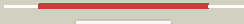



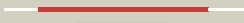



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1026 (-)_1147023_1147982
Date	Wed Jul 31 22:05:09 BST 2019
Unique Job ID	243076502fd27f80

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cerD_	 Alignment		100.0	45	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: possible exopolyphosphatase-like protein; PDBTitle: crystal structure of the exopolyphosphatase-like protein q8g5j2.2 northeast structural genomics consortium target blr13
2	c3mdqA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
3	c2floA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
4	c3hi0B_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: putative exopolyphosphatase; PDBTitle: crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
5	c1t6dB_	 Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: exopolyphosphatase; PDBTitle: miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
6	d1t6ca2	 Alignment		100.0	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
7	d1u6za3	 Alignment		100.0	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
8	d1t6ca1	 Alignment		100.0	35	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
9	d1u6za2	 Alignment		100.0	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
10	c3aapA_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleoside triphosphate diphosphohydrolase i; PDBTitle: crystal structure of lp1ntpdase from legionella pneumophila
11	c5u7xF_	 Alignment		100.0	14	PDB header: hydrolase Chain: F: PDB Molecule: nod factor binding lectin-nucleotide phosphohydrolase; PDBTitle: crystal structure of a nucleoside triphosphate diphosphohydrolase2 (ntpdase) from the legume vigna unguiculata subsp. cylindrica3 (dolichos biflorus) in complex with phosphate and manganese

12	c5u7wA_	Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: apyrase; PDBTitle: crystal structure of a nucleoside triphosphate diphosphohydrolase2 (ntpdase) from the legume trifolium repens in complex with adenine3 and phosphate
13	c3zx2A_	Alignment		100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: ectonucleoside triphosphate diphosphohydrolase 1; PDBTitle: ntpdase1 in complex with decavanadate
14	c3cj9A_	Alignment		99.9	18	PDB header: hydrolase Chain: A; PDB Molecule: ectonucleoside triphosphate diphosphohydrolase 2; PDBTitle: structure of rattus norvegicus ntpdase2 in complex with2 calcium, amp and phosphate
15	c3agrB_	Alignment		99.8	21	PDB header: hydrolase Chain: B; PDB Molecule: nucleoside triphosphate hydrolase; PDBTitle: crystal structure of nucleoside triphosphate hydrolases from neospora2 caninum
16	c4a5bA_	Alignment		99.8	23	PDB header: hydrolase Chain: A; PDB Molecule: nucleoside-triphosphatase 2; PDBTitle: crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
17	c3h1qB_	Alignment		99.1	19	PDB header: structural protein Chain: B; PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrmus hydrogenoformans
18	c5eoxB_	Alignment		99.0	20	PDB header: peptide binding protein Chain: B; PDB Molecule: type 4 fimbrial biogenesis protein pilm; PDBTitle: pseudomonas aeruginosa pilm bound to adp
19	c1e4gT_	Alignment		98.6	18	PDB header: bacterial cell division Chain: T; PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
20	c4j8fA_	Alignment		98.3	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein; PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip
21	c2ychA_	Alignment	not modelled	98.2	18	PDB header: cell cycle Chain: A; PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
22	c3iucC_	Alignment	not modelled	98.2	18	PDB header: chaperone Chain: C; PDB Molecule: heat shock 70kda protein 5 (glucose-regulated PDBTitle: crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
23	c4czeA_	Alignment	not modelled	98.1	20	PDB header: structural protein Chain: A; PDB Molecule: rod shape-determining protein mreB; PDBTitle: c. crescentus mreB, double filament, empty
24	c5tkyA_	Alignment	not modelled	98.1	19	PDB header: chaperone Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
25	c4apwH_	Alignment	not modelled	98.0	17	PDB header: structural protein Chain: H; PDB Molecule: alp12; PDBTitle: alp12 filament structure
26	c5jygA_	Alignment	not modelled	97.9	18	PDB header: structural protein Chain: A; PDB Molecule: actin-like atpase; PDBTitle: cryo-em structure of the mamk filament at 6.5 a
27	c5e84B_	Alignment	not modelled	97.9	16	PDB header: chaperone Chain: B; PDB Molecule: 78 kda glucose-regulated protein; PDBTitle: atp-bound state of bip
28	c4xe7A_	Alignment	not modelled	97.9	12	PDB header: structural protein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: bacillus thuringiensis parm in apo form
29	c5mb9B_	Alignment	not modelled	97.8	13	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of the eukaryotic ribosome associated

					complex (rac),2 a unique hsp70/hsp40 pair
30	c1mwma_	Alignment	not modelled	97.8	14 PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
31	c6izrK_	Alignment	not modelled	97.8	13 PDB header: protein fibril Chain: K: PDB Molecule: putative plasmid segregation protein parm; PDBTitle: whole structure of a 15-stranded parm filament from clostridium2 botulinum
32	c3dwb_	Alignment	not modelled	97.8	16 PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 3; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
33	c2fsnB_	Alignment	not modelled	97.7	14 PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
34	c2v7yA_	Alignment	not modelled	97.7	16 PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
35	c6gfaA_	Alignment	not modelled	97.7	16 PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 105 kda; PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
36	c4pl7B_	Alignment	not modelled	97.6	20 PDB header: structural protein, contractile protein Chain: B: PDB Molecule: actin,thymosin beta-4; PDBTitle: structure of komagataella pastoris actin-thymosin beta4 hybrid
37	c1o1f4_	Alignment	not modelled	97.6	16 PDB header: contractile protein Chain: 4: PDB Molecule: skeletal muscle actin; PDBTitle: molecular models of averaged rigor crossbridges from tomograms of2 insect flight muscle
38	c6igmG_	Alignment	not modelled	97.6	11 PDB header: transcription Chain: G: PDB Molecule: actin-related protein 6; PDBTitle: cryo-em structure of human srcap complex
39	c2p9lA_	Alignment	not modelled	97.5	14 PDB header: structural protein Chain: A: PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
40	c1jcgA_	Alignment	not modelled	97.5	17 PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
41	c1dkgD_	Alignment	not modelled	97.5	18 PDB header: complex (hsp24/hsp70) Chain: D: PDB Molecule: molecular chaperone dnak; PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
42	c3wqtB_	Alignment	not modelled	97.4	15 PDB header: structural genomics Chain: B: PDB Molecule: cell division protein ftsa; PDBTitle: staphylococcus aureus ftsa complexed with amppnp
43	c2khoA_	Alignment	not modelled	97.4	24 PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate
44	c6etxH_	Alignment	not modelled	97.4	9 PDB header: dna binding protein Chain: H: PDB Molecule: actin-related protein 5; PDBTitle: cryo-em structure of the human ino80 complex bound to nucleosome
45	c3qb0C_	Alignment	not modelled	97.4	10 PDB header: structural protein Chain: C: PDB Molecule: actin-related protein 4; PDBTitle: crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
46	c5aftJ_	Alignment	not modelled	97.4	14 PDB header: motor protein Chain: J: PDB Molecule: actin related protein 11; PDBTitle: cryoem structure of dynactin complex at 4.0 angstrom2 resolution
47	c2d0oA_	Alignment	not modelled	97.4	16 PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
48	c5afuB_	Alignment	not modelled	97.2	19 PDB header: motor protein Chain: B: PDB Molecule: dynactin; PDBTitle: cryo-em structure of dynein tail-dynactin-bicd2n complex
49	c3js6A_	Alignment	not modelled	97.2	13 PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
50	c4jd2B_	Alignment	not modelled	97.2	18 PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 2; PDBTitle: crystal structure of bos taurus arp2/3 complex binding with mus2 musculus gmf
51	c4kboA_	Alignment	not modelled	97.1	20 PDB header: signaling protein Chain: A: PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form
52	c6bqwH_	Alignment	not modelled	97.0	14 PDB header: cytosolic protein Chain: H: PDB Molecule: bacterial actin alfa; PDBTitle: alfa filament bound to amppnp
53	c4i6mB_	Alignment	not modelled	97.0	10 PDB header: transcription/hydrolase Chain: B: PDB Molecule: actin-like protein arp9; PDBTitle: structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
54	c3wxiB_	Alignment	not modelled	97.0	18 PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
55	d1e4ft2	Alignment	not modelled	96.9	15 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70

