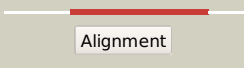

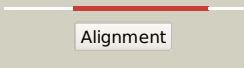

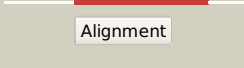

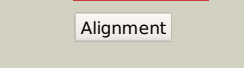

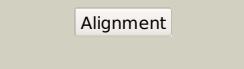

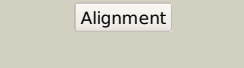

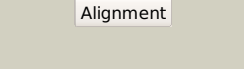

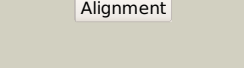

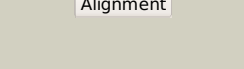

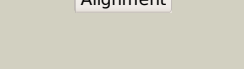
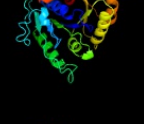
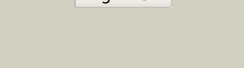



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1229c_(mrp)_1371783_1372955
 Date Wed Jul 31 22:05:32 BST 2019
 Unique Job ID e058abaf9314d521

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6g2gA_	 Alignment		100.0	36	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
2	d2afhe1	 Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
3	c2ph1A_	 Alignment		100.0	39	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
4	c51ljA_	 Alignment		100.0	26	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
5	c4rz3B_	 Alignment		100.0	24	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
6	c3endA_	 Alignment		100.0	20	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
7	d1cp2a_	 Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
8	c3vx3A_	 Alignment		100.0	36	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
9	d1iona_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
10	c3q9lB_	 Alignment		100.0	23	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
11	c6iucC_	 Alignment		100.0	21	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna

12	c3kjgB_	Alignment		100.0	20	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
13	c3ea0B_	Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
14	d1g3ga_	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
15	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
16	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
17	c2bekB_	Alignment		100.0	22	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
18	c2ozeA_	Alignment		100.0	13	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
19	c1hyqA_	Alignment		100.0	27	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
20	d1hyqa_	Alignment		100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
21	c3ez6B_	Alignment	not modelled	100.0	23	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
22	c2xj9B_	Alignment	not modelled	100.0	20	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
23	c3cioA_	Alignment	not modelled	100.0	17	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
24	c4pfsA_	Alignment	not modelled	100.0	23	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
25	c4ru8C_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
26	c3k9gA_	Alignment	not modelled	100.0	15	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
27	c3zq6D_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
28	c3fkqA_	Alignment	not modelled	100.0	16	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
						PDB header: hydrolase

29	c2wooc_	Alignment	not modelled	100.0	17	Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
30	c3ug7D_	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
31	c3la6P_	Alignment	not modelled	100.0	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
32	c1ii0A_	Alignment	not modelled	100.0	13	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
33	c4dzzB_	Alignment	not modelled	100.0	17	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
34	c2vedA_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
35	c5zmfA_	Alignment	not modelled	100.0	18	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
36	c3cwqB_	Alignment	not modelled	100.0	19	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
37	c5bwkA_	Alignment	not modelled	100.0	16	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	c3pg5A_	Alignment	not modelled	100.0	19	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
39	c3ezfA_	Alignment	not modelled	100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
40	c2wojD_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
41	c6bs3A_	Alignment	not modelled	100.0	19	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
42	c3of5A_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
43	d1ihua2	Alignment	not modelled	100.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
44	d1byia_	Alignment	not modelled	100.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
45	c3ibgF_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
46	c6bs5B_	Alignment	not modelled	100.0	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	d1ihua1	Alignment	not modelled	100.0	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
48	c3igfB_	Alignment	not modelled	99.9	19	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
49	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
50	c3fmfA_	Alignment	not modelled	99.9	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
51	c2qmoA_	Alignment	not modelled	99.9	13	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
52	c3lnoA_	Alignment	not modelled	99.7	20	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of domain of unknown function duf59 from2 bacillus anthracis
53	d1uwda_	Alignment	not modelled	99.7	26	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
						PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein;

54	c5irdA_	Alignment	not modelled	99.7	23	PDBTitle: solution structure of rv1466 from mycobacterium tuberculosis, a2 protein associated with [fe-s] complex assembly and repair - seattle3 structural genomics center for infectious disease target4 mytud.17486.a
55	d2cu6a1	Alignment	not modelled	99.7	28	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
56	c5l3qB_	Alignment	not modelled	99.6	17	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
57	c1vmaA_	Alignment	not modelled	99.6	18	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
58	c2qy9A_	Alignment	not modelled	99.6	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
59	c1zu4A_	Alignment	not modelled	99.6	16	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
60	c5l3rC_	Alignment	not modelled	99.5	20	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
61	c3dm5A_	Alignment	not modelled	99.5	13	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.
62	c2og2A_	Alignment	not modelled	99.5	13	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
63	c2cnwF_	Alignment	not modelled	99.4	17	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
64	c6cy1B_	Alignment	not modelled	99.4	19	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
65	c2q9cA_	Alignment	not modelled	99.4	15	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
66	c2yhsA_	Alignment	not modelled	99.4	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
67	c2j7pA_	Alignment	not modelled	99.4	15	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmpnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
68	c3b9qA_	Alignment	not modelled	99.4	13	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
69	c2j37W_	Alignment	not modelled	99.4	11	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
70	c2iy3A_	Alignment	not modelled	99.4	18	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
71	c5gafi_	Alignment	not modelled	99.3	20	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
72	c5l3sF_	Alignment	not modelled	99.3	16	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
73	c2v3cC_	Alignment	not modelled	99.3	22	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
74	c1qzwC_	Alignment	not modelled	99.3	18	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
75	c4ak9A_	Alignment	not modelled	99.3	18	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
76	c3ux2A_	Alignment	not modelled	99.2	11	PDB header: immune system Chain: A: PDB Molecule: mip18 family protein fam96a; PDBTitle: crystal structure of domain-swapped fam96a major dimer
77	c3dmdA_	Alignment	not modelled	99.1	19	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
78	c2j289_	Alignment	not modelled	99.1	19	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs

79	d1qzxa3	Alignment	not modelled	98.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	d1vmaa2	Alignment	not modelled	98.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	d1j8yf2	Alignment	not modelled	98.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
82	c1j8yF_	Alignment	not modelled	98.3	19	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
83	c2px0D_	Alignment	not modelled	98.3	21	PDB header: biosynthetic protein Chain: D; PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
84	c4a0gC_	Alignment	not modelled	98.1	16	PDB header: transferase Chain: C; PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
85	d2qy9a2	Alignment	not modelled	98.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	d1ls1a2	Alignment	not modelled	98.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c2npiB_	Alignment	not modelled	98.0	11	PDB header: transcription Chain: B; PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
88	c5hcnA_	Alignment	not modelled	98.0	15	PDB header: hydrolase Chain: A; PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
89	c4xc8B_	Alignment	not modelled	98.0	19	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)
90	c4a0rB_	Alignment	not modelled	97.9	15	PDB header: transferase Chain: B; PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
91	d1okkd2	Alignment	not modelled	97.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
92	c2h5eB_	Alignment	not modelled	97.9	25	PDB header: translation Chain: B; PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
93	d2qm8a1	Alignment	not modelled	97.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
94	c4ohvA_	Alignment	not modelled	97.8	20	PDB header: rna binding protein Chain: A; PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
95	c4zciA_	Alignment	not modelled	97.8	22	PDB header: gtp-binding protein Chain: A; PDB Molecule: gtp-binding protein typa/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typa
96	c5h7lB_	Alignment	not modelled	97.7	23	PDB header: translation/ribosomal protein Chain: B; PDB Molecule: elongation factor 2; PDBTitle: complex of elongation factor 2-50s ribosomal protein l12
97	c2recB_	Alignment	not modelled	97.6	24	PDB header: helicase PDB COMPND:
98	c4nkrB_	Alignment	not modelled	97.6	22	PDB header: unknown function Chain: B; PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
99	d1x6va3	Alignment	not modelled	97.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'phosphosulfate kinase (APS kinase)
100	d1nija1	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
101	c3hr8A_	Alignment	not modelled	97.5	15	PDB header: recombination Chain: A; PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
102	c2zroA_	Alignment	not modelled	97.5	24	PDB header: hydrolase Chain: A; PDB Molecule: protein reca; PDBTitle: msreca adp form iv
103	c4fn5A_	Alignment	not modelled	97.5	20	PDB header: translation/antibiotic Chain: A; PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyrin2 b
104	c1xp8A_	Alignment	not modelled	97.4	21	PDB header: dna binding protein Chain: A; PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
105	c2ywfA_	Alignment	not modelled	97.4	17	PDB header: translation Chain: A; PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex

					aeolicus
106	d1eg7a_	Alignment	not modelled	97.4	26 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
107	c3wyaA_	Alignment	not modelled	97.3	16 PDB header: translation Chain: A: PDB Molecule: elongation factor 1-alpha; PDBTitle: crystal structure of gdp-bound ef1alpha from pyrococcus horikoshii
108	c3do6B_	Alignment	not modelled	97.3	19 PDB header: ligase Chain: B: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
109	c5a4jC_	Alignment	not modelled	97.3	20 PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t.acetoxydans re1
110	d1yrba1	Alignment	not modelled	97.2	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
111	c4zc0A_	Alignment	not modelled	97.1	11 PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
112	d1xjca_	Alignment	not modelled	97.1	27 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
113	c1xnjB_	Alignment	not modelled	97.1	21 PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
114	d1n0ua2	Alignment	not modelled	97.1	26 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
115	c3bgwD_	Alignment	not modelled	97.1	11 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
116	c1zunB_	Alignment	not modelled	97.0	15 PDB header: transferase Chain: B: PDB Molecule: sulfate adenylate transferase, subunit PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
117	c2f1rA_	Alignment	not modelled	97.0	22 PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
118	c4a1fB_	Alignment	not modelled	97.0	11 PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
119	c3tr5C_	Alignment	not modelled	97.0	14 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
120	d1u94a1	Alignment	not modelled	96.9	28 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)