
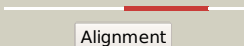

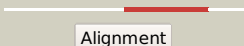







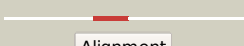












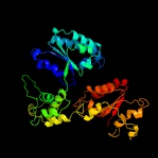

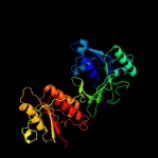


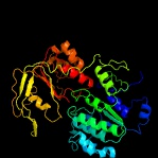


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3894c_(-)_4376440_4380630
Date	Sat Aug 10 22:05:08 BST 2019
Unique Job ID	3aba36baf0978f3a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nh0A_	 Alignment		100.0	31	PDB header: cell cycle Chain: A: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
2	c4n1aE_	 Alignment		100.0	28	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
3	c4lyaA_	 Alignment		100.0	21	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
4	c2iuuE_	 Alignment		100.0	24	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
5	c2iutA_	 Alignment		100.0	24	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
6	c2iusB_	 Alignment		100.0	24	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
7	c4kfuC_	 Alignment		99.9	17	PDB header: hydrolase Chain: C: PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	c4d2iB_	 Alignment		99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-pnp
9	c4ag5A_	 Alignment		99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
10	d1e9ra_	 Alignment		99.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
11	c5g4gF_	 Alignment		99.2	17	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex

12	c6matE_	Alignment		99.2	17	PDB header: ribosomal protein Chain: E; PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
13	c4ag5D_	Alignment		99.1	18	PDB header: hydrolase Chain: D; PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
14	c3cf1C_	Alignment		99.0	15	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
15	c5ifwB_	Alignment		99.0	15	PDB header: signaling protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
16	c3cf2B_	Alignment		99.0	16	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
17	c1u9iA_	Alignment		99.0	15	PDB header: circadian clock protein Chain: A; PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
18	c5e7pA_	Alignment		98.9	16	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
19	c5jwqA_	Alignment		98.8	17	PDB header: transcription regulator Chain: A; PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
20	c1yqtA_	Alignment		98.8	12	PDB header: hydrolyase/translation Chain: A; PDB Molecule: rnaase I inhibitor; PDBTitle: rnaase-I inhibitor
21	c4finA_	Alignment	not modelled	98.5	15	PDB header: atp-binding protein Chain: A; PDB Molecule: etta (yjjk) abcf family protein; PDBTitle: crystal structure of etta (formerly yjjk) - an e. coli abc-type atpase
22	c5zxdB_	Alignment	not modelled	98.5	15	PDB header: translation Chain: B; PDB Molecule: atp-binding cassette sub-family f member 1; PDBTitle: crystal structure of atp-bound human abcf1
23	c3j96F_	Alignment	not modelled	98.4	19	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
24	c3bk7A_	Alignment	not modelled	98.1	15	PDB header: hydrolyase/translation Chain: A; PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-I inhibitor protein from2 pyrococcus abyssi
25	c3l0oB_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: B; PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
26	c3j16B_	Alignment	not modelled	98.1	12	PDB header: ribosome Chain: B; PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
27	c3l0oA_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: A; PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
28	c5w0tA_	Alignment	not modelled	98.1	14	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae

29	c1xwiA_	Alignment	not modelled	98.0	17	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
30	c4b4tj_	Alignment	not modelled	98.0	17	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
31	c2zamA_	Alignment	not modelled	98.0	18	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
32	c6b5cA_	Alignment	not modelled	98.0	21	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
33	c6epcj_	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
34	c5vq9D_	Alignment	not modelled	97.9	18	PDB header: protein binding Chain: D: PDB Molecule: pacchytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
35	c6opcF_	Alignment	not modelled	97.9	16	PDB header: motor protein Chain: F: PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
36	c3d8bB_	Alignment	not modelled	97.9	15	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
37	c3b9pA_	Alignment	not modelled	97.9	14	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
38	c1s3sA_	Alignment	not modelled	97.9	17	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
39	c3hu2C_	Alignment	not modelled	97.9	17	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
40	c4b4tH_	Alignment	not modelled	97.8	22	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
41	c6nyyC_	Alignment	not modelled	97.8	16	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
42	c3vfdA_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
43	c4z8xC_	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
44	c4l16A_	Alignment	not modelled	97.8	19	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
45	d1w5sa2	Alignment	not modelled	97.8	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
46	c1xpuB_	Alignment	not modelled	97.8	13	PDB header: transcription/rna Chain: B: PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
47	c3cmvG_	Alignment	not modelled	97.8	18	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-sdna/dsdna2 structures
48	c4xgcE_	Alignment	not modelled	97.7	14	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
49	c5wc0D_	Alignment	not modelled	97.7	17	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
50	c5kzfj_	Alignment	not modelled	97.7	19	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
51	c3eihB_	Alignment	not modelled	97.7	17	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
52	c5l3rC_	Alignment	not modelled	97.7	12	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
53	c5udbD_	Alignment	not modelled	97.7	18	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 PDB header: immune system