56	c3c7nB	Alignment	not modelled	96.8	17	PDB header: chaperone/chaperone Chain: B: PDB Molecule: heat shock cognate; PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex
57	c2v7zA	Alignment	not modelled	96.7	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock cognate 71 kda protein; PDBTitle: crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
58	c6fhsJ	Alignment	not modelled	96.7	16	PDB header: dna binding protein Chain: J: PDB Molecule: arp5; PDBTitle: cryoem structure of ino80core
59	c4gniA	Alignment	not modelled	96.7	15	PDB header: chaperone Chain: A: PDB Molecule: putative heat shock protein; PDBTitle: structure of the ssz1 atpase bound to atp and magnesium
60	c6gejR	Alignment	not modelled	96.7	14	PDB header: nuclear protein Chain: R: PDB Molecule: actin-like protein arp6; PDBTitle: chromatin remodeler-nucleosome complex at 3.6 a resolution.
61	c4i6mA	Alignment	not modelled	96.7	12	PDB header: transcription/hydrolase Chain: A: PDB Molecule: actin-related protein 7; PDBTitle: structure of arp7-arp9-snf2(hsa)-rtt102 subcomplex of swi/snf2 chromatin remodeler.
62	c6fmlJ	Alignment	not modelled	96.7	14	PDB header: dna binding protein Chain: J: PDB Molecule: actin related protein 5; PDBTitle: cryoem structure ino80core nucleosome complex
63	d2fsja1	Alignment	not modelled	96.4	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
64	c5obuA	Alignment	not modelled	96.4	18	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnak; PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.
65	c3gbtA	Alignment	not modelled	96.3	18	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
66	d2zgya2	Alignment	not modelled	96.3	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
67	d1jcea2	Alignment	not modelled	96.2	33	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
68	c4rtfD	Alignment	not modelled	96.1	18	PDB header: chaperone Chain: D: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv
69	c4fo0A	Alignment	not modelled	95.9	13	PDB header: gene regulation Chain: A: PDB Molecule: actin-related protein 8; PDBTitle: human actin-related protein arp8 in its atp-bound state
70	c2w40C	Alignment	not modelled	95.9	16	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
71	c3d2fC	Alignment	not modelled	95.7	13	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
72	c4am6A	Alignment	not modelled	95.6	23	PDB header: nuclear protein Chain: A: PDB Molecule: actin-like protein arp8; PDBTitle: c-terminal domain of actin-related protein arp8 from s. cerevisiae
73	d2e8aa2	Alignment	not modelled	95.5	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
74	c2zf5O	Alignment	not modelled	95.5	17	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
75	c3ifrB	Alignment	not modelled	95.2	15	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
76	c3zyyY	Alignment	not modelled	95.1	19	PDB header: iron-sulfur-binding protein Chain: Y: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
77	d1bupa2	Alignment	not modelled	95.0	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
78	c3zyyX	Alignment	not modelled	94.8	15	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
79	c3gg4B	Alignment	not modelled	94.7	21	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
80	c4cj7B	Alignment	not modelled	94.6	18	PDB header: structural protein Chain: B: PDB Molecule: actin/actin family protein; PDBTitle: structure of crenactin, an archeal actin-like protein
81	c3slcA	Alignment	not modelled	94.4	18	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
82	c3hz6A	Alignment	not modelled	94.0	19	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium

						violaceum
83	d1dkgd2	Alignment	not modelled	93.9	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
84	d2p3ra1	Alignment	not modelled	93.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
85	c2cgkB	Alignment	not modelled	93.8	13	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia coli in an2 open uncomplexed conformation.
86	c3ezwD	Alignment	not modelled	93.7	19	PDB header: transferase Chain: D: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
87	c2e2pA	Alignment	not modelled	93.5	14	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
88	c3uleB	Alignment	not modelled	93.4	24	PDB header: structural protein Chain: B: PDB Molecule: actin-related protein 2; PDBTitle: structure of bos taurus arp2/3 complex with bound inhibitor ck-869 and2 atp
89	c1nbwA	Alignment	not modelled	93.3	26	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
90	c2nlxA	Alignment	not modelled	93.3	16	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
91	c4xhpA	Alignment	not modelled	93.0	22	PDB header: structural protein Chain: A: PDB Molecule: parm hybrid fusion protein; PDBTitle: bacillus thuringiensis parm hybrid protein with adp, containing two2 parm mutants
92	c1glbG	Alignment	not modelled	93.0	19	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
93	c3g25B	Alignment	not modelled	92.7	19	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
94	c3h6eB	Alignment	not modelled	92.5	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
95	c2d4wA	Alignment	not modelled	92.5	23	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
96	c3flcX	Alignment	not modelled	92.5	19	PDB header: transferase Chain: X: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
97	c1x3nA	Alignment	not modelled	91.5	25	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
98	d2ewsA1	Alignment	not modelled	91.4	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
99	c4htIA	Alignment	not modelled	91.3	17	PDB header: transferase Chain: A: PDB Molecule: beta-glucoside kinase; PDBTitle: lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
100	c5vm1A	Alignment	not modelled	90.9	15	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of a xylolose kinase from brucella ovis
101	d1nm1a2	Alignment	not modelled	90.6	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
102	c4e1jA	Alignment	not modelled	90.4	17	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
103	c2qm1D	Alignment	not modelled	90.4	16	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
104	d1e4ft1	Alignment	not modelled	90.1	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
105	c3i8bA	Alignment	not modelled	90.0	21	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
106	d2hf3a2	Alignment	not modelled	89.9	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
107	c5ya2A	Alignment	not modelled	89.9	20	PDB header: structural protein Chain: A: PDB Molecule: autoinducer-2 kinase; PDBTitle: crystal structure of lsrk-hpr complex with adp
108	d1huxa	Alignment	not modelled	89.3	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like

109	c2p9kB	Alignment	not modelled	89.0	24	PDB header: structural protein Chain: B: PDB Molecule: actin-like protein 2; PDBTitle: crystal structure of bovine arp2/3 complex co-crystallized with atp2 and crosslinked with glutaraldehyde
110	c3jvpA	Alignment	not modelled	88.9	17	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
111	d1zc6a1	Alignment	not modelled	88.4	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
112	c1hpmA	Alignment	not modelled	88.2	17	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 7o kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
113	c4c23A	Alignment	not modelled	87.6	14	PDB header: transferase Chain: A: PDB Molecule: l-fucose kinase fuck; PDBTitle: l-fucose kinase
114	c5hv7A	Alignment	not modelled	87.6	14	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
115	d1yaga2	Alignment	not modelled	87.5	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
116	d1k8kb1	Alignment	not modelled	87.4	32	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
117	d2fxua2	Alignment	not modelled	87.2	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
118	c4ijaA	Alignment	not modelled	87.2	9	PDB header: protein binding Chain: A: PDB Molecule: xylr protein; PDBTitle: structure of s. aureus methicillin resistance factor mec2
119	c2dpmB	Alignment	not modelled	87.1	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
120	c1tuuA	Alignment	not modelled	86.4	19	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs