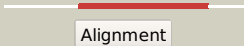

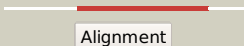

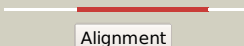
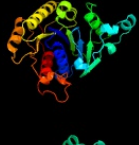






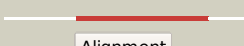











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3860_(-)_4336955_4338127
Date	Sat Aug 10 22:05:04 BST 2019
Unique Job ID	9e104dd742016a51

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2afhe1	 Alignment		100.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
2	c3endA	 Alignment		100.0	15	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
3	d1cp2a	 Alignment		100.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
4	c3ea0B	 Alignment		100.0	15	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
5	c4rz3B	 Alignment		100.0	17	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
6	c3ez6B	 Alignment		100.0	19	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
7	c511jA	 Alignment		100.0	19	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
8	c3q91B	 Alignment		100.0	15	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
9	d1iona	 Alignment		100.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
10	d1g3qa	 Alignment		100.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
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	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
13	c1hyqA_	Alignment		100.0	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
14	c3kjgB_	Alignment		100.0	17	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
15	c3fkqA_	Alignment		100.0	12	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
16	c6iucC_	Alignment		100.0	16	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
17	c6nonB_	Alignment		100.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
18	c2bekB_	Alignment		100.0	19	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
19	c3vx3A_	Alignment		100.0	21	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1
20	c3ezfA_	Alignment		100.0	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
21	c6g2gA_	Alignment	not modelled	100.0	19	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
22	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
23	c2ph1A_	Alignment	not modelled	100.0	19	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
24	c4v02B_	Alignment	not modelled	100.0	15	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
25	c3pg5A_	Alignment	not modelled	99.9	24	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
26	c3la6P_	Alignment	not modelled	99.9	16	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
27	c2wojD_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
28	c3cioA_	Alignment	not modelled	99.9	16	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk

29	c2xj9B_	Alignment	not modelled	99.9	15	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
30	c4ru8C_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
31	c4pfsA_	Alignment	not modelled	99.9	21	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	c2vedA_	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
33	c6bs3A_	Alignment	not modelled	99.9	23	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
34	c3zq6D_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
35	c4dzzB_	Alignment	not modelled	99.9	14	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
36	c2wooC_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
37	c5bwkA_	Alignment	not modelled	99.9	17	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
38	d1byia_	Alignment	not modelled	99.9	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
39	d1ihua1	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
40	d1ihua2	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	c1ii0A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
42	c5zmfA_	Alignment	not modelled	99.9	22	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
43	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
44	c3ug7D_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
45	c3io3A_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
46	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
47	c3ibgF_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
48	c3of5A_	Alignment	not modelled	99.8	9	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
49	c2qmoA_	Alignment	not modelled	99.8	12	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
50	c3igfB_	Alignment	not modelled	99.8	16	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	15	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	c5l3qB_	Alignment	not modelled	99.4	16	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
53	c2qy9A_	Alignment	not modelled	99.2	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 PDB header: protein transport

54	c1zu4A_	Alignment	not modelled	99.2	12	Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsyl from mycoplasma mycoides-space2 group p21212
55	c5l3rC_	Alignment	not modelled	99.2	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 ftsyl from2 arabidopsis thaliana
56	c1vmaA_	Alignment	not modelled	99.1	19	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: crystal structure of cell division protein ftsyl (tm0570) from2 thermotoga maritima at 1.60 a resolution
57	c2cnwF_	Alignment	not modelled	99.1	20	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsyl; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsyl
58	c2og2A_	Alignment	not modelled	99.1	14	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsyl from arabidopsis2 thaliana
59	c2j7pA_	Alignment	not modelled	99.1	19	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyl
60	c3dm5A_	Alignment	not modelled	99.1	16	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.
61	c6cy1B_	Alignment	not modelled	99.0	17	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsyl; PDBTitle: crystal structure of signal recognition particle receptor ftsyl from2 elizabethkingia anophelis
62	c2iy3A_	Alignment	not modelled	99.0	18	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
63	c5l3sF_	Alignment	not modelled	99.0	20	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsyl; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsyl
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	c2q9cA_	Alignment	not modelled	99.0	20	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: structure of ftsyl:gmppnp with mgcl complex
66	c2yhsA_	Alignment	not modelled	99.0	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsyl; PDBTitle: structure of the e. coli srp receptor ftsyl
67	c5gafi_	Alignment	not modelled	99.0	18	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
68	c2j37W_	Alignment	not modelled	99.0	18	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
69	c1qzwC_	Alignment	not modelled	98.9	15	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
70	c4ak9A_	Alignment	not modelled	98.9	16	PDB header: protein transport Chain: A: PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsyl from physcomitrella patens
71	c2v3cC_	Alignment	not modelled	98.8	17	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
72	c3dmdA_	Alignment	not modelled	98.7	16	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
73	d1qzxa3	Alignment	not modelled	98.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	c2j289_	Alignment	not modelled	98.6	13	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
75	c2px0D_	Alignment	not modelled	98.4	18	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
76	d1vmaa2	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c5hcnA_	Alignment	not modelled	98.0	18	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
78	c4xc8B_	Alignment	not modelled	98.0	15	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)
79	c2npiB_	Alignment	not modelled	97.9	16	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex

80	d2qm8a1	Alignment	not modelled	97.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	c4a0gC	Alignment	not modelled	97.7	13	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from <i>Arabidopsis thaliana</i> in its apo form.
82	d2qy9a2	Alignment	not modelled	97.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	c4ohvA	Alignment	not modelled	97.7	15	PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
84	c2f1rA	Alignment	not modelled	97.6	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
85	c4nkrB	Alignment	not modelled	97.6	19	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of <i>Bacillus subtilis</i> mobb
86	d1okkd2	Alignment	not modelled	97.5	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c3cr8C	Alignment	not modelled	97.5	13	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from <i>Thiobacillus denitrificans</i>
88	c2h5eB	Alignment	not modelled	97.5	19	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of <i>E. coli</i> polypeptide release factor rf3
89	c2recB	Alignment	not modelled	97.4	18	PDB header: helicase PDB COMPND:
90	d1x6va3	Alignment	not modelled	97.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'-phosphosulfate kinase (APS kinase)
91	c3tr5C	Alignment	not modelled	97.4	14	PDB header: translation Chain: C: PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from <i>Coxiella burnetii</i>
92	d1yrba1	Alignment	not modelled	97.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
93	c1xjqA	Alignment	not modelled	97.4	16	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: adp complex of human paps synthetase 1
94	d1ls1a2	Alignment	not modelled	97.4	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
95	d1nifa	Alignment	not modelled	97.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
96	c1xnjB	Alignment	not modelled	97.3	16	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
97	c5dn8A	Alignment	not modelled	97.3	17	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from <i>Coxiella burnetii</i> in complex with gdp.
98	c4fn5A	Alignment	not modelled	97.3	20	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (<i>Pseudomonas aeruginosa</i>) in complex with argyrin2 b
99	d1xjca	Alignment	not modelled	97.3	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	c2dy1A	Alignment	not modelled	97.2	20	PDB header: signaling protein, translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of ef-g-2 from <i>Thermus thermophilus</i>
101	c3degC	Alignment	not modelled	97.2	13	PDB header: ribosome Chain: C: PDB Molecule: gtp-binding protein lepa; PDBTitle: complex of elongating <i>Escherichia coli</i> 70s ribosome and ef4(lepa)-2 gmppnp
102	c4zc0A	Alignment	not modelled	97.2	13	PDB header: helicase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
103	c3bgwD	Alignment	not modelled	97.2	13	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
104	d2dy1a2	Alignment	not modelled	97.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
105	c1xp8A	Alignment	not modelled	97.2	18	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s PDB header: elongation factor

106	c2bm0A_	Alignment	not modelled	97.1	17	Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
107	d1nija1	Alignment	not modelled	97.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
108	d1mo6a1	Alignment	not modelled	97.1	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
109	c3vr1B_	Alignment	not modelled	97.0	12	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor 3; PDBTitle: crystal structure analysis of the translation factor rf3
110	c1mkya_	Alignment	not modelled	97.0	19	PDB header: ligand binding protein Chain: A: PDB Molecule: probable gtp-binding protein enga; PDBTitle: structural analysis of the domain interactions in der, a switch2 protein containing two gtpase domains
111	c4zciA_	Alignment	not modelled	97.0	20	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
112	c5h7lB_	Alignment	not modelled	97.0	13	PDB header: translation/ribosomal protein Chain: B: PDB Molecule: elongation factor 2; PDBTitle: complex of elongation factor 2-50s ribosomal protein l12
113	d1j8yf2	Alignment	not modelled	97.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
114	c2ywfA_	Alignment	not modelled	97.0	13	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
115	c2vyeA_	Alignment	not modelled	97.0	14	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dna-c-ssdna complex
116	c1fnnB_	Alignment	not modelled	97.0	20	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
117	c4wiaA_	Alignment	not modelled	97.0	7	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
118	c1d2eA_	Alignment	not modelled	96.9	28	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	d1odfa_	Alignment	not modelled	96.9	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
120	c4nmnA_	Alignment	not modelled	96.9	13	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution