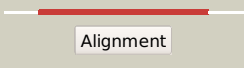

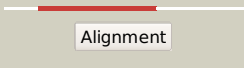

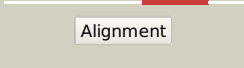

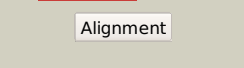

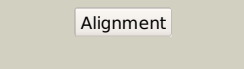
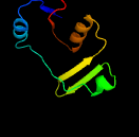
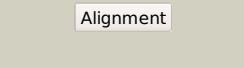

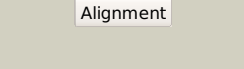

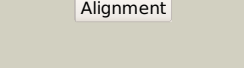

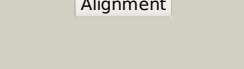
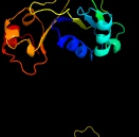
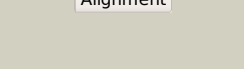

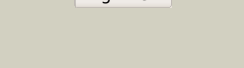





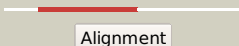
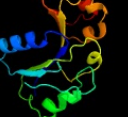
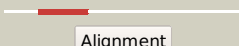





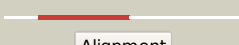







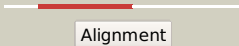
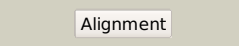
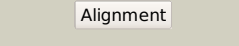





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0106 (-)_124371_125567
Date	Tue Jul 23 14:50:14 BST 2019
Unique Job ID	2102d082ffb7a9ef

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nija_	 Alignment		100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
2	d1nija1	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
3	d1nija2	 Alignment		99.8	18	Fold: Hypothetical protein YjiA, C-terminal domain Superfamily: Hypothetical protein YjiA, C-terminal domain Family: Hypothetical protein YjiA, C-terminal domain
4	c4lpsA_	 Alignment		99.0	13	PDB header: metal binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein hypb; PDBTitle: crystal structure of hypb from helicobacter pylori in complex with2 nickel
5	c4nkrB_	 Alignment		98.7	20	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
6	c4xc8B_	 Alignment		98.7	16	PDB header: isomerase Chain: B: PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
7	c2hf9A_	 Alignment		98.6	15	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
8	c5xktA_	 Alignment		98.4	14	PDB header: hydrolase Chain: A: PDB Molecule: urease accessory protein ureg; PDBTitle: klebsiella pneumoniae ureg in complex with gmppnp and nickel
9	c4hi0F_	 Alignment		98.4	12	PDB header: metal binding protein Chain: F: PDB Molecule: urease accessory protein ureg; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h/g complex
10	c5ck3D_	 Alignment		98.4	8	PDB header: signaling protein Chain: D: PDB Molecule: putative signal recognition particle protein; PDBTitle: signal recognition particle receptor srb-gtp/srx complex from2 chaetomium thermophilum
11	d2qm8a1	 Alignment		98.2	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like

12	c3nxsA_	 Alignment		98.2	11	PDB header: transport protein Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
13	d1yrba1	 Alignment		98.2	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
14	c2wsmB_	 Alignment		98.1	19	PDB header: metal binding protein Chain: B: PDB Molecule: hydrogenase expression/formation protein (hyhb); PDBTitle: crystal structure of hydrogenase maturation factor hyhb from2 archaeoglobus fulgidus
15	c2f1rA_	 Alignment		97.5	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
16	d2p67a1	 Alignment		97.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
17	c5hcnA_	 Alignment		97.3	8	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
18	d2dy1a2	 Alignment		97.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
19	c3md0A_	 Alignment		97.0	12	PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system atpase from2 mycobacterium tuberculosis bound to gdp (a ras-like gtpase3 superfamily protein)
20	c5l3rC_	 Alignment		96.9	17	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
21	c5ady6_	 Alignment	not modelled	96.8	13	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
22	c5l3qB_	 Alignment	not modelled	96.7	13	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
23	c5mvfA_	 Alignment	not modelled	96.7	21	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein 4; PDBTitle: active structure of ehd4 complexed with adp
24	c5l3sF_	 Alignment	not modelled	96.6	13	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
25	c2e87A_	 Alignment	not modelled	96.5	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1320; PDBTitle: crystal structure of hypothetical gtp-binding protein ph1320 from2 pyrococcus horikoshii ot3, in complex with gdp
26	d1qzxa3	 Alignment	not modelled	96.5	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
27	c3dmdA_	 Alignment	not modelled	96.2	13	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
28	c4n3nA_	 Alignment	not modelled	96.2	8	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 5b-like protein,

						PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-1116) from chaetomium thermophilum, apo form
29	d1vmaa2	Alignment	not modelled	96.1	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	c1g7tA_	Alignment	not modelled	95.9	12	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if2/eif5b; PDBTitle: x-ray structure of translation initiation factor if2/eif5b2 complexed with gdnpp
31	c2iy3A_	Alignment	not modelled	95.9	14	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
32	c2qptA_	Alignment	not modelled	95.8	19	PDB header: endocytosis Chain: A: PDB Molecule: eh domain-containing protein-2; PDBTitle: crystal structure of an ehd atpase involved in membrane remodelling
33	c2wwwB_	Alignment	not modelled	95.8	18	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
34	c2qagB_	Alignment	not modelled	95.8	13	PDB header: cell cycle, structural protein Chain: B: PDB Molecule: septin-6; PDBTitle: crystal structure of human septin trimer 2/6/7
35	c3wbkB_	Alignment	not modelled	95.8	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b; PDBTitle: crystal structure analysis of eukaryotic translation initiation factor2 5b and 1a complex
36	c3vr1B_	Alignment	not modelled	95.8	10	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
37	d1ls1a2	Alignment	not modelled	95.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
38	c3b9qA_	Alignment	not modelled	95.7	20	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
39	c4zciA_	Alignment	not modelled	95.7	16	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
40	c2v3cC_	Alignment	not modelled	95.6	8	PDB header: signaling protein Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
41	c1zu4A_	Alignment	not modelled	95.6	11	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
42	c4ak9A_	Alignment	not modelled	95.4	16	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsyt from physcomitrella patens
43	c2qthA_	Alignment	not modelled	95.4	16	PDB header: nucleotide binding protein Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of a gtp-binding protein from the hyperthermophilic2 archaeon sulfolobus solfataricus in complex with gdp
44	c2qy9A_	Alignment	not modelled	95.2	13	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsyt
45	c2bm0A_	Alignment	not modelled	95.2	17	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
46	c4upyB_	Alignment	not modelled	95.2	15	PDB header: ribosome Chain: B: PDB Molecule: eif5b; PDBTitle: mammalian 80s hcv-ires initiation complex with eif5b pre-like state
47	c3jcrB_	Alignment	not modelled	95.1	11	PDB header: splicing Chain: B: PDB Molecule: hsnu114; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snnp complex
48	c1egaB_	Alignment	not modelled	95.0	15	PDB header: hydrolase Chain: B: PDB Molecule: protein (gtp-binding protein era); PDBTitle: crystal structure of a widely conserved gtpase era
49	c2wooC_	Alignment	not modelled	95.0	14	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
50	c3degC_	Alignment	not modelled	94.9	12	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
51	c2q9cA_	Alignment	not modelled	94.9	18	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of ftsyt:gmppnp with mgcl complex
52	c2ywfA_	Alignment	not modelled	94.9	11	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
53	c1wb1C_	Alignment	not modelled	94.8	12	PDB header: protein synthesis Chain: C: PDB Molecule: translation elongation factor selb; PDBTitle: crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein;