54	c4kxfF_	Alignment	not modelled	97.7	12	Chain: F; PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlr4 reveals its autoinhibition mechanism
55	c2ce7B_	Alignment	not modelled	97.6	23	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
56	c5l3sF_	Alignment	not modelled	97.6	12	PDB header: protein transport Chain: F; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
57	c4xgcD_	Alignment	not modelled	97.6	13	PDB header: dna binding protein Chain: D; PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
58	c1iy2A_	Alignment	not modelled	97.6	21	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
59	c4b4tK_	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: K; PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
60	c4yerB_	Alignment	not modelled	97.6	19	PDB header: hydrolase Chain: B; PDB Molecule: abc transporter atp-binding protein; PDBTitle: crystal structure of an abc transporter atp-binding protein (tm_1403)2 from thermotoga maritima msb8 at 2.35 a resolution
61	c5mpaL_	Alignment	not modelled	97.6	13	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
62	c6hecH_	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: H; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
63	c4lcbA_	Alignment	not modelled	97.6	22	PDB header: protein transport Chain: A; PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
64	c6epdM_	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
65	c2dhrC_	Alignment	not modelled	97.5	19	PDB header: hydrolase Chain: C; PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
66	d1xpuA3	Alignment	not modelled	97.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
67	c2j7pA_	Alignment	not modelled	97.5	15	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
68	c5gjqL_	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
69	c3ldaA_	Alignment	not modelled	97.5	16	PDB header: dna binding protein Chain: A; PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
70	c5vy9C_	Alignment	not modelled	97.5	17	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
71	d1nlfa_	Alignment	not modelled	97.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
72	c4b4tM_	Alignment	not modelled	97.4	18	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
73	c6azyA_	Alignment	not modelled	97.4	17	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
74	c3sylB_	Alignment	not modelled	97.4	14	PDB header: chaperone Chain: B; PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
75	c4b4tL_	Alignment	not modelled	97.4	13	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
76	c3dmdA_	Alignment	not modelled	97.4	13	PDB header: transport protein Chain: A; PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
77	c2iw3B_	Alignment	not modelled	97.4	16	PDB header: translation Chain: B; PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
78	c4xguB_	Alignment	not modelled	97.4	14	PDB header: atp-binding protein Chain: B; PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
79	c2cnwF_	Alignment	not modelled	97.4	12	PDB header: signal recognition Chain: F; PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy

80	c2vyzA	Alignment	not modelled	97.4	16	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
81	c2q6tB	Alignment	not modelled	97.4	12	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
82	c2it1B	Alignment	not modelled	97.4	21	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
83	d1ji0a	Alignment	not modelled	97.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
84	d1tf7a2	Alignment	not modelled	97.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
85	c2ja1A	Alignment	not modelled	97.3	13	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
86	d2ce7a2	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
87	c5t0gA	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
88	c3te6A	Alignment	not modelled	97.3	12	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
89	c4b4tl	Alignment	not modelled	97.3	21	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
90	c5l3qB	Alignment	not modelled	97.3	21	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
91	c3fvqB	Alignment	not modelled	97.3	20	PDB header: hydrolase Chain: B: PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc complexed with2 atp
92	c2v1uA	Alignment	not modelled	97.3	14	PDB header: replication Chain: A: PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
93	c4ypnA	Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: A: PDB Molecule: lon protease; PDBTitle: crystal structure of a lon fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
94	c3bh0A	Alignment	not modelled	97.3	15	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
95	c5x06G	Alignment	not modelled	97.3	8	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
96	c3ux8A	Alignment	not modelled	97.3	17	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
97	c4kxfl	Alignment	not modelled	97.2	13	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
98	c5uj7B	Alignment	not modelled	97.2	10	PDB header: dna binding protein Chain: B: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
99	c3gfoA	Alignment	not modelled	97.2	19	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of the abc2 transporter complex cbionq.
100	d1b0ua	Alignment	not modelled	97.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
101	c2r65A	Alignment	not modelled	97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsH homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsH2 adp complex
102	c1oxtb	Alignment	not modelled	97.2	20	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
103	c5nj3B	Alignment	not modelled	97.2	14	PDB header: transport protein Chain: B: PDB Molecule: atp-binding cassette sub-family g member 2; PDBTitle: structure of an abc transporter: complete structure
104	c6amxA	Alignment	not modelled	97.2	18	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucleotide binding domain of o-antigen2 polysaccharide abc-transporter
						PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding

105	c2pcjB_	Alignment	not modelled	97.2	16	protein Iold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
106	c1r6bX_	Alignment	not modelled	97.2	13	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
107	d1fnna2	Alignment	not modelled	97.2	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	c4p31B_	Alignment	not modelled	97.2	20	PDB header: hydrolase Chain: B: PDB Molecule: lipopolysaccharide export system atp-binding protein lptb; PDBTitle: crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium
109	c2x8aA_	Alignment	not modelled	97.2	12	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
110	c2qbyA_	Alignment	not modelled	97.1	10	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
111	c1vmaA_	Alignment	not modelled	97.1	15	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
112	d1n0wa_	Alignment	not modelled	97.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
113	c4tqvO_	Alignment	not modelled	97.1	15	PDB header: transport protein Chain: O: PDB Molecule: algs; PDBTitle: crystal structure of a bacterial abc transporter involved in the2 import of the acidic polysaccharide alginate
114	c2yz2B_	Alignment	not modelled	97.1	23	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
115	c3d31B_	Alignment	not modelled	97.1	20	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding protein; PDBTitle: modbc from methanosarcina acetivorans
116	c5udb9_	Alignment	not modelled	97.1	15	PDB header: replication Chain: 9: PDB Molecule: cell division control protein 6; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
117	c2px0D_	Alignment	not modelled	97.1	20	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmpnpn/mg(2+)
118	d2qy9a2	Alignment	not modelled	97.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
119	c5l22B_	Alignment	not modelled	97.1	16	PDB header: protein transport Chain: B: PDB Molecule: abc transporter (hlyb subfamily); PDBTitle: prtD t1ss abc transporter
120	c3pvsA_	Alignment	not modelled	97.1	19	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa