


















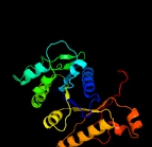




Phyre2

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Description	RVBD3876 (-)_4353188_4355188
Date	Sat Aug 10 22:05:06 BST 2019
Unique Job ID	84be79a9517a6b18

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ea0B_	 Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
2	d2afhe1	 Alignment		100.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
3	c3endA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
4	c51ljA_	 Alignment		100.0	20	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
5	d1cp2a_	 Alignment		100.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
6	c4rz3B_	 Alignment		100.0	20	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
7	c3q9lB_	 Alignment		100.0	18	PDB header: cell cycle, hydrolase Chain: B: PDB Molecule: septum site-determining protein mind; PDBTitle: the structure of the dimeric e.coli mind-atp complex
8	d1iona_	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
9	d1g3qa_	 Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
10	c3fkqA_	 Alignment		100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
11	c2ozeA_	 Alignment		100.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes

12	d1hyqa_	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
13	c1hyqA_	Alignment		100.0	23	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
14	c3ez6B_	Alignment		100.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
15	c6iucC_	Alignment		100.0	20	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
16	c2bekB_	Alignment		100.0	20	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
17	c6nonB_	Alignment		100.0	18	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
18	c3vx3A_	Alignment		100.0	20	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [hife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
19	c2ph1A_	Alignment		100.0	16	PDB header: ligand binding protein Chain: A: PDB Molecule: nucleotide-binding protein; PDBTitle: crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
20	c4v02B_	Alignment		100.0	21	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
21	c6g2gA_	Alignment	not modelled	100.0	15	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
22	c3kjgB_	Alignment	not modelled	100.0	22	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
23	c3k9gA_	Alignment	not modelled	100.0	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
24	c2wojD_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
25	c3cioA_	Alignment	not modelled	100.0	16	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
26	c3ezfA_	Alignment	not modelled	100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
27	c2xj9B_	Alignment	not modelled	100.0	17	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
28	c3la6P_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: P: PDB Molecule: tyrosine-protein kinase wzc; PDBTitle: octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
						PDB header: hydrolase

29	c3zq6D_	Alignment	not modelled	100.0	20	Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
30	c3pg5A_	Alignment	not modelled	99.9	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
31	c4pfsA_	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
32	c4ru8C_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
33	d1byia_	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
34	c2vedA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
35	c2wooC_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
36	c4dzzB_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
37	c3ug7D_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
38	c5bwkA_	Alignment	not modelled	99.9	21	PDB header: hydrolase/transport Chain: A: PDB Molecule: atpase get3; PDBTitle: 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae
39	c6bs3A_	Alignment	not modelled	99.9	21	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
40	d1ihua1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
41	d1ihua2	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
42	c1ii0A_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
43	c6bs5B_	Alignment	not modelled	99.9	25	PDB header: unknown function Chain: B: PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
44	c3ibgF_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
45	c5zmfA_	Alignment	not modelled	99.9	17	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
46	c3io3A_	Alignment	not modelled	99.9	18	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
47	c3of5A_	Alignment	not modelled	99.9	10	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
48	c3cwqB_	Alignment	not modelled	99.9	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: para family chromosome partitioning protein; PDBTitle: crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
49	c2qmoA_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
50	c3igfB_	Alignment	not modelled	99.8	14	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
51	c3fmfA_	Alignment	not modelled	99.8	17	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
52	c2qy9A_	Alignment	not modelled	99.3	17	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
53	c5l3qB_	Alignment	not modelled	99.3	18	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
						PDB header: protein transport

54	c1zu4A_	Alignment	not modelled	99.3	17	Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
55	c1vmaA_	Alignment	not modelled	99.2	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
56	c2cnwF_	Alignment	not modelled	99.2	17	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
57	c5l3sF_	Alignment	not modelled	99.2	24	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
58	c5l3rC_	Alignment	not modelled	99.2	14	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
59	c2og2A_	Alignment	not modelled	99.2	19	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
60	c2yhsA_	Alignment	not modelled	99.1	15	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
61	c2q9cA_	Alignment	not modelled	99.1	21	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
62	c6cy1B_	Alignment	not modelled	99.1	16	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
63	c2j7pA_	Alignment	not modelled	99.0	18	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
64	c3b9qA_	Alignment	not modelled	99.0	16	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyl from arabidopsis thaliana
65	c2iy3A_	Alignment	not modelled	99.0	20	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
66	c5gafi_	Alignment	not modelled	99.0	19	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
67	c3dm5A_	Alignment	not modelled	99.0	14	PDB header: rna binding protein, transport protein Chain: A: PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
68	c2j37W_	Alignment	not modelled	99.0	17	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
69	c4ak9A_	Alignment	not modelled	99.0	20	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
70	c1qzwC_	Alignment	not modelled	98.9	16	PDB header: signaling protein/rna Chain: C: PDB Molecule: signal recognition 54 kda protein; PDBTitle: crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
71	c3dmdA_	Alignment	not modelled	98.8	18	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
72	c2v3cC_	Alignment	not modelled	98.7	16	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
73	c2j289_	Alignment	not modelled	98.7	18	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
74	d1vmaa2	Alignment	not modelled	98.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	d1qzxa3	Alignment	not modelled	98.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d2qm8a1	Alignment	not modelled	98.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c4xc8B_	Alignment	not modelled	98.4	21	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)
78	c2npiB_	Alignment	not modelled	98.4	18	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
79	c2px0D_	Alignment	not modelled	98.2	22	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)

80	d2qy9a2	Alignment	not modelled	98.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	c2h5eB	Alignment	not modelled	98.1	22	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
82	c3tr5C	Alignment	not modelled	98.1	22	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
83	c3cr8C	Alignment	not modelled	98.0	24	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans
84	c5hcnA	Alignment	not modelled	98.0	14	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
85	d1nija1	Alignment	not modelled	97.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	c4a0gC	Alignment	not modelled	97.9	17	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxonanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
87	d2p67a1	Alignment	not modelled	97.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
88	d1j8yf2	Alignment	not modelled	97.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	c1j8yF	Alignment	not modelled	97.8	16	PDB header: signaling protein Chain: F: PDB Molecule: signal recognition 54 kda protein; PDBTitle: signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
90	d1nlfa	Alignment	not modelled	97.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
91	c4ohvA	Alignment	not modelled	97.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
92	c4zciA	Alignment	not modelled	97.7	23	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
93	c4fn5A	Alignment	not modelled	97.7	20	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyri2 b
94	c2j69D	Alignment	not modelled	97.7	15	PDB header: hydrolase Chain: D: PDB Molecule: bacterial dynamin-like protein; PDBTitle: bacterial dynamin-like protein bdlp
95	c4wiaA	Alignment	not modelled	97.7	8	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
96	c5dn8A	Alignment	not modelled	97.7	25	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
97	c2ywfA	Alignment	not modelled	97.6	24	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
98	c2dy1A	Alignment	not modelled	97.6	22	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from thermus thermophilus
99	c2recB	Alignment	not modelled	97.6	21	PDB header: helicase PDB COMPND:
100	c1zunB	Alignment	not modelled	97.6	19	PDB header: transferase Chain: B: PDB Molecule: sulfate adenylyltransferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
101	c4zc0A	Alignment	not modelled	97.6	9	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
102	c3bgwD	Alignment	not modelled	97.5	10	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
103	c2j3eA	Alignment	not modelled	97.5	14	PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components atoc33 and pstoc159
104	c4zu9A	Alignment	not modelled	97.5	20	PDB header: translation Chain: A: PDB Molecule: elongation factor selb; PDBTitle: crystal structure of bacterial selenocysteine-specific elongation2 factor ef-sec
105	d1yrba1	Alignment	not modelled	97.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
						Fold: P-loop containing nucleoside triphosphate hydrolases

106	d2dy1a2	Alignment	not modelled	97.5	25	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
107	c4nkrB_	Alignment	not modelled	97.5	15	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
108	c1mj1A_	Alignment	not modelled	97.5	18	PDB header: ribosome Chain: A: PDB Molecule: elongation factor tu; PDBTitle: fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
109	d1h65a_	Alignment	not modelled	97.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
110	c5ady6_	Alignment	not modelled	97.5	26	PDB header: ribosome Chain: 6: PDB Molecule: gtpase hflx; PDBTitle: cryo-em structures of the 50s ribosome subunit bound with hflx
111	c1nijA_	Alignment	not modelled	97.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
112	c2bm0A_	Alignment	not modelled	97.5	17	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
113	c2vyeA_	Alignment	not modelled	97.5	10	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dna-ssdna complex
114	d2bv3a2	Alignment	not modelled	97.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
115	c2wwwB_	Alignment	not modelled	97.5	14	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
116	c3jcrB_	Alignment	not modelled	97.5	17	PDB header: splicing Chain: B: PDB Molecule: hsnu114; PDBTitle: 3d structure determination of the human*u4/u6.u5* tri-snrrp complex
117	c4aurA_	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: A: PDB Molecule: leoa; PDBTitle: leoa bacterial dynamin gtpase from etec
118	c1d2eA_	Alignment	not modelled	97.5	26	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
119	c2f1rA_	Alignment	not modelled	97.5	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
120	c4lpsA_	Alignment	not modelled	97.5	14	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