54	c3dm5A_	Alignment	not modelled	94.8	13	PDBTitle: structures of srp54 and srp19, the two proteins assembling the 2 ribonucleic core of the signal recognition particle from the archaeon 3 pyrococcus furiosus.
55	c3cioA_	Alignment	not modelled	94.7	15	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
56	c3la6P_	Alignment	not modelled	94.7	13	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound 2 adp
57	c2h5eB_	Alignment	not modelled	94.7	17	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
58	c4b3xA_	Alignment	not modelled	94.6	10	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: bacterial translation initiation factor if2 (1-363), apo form
59	c3gehA_	Alignment	not modelled	94.5	20	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
60	c2gzaB_	Alignment	not modelled	94.4	14	PDB header: hydrolase Chain: B: PDB Molecule: type iv secretion system protein virb11; PDBTitle: crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
61	c3agiC_	Alignment	not modelled	94.3	9	PDB header: translation/hydrolase Chain: C: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
62	c4ii7D_	Alignment	not modelled	94.3	15	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaeum assembly atpase flai
63	c2px0D_	Alignment	not modelled	94.0	11	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnp/mg(2+)
64	c2cnwF_	Alignment	not modelled	93.8	14	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
65	c6em5b_	Alignment	not modelled	93.8	16	PDB header: ribosome Chain: B: PDB Molecule: 60s ribosomal protein l3; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the 2 assembly pathway of nucleolar pre-60s ribosomes
66	c3k53B_	Alignment	not modelled	93.7	21	PDB header: metal transport Chain: B: PDB Molecule: ferrous iron transport protein b; PDBTitle: crystal structure of nfeob from p. furiosus
67	c2xexA_	Alignment	not modelled	93.7	23	PDB header: translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor 2 g
68	d1g6oa_	Alignment	not modelled	93.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	c1xzqA_	Alignment	not modelled	93.5	13	PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
70	c5z58C_	Alignment	not modelled	93.4	13	PDB header: splicing Chain: C: PDB Molecule: 116 kda u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
71	c5k0yS_	Alignment	not modelled	93.4	11	PDB header: translation Chain: S: PDB Molecule: eukaryotic initiation factor 2 gamma subunit (eif2-gamma); PDBTitle: m48s late-stage initiation complex, purified from rabbit reticulocytes2 lysates, displaying eif2 ternary complex and eif3 i and g subunits3 relocated to the intersubunit face
72	c1d2eA_	Alignment	not modelled	93.4	10	PDB header: rna binding protein Chain: A: PDB Molecule: elongation factor tu (ef-tu); PDBTitle: crystal structure of mitochondrial ef-tu in complex with gdp
73	c3qq5A_	Alignment	not modelled	93.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: small gtp-binding protein; PDBTitle: crystal structure of the [fefe]-hydrogenase maturation protein hydf
74	d1jala1	Alignment	not modelled	93.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
75	c6cy1B_	Alignment	not modelled	93.2	12	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from 2 elizabethkingia anophelis
76	d1n0ua2	Alignment	not modelled	93.2	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
77	c2oaq1_	Alignment	not modelled	93.0	21	PDB header: hydrolase Chain: 1: PDB Molecule: type ii secretion system protein; PDBTitle: crystal structure of the archaeal secretion atpase gspe in complex2 with phosphate
78	c3j4jA_	Alignment	not modelled	93.0	13	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: model of full-length t. thermophilus translation initiation factor 22 refined against its cryo-em density from a 30s initiation complex map
79	c1g7cA_	Alignment	not modelled	93.0	6	PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha;

						PDBTitle: yeast eef1a:eef1ba in complex with gdpnp
80	c3lxxA_	Alignment	not modelled	92.9	16	PDB header: immune system Chain: A: PDB Molecule: gtpase imap family member 4; PDBTitle: crystal structure of human gtpase imap family member 4
81	c2j7pA_	Alignment	not modelled	92.8	17	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
82	c4zu9A_	Alignment	not modelled	92.6	14	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
83	c5h7lB_	Alignment	not modelled	92.6	20	PDB header: translation/ribosomal protein Chain: B: PDB Molecule: elongation factor 2; PDBTitle: complex of elongation factor 2-50s ribosomal protein l12
84	c2j37W_	Alignment	not modelled	92.3	11	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
85	c5gafi_	Alignment	not modelled	92.3	13	PDB header: ribosome Chain: l: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
86	c2og2A_	Alignment	not modelled	92.2	18	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
87	d1rkba_	Alignment	not modelled	92.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
88	c2xj9B_	Alignment	not modelled	91.9	11	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
89	c2rdo7_	Alignment	not modelled	91.6	12	PDB header: ribosome Chain: 7: PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdpnp) and rrf bound
90	d2afhe1	Alignment	not modelled	91.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
91	c4phtC_	Alignment	not modelled	91.2	18	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspl from the2 vibrio vulnificus type ii secretion system
92	c2yhsA_	Alignment	not modelled	91.2	16	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
93	c1r5nA_	Alignment	not modelled	91.1	8	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor gtp- PDBTitle: crystal structure analysis of sup35 complexed with gdp
94	c2bvnB_	Alignment	not modelled	91.1	15	PDB header: elongation factor Chain: B: PDB Molecule: elongation factor tu; PDBTitle: e. coli ef-tu:gdpnp in complex with the antibiotic enacyloxin iia
95	c3tr5C_	Alignment	not modelled	90.9	13	PDB header: translation Chain: C: PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
96	c5izkB_	Alignment	not modelled	90.8	17	PDB header: translation Chain: B: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: the crystal structure of human eefsec in complex with gdp
97	c1vmaA_	Alignment	not modelled	90.6	17	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
98	d1g7sa4	Alignment	not modelled	90.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
99	c3akcA_	Alignment	not modelled	90.3	11	PDB header: transferase Chain: A: PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
100	c5f4hF_	Alignment	not modelled	90.3	22	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
101	c3ibgF_	Alignment	not modelled	90.1	15	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
102	c3b8hA_	Alignment	not modelled	90.0	13	PDB header: biosynthetic protein/transferase Chain: A: PDB Molecule: elongation factor 2; PDBTitle: structure of the eef2-exoa(e546a)-nad+ complex
103	c2dy1A_	Alignment	not modelled	89.7	21	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
104	c2q3fB_	Alignment	not modelled	89.2	4	PDB header: protein binding Chain: B: PDB Molecule: ras-related gtp-binding protein d; PDBTitle: x-ray crystal structure of putative human ras-related gtp2 binding d in complex with gmppnp
105	c4ehxA_	Alignment	not modelled	89.2	16	PDB header: transferase Chain: A: PDB Molecule: tetraacyldisaccharide 4'-kinase; PDBTitle: crystal structure of lpxk from aquifex aeolicus at 1.9 angstrom2 resolution

106	c3j38z_	Alignment	not modelled	89.1	14	PDB header: ribosome Chain: Z: PDB Molecule: 40s ribosomal protein s25; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
107	d1p9ra_	Alignment	not modelled	89.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
108	c3jvvA_	Alignment	not modelled	89.1	33	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-ppc
109	c5fl3A_	Alignment	not modelled	89.0	20	PDB header: transport protein Chain: A: PDB Molecule: pili retraction protein pilt; PDBTitle: pilt2 from thermus thermophilus
110	c2gc6A_	Alignment	not modelled	88.9	14	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
111	c5it5B_	Alignment	not modelled	88.8	22	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
112	d1e8ca3	Alignment	not modelled	88.7	11	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
113	d2qy9a2	Alignment	not modelled	88.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
114	c5uz4Z_	Alignment	not modelled	88.4	20	PDB header: ribosome/hydrolase Chain: Z: PDB Molecule: small ribosomal subunit biogenesis gtpase rsga; PDBTitle: the cryo-em structure of yjeq bound to the 30s subunit suggests a2 fidelity checkpoint function for this protein in ribosome assembly
115	c2elfA_	Alignment	not modelled	88.3	13	PDB header: translation Chain: A: PDB Molecule: protein translation elongation factor 1a; PDBTitle: crystal structure of the selb-like elongation factor ef-pyl from2 methanosarcina mazei
116	c3zq6D_	Alignment	not modelled	88.1	20	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
117	c4xrpA_	Alignment	not modelled	88.0	19	PDB header: protein binding Chain: A: PDB Molecule: pnkp1; PDBTitle: structure of the pnkp1/rnl/hen1 rna repair complex
118	c4kssC_	Alignment	not modelled	87.4	18	PDB header: protein transport Chain: C: PDB Molecule: type ii secretion system protein e, hemolysin-coregulated PDBTitle: crystal structure of vibrio cholerae atpase gspse hexamer
119	d1kgda_	Alignment	not modelled	87.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
120	c5d6aA_	Alignment	not modelled	87.4	13	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase of the abc class; PDBTitle: 2.7 angstrom crystal structure of abc transporter atpase from vibrio2 vulnificus in complex with adenylyl-imidodiphosphate (amp-pnp)