

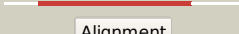

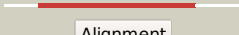



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2510c_(-)_2825498_2827099
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	63d7850ee0ec7dd0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4d2iB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfobolus solfataricus bound to amp-pnp
2	c4ag5A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
3	d1e9ra_	 Alignment		100.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
4	c2iuuE_	 Alignment		100.0	19	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
5	c2iutA_	 Alignment		100.0	19	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
6	c4ag5D_	 Alignment		100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
7	c2iusB_	 Alignment		100.0	24	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
8	c4kfuC_	 Alignment		99.9	19	PDB header: hydrolase Chain: C: PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfobolus turreted2 icosahedral virus 2 in complex with amppcp
9	c4nh0A_	 Alignment		99.9	21	PDB header: cell cycle Chain: A: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
10	c4n1aE_	 Alignment		99.8	21	PDB header: protein binding/protein binding Chain: E: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
11	c4lyvA_	 Alignment		99.7	15	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)

12	c4ag6D_	Alignment		98.8	18	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
13	d2ve8a1	Alignment		98.8	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
14	d2j5pa1	Alignment		98.8	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
15	c2r2aB_	Alignment		98.7	19	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
16	c3b9pA_	Alignment		97.9	26	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
17	c2w0mA_	Alignment		97.9	15	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfobolus solfataricus p2
18	d2i3ba1	Alignment		97.7	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
19	c6n9IA_	Alignment		97.6	13	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
20	c5dcfA_	Alignment		97.6	5	PDB header: recombination Chain: A: PDB Molecule: tyrosine recombinase xerd,dna translocase ftsk; PDBTitle: c-terminal domain of xerd recombinase in complex with gamma domain of f2 ftsk
21	d1byia_	Alignment	not modelled	97.6	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
22	c5udbD_	Alignment	not modelled	97.6	28	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
23	d1vmaa2	Alignment	not modelled	97.5	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
24	d2qy9a2	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
25	c4kssC_	Alignment	not modelled	97.4	35	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
26	c5l3qB_	Alignment	not modelled	97.4	33	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
27	c5fl3A_	Alignment	not modelled	97.4	22	PDB header: transport protein Chain: A: PDB Molecule: pili retraction protein pilt; PDBTitle: pilt2 from thermus thermophilus
28	c4xgcD_	Alignment	not modelled	97.4	21	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
						Fold: P-loop containing nucleoside triphosphate hydrolases

29	d1g6oa_	Alignment	not modelled	97.3	23	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
30	c4nkrB_	Alignment	not modelled	97.3	23	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
31	c5f4hF_	Alignment	not modelled	97.3	29	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
32	c3jvvA_	Alignment	not modelled	97.3	29	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-ppc
33	d1p9ra_	Alignment	not modelled	97.3	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
34	c2ja1A_	Alignment	not modelled	97.3	16	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
35	d1okkd2	Alignment	not modelled	97.3	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
36	c3of5A_	Alignment	not modelled	97.3	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
37	c5l3rC_	Alignment	not modelled	97.2	30	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
38	d1np6a_	Alignment	not modelled	97.2	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
39	c4phtC_	Alignment	not modelled	97.2	29	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
40	c2cnwF_	Alignment	not modelled	97.2	30	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
41	c5it5B_	Alignment	not modelled	97.2	21	PDB header: transport protein Chain: B: PDB Molecule: atp binding motif-containing protein pilf; PDBTitle: thermus thermophilus pilb core atpase region
42	c5l3sF_	Alignment	not modelled	97.2	22	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
43	c1zu4A_	Alignment	not modelled	97.2	36	PDB header: protein transport Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
44	c6cy1B_	Alignment	not modelled	97.2	31	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
45	c5zfqa_	Alignment	not modelled	97.2	32	PDB header: transport protein Chain: A: PDB Molecule: twitching motility pilus retraction protein; PDBTitle: crystal structure of pilt-4, a retraction atpase motor of type iv2 pilus , from geobacter sulfurreducens
46	c2j7pA_	Alignment	not modelled	97.2	27	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
47	c2q9cA_	Alignment	not modelled	97.2	31	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
48	c2gzaB_	Alignment	not modelled	97.2	25	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
49	c1vmaA_	Alignment	not modelled	97.2	33	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
50	c2qy9A_	Alignment	not modelled	97.2	36	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
51	d1qzxa3	Alignment	not modelled	97.2	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
52	c3b9qA_	Alignment	not modelled	97.1	39	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyl from arabidopsis thaliana
53	c5tshF_	Alignment	not modelled	97.1	29	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
54	c2yhsA_	Alignment	not modelled	97.1	36	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
55	c3u5zM_	Alignment	not modelled	97.1	22	PDB header: dna binding protein/dna Chain: M: PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the

