	not modelled	100.0	20	<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 after2 branching
66	<a href="#">c5h7lB</a>	Alignment	not modelled	100.0	23	<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
67	<a href="#">c5z58C</a>	Alignment	not modelled	100.0	23	<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 bact) at 4.92 angstrom.
68	<a href="#">c3jb9B</a>	Alignment	not modelled	100.0	25	<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
69	<a href="#">c2h5eB</a>	Alignment	not modelled	100.0	23	<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
70	<a href="#">c5ancK</a>	Alignment	not modelled	100.0	28	<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
71	<a href="#">c1m8pB</a>	Alignment	not modelled	100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> crystal structure of p. chrysogenum atp sulfurylase in the t-state
72	<a href="#">d1zunb3</a>	Alignment	not modelled	100.0	58	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
73	<a href="#">c1xjqA</a>	Alignment	not modelled	100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional 3'-phosphoadenosine 5'-phosphosulfate <b>PDBTitle:</b> adp complex of human paps synthetase 1
74	<a href="#">c6notB</a>	Alignment	not modelled	100.0	24	<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) from2 rickettsia prowazekii
75	<a href="#">c2gksB</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional sat/aps kinase; <b>PDBTitle:</b> crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
76	<a href="#">c3cr8C</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfate adenylyltransferase, adenylylsulfate kinase; <b>PDBTitle:</b> hexameric aps kinase from thiobacillus denitrificans
77	<a href="#">d1jnya3</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
78	<a href="#">c3uieB</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> adenylyl-sulfate kinase 1, chloroplastic; <b>PDBTitle:</b> crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with ampnpn and aps

79	<a href="#">c4bzbB</a>	Alignment	not modelled	100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional enzyme cysn/cytc; <b>PDBTitle:</b> structure of the mycobacterium tuberculosis aps kinase cysc2 in complex with adp
80	<a href="#">d1r5ba3</a>	Alignment	not modelled	100.0	38	<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="#">d1m7ga</a>	Alignment	not modelled	100.0	46	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'-phosphosulfate kinase (APS kinase)
82	<a href="#">c5cb6A</a>	Alignment	not modelled	100.0	49	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable adenylyl-sulfate kinase; <b>PDBTitle:</b> structure of adenosine-5'-phosphosulfate kinase
83	<a href="#">c2yvua</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable adenylyl-sulfate kinase; <b>PDBTitle:</b> crystal structure of ape1195
84	<a href="#">d1x6va3</a>	Alignment	not modelled	100.0	47	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'-phosphosulfate kinase (APS kinase)
85	<a href="#">d2c78a3</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
86	<a href="#">d1zunb2</a>	Alignment	not modelled	100.0	44	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
87	<a href="#">d1m8pa3</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain
88	<a href="#">d1m7gb</a>	Alignment	not modelled	99.9	47	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Adenosine-5'-phosphosulfate kinase (APS kinase)
89	<a href="#">d1jnva2</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
90	<a href="#">d2dy1a2</a>	Alignment	not modelled	99.9	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="#">d1f60a2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
92	<a href="#">d1n0ua2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
93	<a href="#">d1d2ea3</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
94	<a href="#">c6b8vA</a>	Alignment	not modelled	99.9	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylylsulfate kinase; <b>PDBTitle:</b> crystal structure of adenylyl-sulfate kinase from cryptococcus2 neoformans
95	<a href="#">d1g8fa3</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain
96	<a href="#">c1mkyA</a>	Alignment	not modelled	99.9	29	<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
97	<a href="#">d2bv3a2</a>	Alignment	not modelled	99.9	24	<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="#">c1g8gB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfate adenylyltransferase; <b>PDBTitle:</b> atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
99	<a href="#">c2higA</a>	Alignment	not modelled	99.9	26	<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
100	<a href="#">c5dn8A</a>	Alignment	not modelled	99.9	36	<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.
101	<a href="#">d1zunb1</a>	Alignment	not modelled	99.9	50	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
102	<a href="#">c3j8gX</a>	Alignment	not modelled	99.9	32	<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
103	<a href="#">d1efca3</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> G proteins
104	<a href="#">d1knqa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Gluconate kinase
105	<a href="#">c2e87A</a>	Alignment	not modelled	99.9	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 <b>PDB header:</b> unknown function



106	<a href="#">c2rhmD_</a>	Alignment	not modelled	99.9	16	<b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
107	<a href="#">d1kk1a1</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
108	<a href="#">d1jnya1</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
109	<a href="#">c3t61A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconokinase; <b>PDBTitle:</b> crystal structure of a gluconokinase from sinorhizobium meliloti 1021
110	<a href="#">c4eunA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> thermoreistant glucokinase; <b>PDBTitle:</b> crystal structure of a sugar kinase (target efi-502144 from janibacter2 sp. htcc2649), unliganded structure
111	<a href="#">d1kk1a3</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
112	<a href="#">d1f60a1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
113	<a href="#">c2qthA_</a>	Alignment	not modelled	99.8	21	<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
114	<a href="#">d1bifa1</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> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
115	<a href="#">c2pt5D_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> shikimate kinase; <b>PDBTitle:</b> crystal structure of shikimate kinase (aq_2177) from aquifex aeolicus2 vf5
116	<a href="#">d1s0ua1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
117	<a href="#">c2vliB_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> antibiotic resistance protein; <b>PDBTitle:</b> structure of deinococcus radiodurans tunicamycin resistance protein
118	<a href="#">c4xrpA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> pnkp1; <b>PDBTitle:</b> structure of the pnkp1/rnl/hen1 rna repair complex
119	<a href="#">d1d2ea1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
120	<a href="#">d1efca1</a>	Alignment	not modelled	99.8	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors