



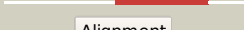

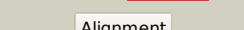

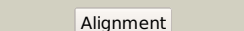

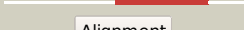
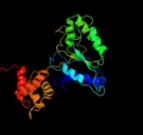



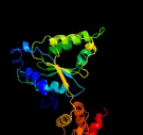








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0282 (-)_342130_344025
Date	Tue Jul 23 14:50:34 BST 2019
Unique Job ID	a71a657dd4c742b0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sylB_	 Alignment		100.0	36	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
2	c6matE_	 Alignment		100.0	22	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
3	c5e7pA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
4	c5g4gF_	 Alignment		100.0	23	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
5	c3cf1C_	 Alignment		100.0	27	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alpha
6	c6nyyC_	 Alignment		100.0	19	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
7	c3hu2C_	 Alignment		100.0	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
8	c2dhrC_	 Alignment		100.0	24	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
9	c5kzfj_	 Alignment		100.0	21	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
10	c6epdM_	 Alignment		100.0	21	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
11	c1s3sA_	 Alignment		100.0	21	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

12	c4f3vB_	Alignment		100.0	25	PDB header: protein transport Chain: B; PDB Molecule: esx-1 secretion system protein eccA1; PDBTitle: crystal structure of n-terminal domain of eccA1 atpase from esx-12 secretion system of mycobacterium tuberculosis
13	c4b4tH_	Alignment		100.0	19	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
14	c6epcJ_	Alignment		99.9	24	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
15	c4b4tI_	Alignment		99.9	22	PDB header: hydrolase Chain: I; PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	c6genX_	Alignment		99.9	24	PDB header: nuclear protein Chain: X; PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
17	c6az0A_	Alignment		99.9	16	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
18	c3b9pA_	Alignment		99.9	24	PDB header: hydrolase Chain: A; PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
19	c1xwiA_	Alignment		99.9	20	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
20	c3eihB_	Alignment		99.9	22	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
21	c6nyyA_	Alignment	not modelled	99.9	20	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
22	c4b4tL_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
23	c4b4tJ_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: J; PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
24	c4l16A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
25	c4z8xC_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
26	c5w0tA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
27	c2ce7B_	Alignment	not modelled	99.9	22	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
28	c6hecH_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: H; PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
						PDB header: transport protein

29	c3cf2B_	Alignment	not modelled	99.9	20	Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
30	c5ifwB_	Alignment	not modelled	99.9	22	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
31	c4b4tK_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
32	c5gjqL_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
33	c3d8bB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
34	c5t0gA_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
35	c5mpaL_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
36	c4b4tM_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
37	c3pxiB_	Alignment	not modelled	99.9	24	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca108:clpc
38	c4xguB_	Alignment	not modelled	99.9	15	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
39	c5oafB_	Alignment	not modelled	99.9	21	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexamer in ino80 complex
40	c2c9oA_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
41	d1e32a2	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c3j96F_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
43	c2zamA_	Alignment	not modelled	99.9	17	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
44	c1iy2A_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
45	d1g41a_	Alignment	not modelled	99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
46	c4bujF_	Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: F: PDB Molecule: superkiller protein 3; PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex
47	c6b5cA_	Alignment	not modelled	99.9	18	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
48	d2ce7a2	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c3vfdA_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
50	c5vq9D_	Alignment	not modelled	99.9	14	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
51	c6azyA_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
52	c3pfiB_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
53	c5dseC_	Alignment	not modelled	99.9	12	PDB header: protein binding Chain: C: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
54	c3h4mC_	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase

55	c5wc0D_	Alignment	not modelled	99.9	24	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
56	c3pvsA_	Alignment	not modelled	99.9	24	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
57	c6mdnF_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: the 20s supercomplex engaging the snap-25 n-terminus (class 2)
58	c1qvrB_	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: B: PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
59	c1r6bX_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: X: PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
60	c4ciuA_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
61	c2xpiA_	Alignment	not modelled	99.9	11	PDB header: cell cycle Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9; PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1
62	c4hnxA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata acetyltransferase complex bound to ppgpp
63	c6c95A_	Alignment	not modelled	99.9	11	PDB header: transferase Chain: A: PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit; PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk
64	c5kneA_	Alignment	not modelled	99.9	24	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
65	c5kneF_	Alignment	not modelled	99.9	16	PDB header: chaperone Chain: F: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
66	c5d4wB_	Alignment	not modelled	99.9	19	PDB header: chaperone Chain: B: PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
67	c5vy9C_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
68	c5ubvB_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
69	c4ww4B_	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
70	d1ixza_	Alignment	not modelled	99.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
71	c2c9oC_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
72	c2r65A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
73	c4lcbA_	Alignment	not modelled	99.9	20	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
74	c6djuA_	Alignment	not modelled	99.9	23	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
75	d1w3ba_	Alignment	not modelled	99.9	14	Fold: alpha-alpha superhelix Superfamily: TPR-like Family: Tetratricopeptide repeat (TPR)
76	d1ofha_	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
77	c4ww4A_	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
78	c5dseA_	Alignment	not modelled	99.9	27	PDB header: protein binding Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b; PDBTitle: crystal structure of the ttc7b/hyccin complex
79	c3zw6B_	Alignment	not modelled	99.9	14	PDB header: photosynthesis Chain: B: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
80	c5jqyA_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartyl/asparaginyl beta-hydroxylase; PDBTitle: aspartyl/asparaginyl beta-hydroxylase (asph)oxygenase and tpr domains2 in complex with manganese, n-oxalylglycine and

						factor x substrate3 peptide fragment(39mer-4ser)
81	c5nnrD_	Alignment	not modelled	99.9	13	PDB header: transferase Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein; PDBTitle: structure of naa15/naa10 bound to hypk-thb
82	c6em8F_	Alignment	not modelled	99.9	21	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
83	c5ganJ_	Alignment	not modelled	99.9	9	PDB header: transcription Chain: J: PDB Molecule: pre-mrna-splicing factor 6; PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
84	c2qz4A_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
85	d1qvra3	Alignment	not modelled	99.9	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c6opcF_	Alignment	not modelled	99.9	21	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)
87	c4ui9C_	Alignment	not modelled	99.9	12	PDB header: cell cycle Chain: C: PDB Molecule: cell division cycle protein 23 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
88	d1um8a_	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
89	c6e111_	Alignment	not modelled	99.9	24	PDB header: protein transport Chain: 1: PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
90	d1r6bx3	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
91	c4kvmA_	Alignment	not modelled	99.9	14	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1; PDBTitle: the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog
92	c3iegB_	Alignment	not modelled	99.9	17	PDB header: chaperone Chain: B: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of p58(ipk) tpr domain at 2.5 a
93	c5kneD_	Alignment	not modelled	99.9	16	PDB header: chaperone Chain: D: PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
94	c6blbA_	Alignment	not modelled	99.9	27	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
95	c1in8A_	Alignment	not modelled	99.9	31	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
96	c6djvE_	Alignment	not modelled	99.9	22	PDB header: chaperone Chain: E: PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 2
97	d1r6bx2	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
98	c3pxgA_	Alignment	not modelled	99.9	26	PDB header: protein binding Chain: A: PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca121 and clpc1-485 complex
99	c3hteC_	Alignment	not modelled	99.9	18	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
100	c4ui9K_	Alignment	not modelled	99.9	11	PDB header: cell cycle Chain: K: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
101	d1in4a2	Alignment	not modelled	99.9	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
102	c2x8aA_	Alignment	not modelled	99.9	18	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
103	c3fp4A_	Alignment	not modelled	99.8	22	PDB header: transport protein Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w; PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment
104	d1jbka_	Alignment	not modelled	99.8	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
105	c4d2qC_	Alignment	not modelled	99.8	19	PDB header: chaperone Chain: C: PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
106	d1r7ra3	Alianment	not modelled	99.8	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

					Family: Extended AAA-ATPase domain
107	d1g8pa_	Alignment	not modelled	99.8	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	d1lv7a_	Alignment	not modelled	99.8	20 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	c2r44A_	Alignment	not modelled	99.8	15 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
110	c6qi8E_	Alignment	not modelled	99.8	17 PDB header: chaperone Chain: E: PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
111	c5o9zG_	Alignment	not modelled	99.8	10 PDB header: splicing Chain: G: PDB Molecule: pre-mrna-processing factor 6; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for 2 activation (b complex)
112	c4r7sA_	Alignment	not modelled	99.8	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tetratricopeptide repeat protein; PDBTitle: crystal structure of a tetratricopeptide repeat protein (parmer_03812)2 from parabacteroides merdae atcc 43184 at 2.39 a resolution
113	c3pe3D_	Alignment	not modelled	99.8	14 PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
114	c6em8H_	Alignment	not modelled	99.8	24 PDB header: chaperone Chain: H: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
115	c2p65A_	Alignment	not modelled	99.8	25 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
116	c3hymB_	Alignment	not modelled	99.8	14 PDB header: cell cycle, ligase Chain: B: PDB Molecule: cell division cycle protein 16 homolog; PDBTitle: insights into anaphase promoting complex tpr subdomain2 assembly from a cdc26-apc6 structure
117	c1fchB_	Alignment	not modelled	99.8	18 PDB header: signaling protein Chain: B: PDB Molecule: peroxisomal targeting signal 1 receptor; PDBTitle: crystal structure of the pts1 complexed to the tpr region2 of human pex5
118	c2y4tA_	Alignment	not modelled	99.8	12 PDB header: chaperone Chain: A: PDB Molecule: dnaj homolog subfamily c member 3; PDBTitle: crystal structure of the human co-chaperone p58(ipk)
119	c3draA_	Alignment	not modelled	99.8	7 PDB header: transferase Chain: A: PDB Molecule: protein PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
120	c4ypnA_	Alignment	not modelled	99.8	24 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