						t4 clamp,2 primer-template dna, and atp analog
56	c2f1rA_	Alignment	not modelled	97.1	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
57	c4ak9A_	Alignment	not modelled	97.1	42	PDB header: protein transport Chain: A: PDB Molecule: cpfts; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
58	d1ls1a2	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
59	c2og2A_	Alignment	not modelled	97.0	39	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
60	c2oaq1_	Alignment	not modelled	97.0	25	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
61	c3dmdA_	Alignment	not modelled	97.0	34	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
62	c2gszE_	Alignment	not modelled	97.0	20	PDB header: protein transport Chain: E: PDB Molecule: witching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per asymmetric unit
63	c5ywwA_	Alignment	not modelled	97.0	36	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archaeal ruvb-like holiday junction helicase
64	c5hcnA_	Alignment	not modelled	97.0	23	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
65	c1xp8A_	Alignment	not modelled	97.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
66	d1u94a1	Alignment	not modelled	97.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
67	c4ii7D_	Alignment	not modelled	97.0	25	PDB header: hydrolase Chain: D: PDB Molecule: flai atpase; PDBTitle: archaellum assembly atpase flai
68	c2iy3A_	Alignment	not modelled	97.0	27	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
69	c5bq5A_	Alignment	not modelled	97.0	26	PDB header: atp-binding protein Chain: A: PDB Molecule: insertion sequence is5376 putative atp-binding protein; PDBTitle: crystal structure of the istb aaa+ domain bound to adp-bef3
70	c3a4mB_	Alignment	not modelled	96.9	24	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
71	c2eyuA_	Alignment	not modelled	96.9	21	PDB header: protein transport Chain: A: PDB Molecule: witching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
72	c3dm5A_	Alignment	not modelled	96.9	30	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.
73	d1xp8a1	Alignment	not modelled	96.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
74	c5x06G_	Alignment	not modelled	96.9	23	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
75	c5eaxB_	Alignment	not modelled	96.9	36	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna replication atp-dependent helicase/nuclease dna2; PDBTitle: crystal structure of dna2 in complex with an ssdna
76	c4ry2A_	Alignment	not modelled	96.8	19	PDB header: transport protein/hydrolase Chain: A: PDB Molecule: abc-type bacteriocin transporter; PDBTitle: crystal structure of the peptidase-containing abc transporter pcat1
77	c1xx6B_	Alignment	not modelled	96.8	14	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
78	c3bh0A_	Alignment	not modelled	96.8	16	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
79	c2j37W_	Alignment	not modelled	96.8	25	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
80	c2qmoA_	Alignment	not modelled	96.8	25	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori

81	c3upuC	Alignment	not modelled	96.8	28	PDB header: hydrolase/dna Chain: C; PDB Molecule: atp-dependent dna helicase dda; PDBTitle: crystal structure of the t4 phage sf1b helicase dda
82	d1cp2a	Alignment	not modelled	96.7	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	c3c8uA	Alignment	not modelled	96.7	31	PDB header: transferase Chain: A; PDB Molecule: fructokinase; PDBTitle: crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
84	d1rz3a	Alignment	not modelled	96.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
85	c5he8J	Alignment	not modelled	96.7	31	PDB header: protein binding Chain: J; PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
86	c6qelB	Alignment	not modelled	96.7	26	PDB header: replication Chain: B; PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
87	c3bgwD	Alignment	not modelled	96.7	15	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
88	d1xjca	Alignment	not modelled	96.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
89	d1pjra1	Alignment	not modelled	96.6	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
90	c1zuiA	Alignment	not modelled	96.6	31	PDB header: transferase Chain: A; PDB Molecule: shikimate kinase; PDBTitle: structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
91	d2qm8a1	Alignment	not modelled	96.6	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
92	c5cb6A	Alignment	not modelled	96.6	24	PDB header: transferase Chain: A; PDB Molecule: probable adenylyl-sulfate kinase; PDBTitle: structure of adenosine-5'-phosphosulfate kinase
93	c3oiyB	Alignment	not modelled	96.6	21	PDB header: isomerase Chain: B; PDB Molecule: reverse gyrase helicase domain; PDBTitle: helicase domain of reverse gyrase from thermotoga maritima
94	c6gefB	Alignment	not modelled	96.6	24	PDB header: hydrolase Chain: B; PDB Molecule: type iv secretion system protein dotb; PDBTitle: x-ray structure of the yersinia pseudotuberculosis atpase dotb
95	c3fmfA	Alignment	not modelled	96.6	32	PDB header: ligase Chain: A; PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
96	d1l8qa2	Alignment	not modelled	96.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c3gp8A	Alignment	not modelled	96.5	28	PDB header: hydrolase/dna Chain: A; PDB Molecule: exodeoxyribonuclease v, subunit recd, putative; PDBTitle: crystal structure of the binary complex of recd2 with dna
98	c4nmnA	Alignment	not modelled	96.5	21	PDB header: replication Chain: A; PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
99	c2px0D	Alignment	not modelled	96.5	26	PDB header: biosynthetic protein Chain: D; PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnpn/mg(2+)
100	d1uaaa1	Alignment	not modelled	96.5	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
101	d1khta	Alignment	not modelled	96.5	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
102	c3ifuA	Alignment	not modelled	96.5	19	PDB header: hydrolase Chain: A; PDB Molecule: dna helicase ii; PDBTitle: crystal structure of e. coli uvrd
103	c3bosA	Alignment	not modelled	96.5	9	PDB header: hydrolase regulator,dna binding protein Chain: A; PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
104	c4b3gA	Alignment	not modelled	96.5	31	PDB header: hydrolase/rna Chain: A; PDB Molecule: dna-binding protein smubp-2; PDBTitle: crystal structure of ighmbp2 helicase in complex with rna
105	c3hr8A	Alignment	not modelled	96.5	18	PDB header: recombination Chain: A; PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
106	c3h1tA	Alignment	not modelled	96.5	29	PDB header: hydrolase Chain: A; PDB Molecule: type i site-specific restriction-modification PDBTitle: the fragment structure of a putative hsr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016 PDB header: transferase

107	c3tqcB	Alignment	not modelled	96.5	25	Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the pantothenate kinase (coaa) from coxiella burnetii
108	c4wiaA	Alignment	not modelled	96.5	16	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
109	c6c90A	Alignment	not modelled	96.5	22	PDB header: hydrolase/rna binding protein Chain: A: PDB Molecule: exosome rna helicase mtr4,exosome rna helicase mtr4; PDBTitle: human mtr4 helicase in complex with zcchc8-ctd
110	c4y0aA	Alignment	not modelled	96.4	34	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: shikimate kinase; PDBTitle: shikimate kinase from acinetobacter baumannii in complex with2 shikimate
111	c5ep4A	Alignment	not modelled	96.4	17	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
112	c5exsA	Alignment	not modelled	96.4	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator fleq; PDBTitle: aaa+ atpase fleq from pseudomonas aeruginosa bound to atp-gamma-s
113	d1g41a	Alignment	not modelled	96.4	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
114	c2qq0B	Alignment	not modelled	96.4	22	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
115	d1gkub1	Alignment	not modelled	96.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Helicase-like "domain" of reverse gyrase
116	c2v3cC	Alignment	not modelled	96.4	28	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
117	c3nxsA	Alignment	not modelled	96.4	30	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
118	c2ce7B	Alignment	not modelled	96.4	32	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
119	c2zroA	Alignment	not modelled	96.4	21	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
120	c4cbhC	Alignment	not modelled	96.3	21	PDB header: hydrolase Chain: C: PDB Molecule: serine protease ns3; PDBTitle: pestivirus ns3 helicase