
































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h1qB_	 Alignment		100.0	43	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from <i>Carboxydothermus hydrogenoformans</i>
2	c1e4gT_	 Alignment		100.0	17	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from <i>Thermotoga maritima</i>
3	c2v7yA_	 Alignment		100.0	25	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnaK; PDBTitle: crystal structure of the molecular chaperone dnaK from <i>Geobacillus kaustophilus</i> hta426 in post-atp hydrolysis state
4	c3d2fC_	 Alignment		100.0	22	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
5	c2khoA_	 Alignment		100.0	27	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of <i>E. coli</i> hsp70 (dnaK) chaperone2 (1-605) complexed with adp and substrate
6	c1jcgA_	 Alignment		100.0	25	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from <i>Thermotoga maritima</i> , amppnp
7	c1dkgD_	 Alignment		100.0	25	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
8	c2ychA_	 Alignment		100.0	22	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilM; PDBTitle: pilM-pilN type IV pilus biogenesis complex
9	c2v7zA_	 Alignment		100.0	24	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 <i>Rattus norvegicus</i> in post-atp hydrolysis state
10	c3iucC_	 Alignment		100.0	24	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
11	c1hpmA_	 Alignment		100.0	24	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (N-terminal) of 70 kDa heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. II. potassium binds specifically in the3 atpase active site

12	dlhuxa_	Alignment		100.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
13	c2d0oA_	Alignment		99.9	19	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
14	c1o1f4_	Alignment		99.9	17	PDB header: contractile protein Chain: 4: PDB Molecule: skeletal muscle actin; PDBTitle: molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
15	c1mwmA_	Alignment		99.9	17	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
16	c3dwlB_	Alignment		99.9	17	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
17	dljcea2	Alignment		99.9	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
18	d1e4ft2	Alignment		99.9	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
19	c2p9lA_	Alignment		99.9	19	PDB header: structural protein Chain: A: PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
20	c2fsnB_	Alignment		99.8	20	PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
21	d1dkgd2	Alignment	not modelled	99.8	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
22	c3qb0C_	Alignment	not modelled	99.8	19	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
23	d1bupa2	Alignment	not modelled	99.8	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
24	d2e8aa2	Alignment	not modelled	99.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
25	c3js6A_	Alignment	not modelled	99.7	13	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
26	d2ewsal	Alignment	not modelled	99.7	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
27	c2e2pA_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
28	d2zgaya2	Alignment	not modelled	99.6	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
29	c3hz6A_	Alignment	not modelled	99.6	20	PDB header: transferase Chain: A: PDB Molecule: xylulokinase;

29	c3hzvA_	Alignment	not modelled	99.6	20	PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
30	c2nlxA_	Alignment	not modelled	99.6	16	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
31	c3ifrB_	Alignment	not modelled	99.6	21	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
32	c3gbtA_	Alignment	not modelled	99.6	20	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
33	d1e4ft1	Alignment	not modelled	99.5	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
34	c2dpnB_	Alignment	not modelled	99.5	22	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
35	c3gg4B_	Alignment	not modelled	99.5	23	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
36	d1jcea1	Alignment	not modelled	99.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
37	c2zf5O_	Alignment	not modelled	99.5	22	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
38	c2ch5D_	Alignment	not modelled	99.5	12	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
39	c3flcX_	Alignment	not modelled	99.5	17	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
40	c3g25B_	Alignment	not modelled	99.4	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.
41	c2w40C_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
42	c2qm1D_	Alignment	not modelled	99.4	16	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
43	c3i8bA_	Alignment	not modelled	99.4	20	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
44	c3ezwD_	Alignment	not modelled	99.4	20	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
45	c2d4wA_	Alignment	not modelled	99.4	22	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
46	d1nm1a2	Alignment	not modelled	99.4	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
47	d2fxua2	Alignment	not modelled	99.4	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
48	d2fsja1	Alignment	not modelled	99.4	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
49	c2ap1A_	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
50	c1glbG_	Alignment	not modelled	99.4	16	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
51	c2p9kB_	Alignment	not modelled	99.3	21	PDB header: structural protein Chain: B: PDB Molecule: actin-like protein 2; PDBTitle: crystal structure of bovine arp2/3 complex co-crystallized2 with atp and crosslinked with glutaraldehyde
52	d2hf3a2	Alignment	not modelled	99.3	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
53	c2aa4B_	Alignment	not modelled	99.3	15	PDB header: transferase Chain: B: PDB Molecule: putative n-acetylmannosamine kinase; PDBTitle: crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
54	c2ivoC_	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
						PDB header: transferase

55	c3jvpA_	Alignment	not modelled	99.3	19	Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
56	c3hi0B_	Alignment	not modelled	99.3	17	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
57	c1z05A_	Alignment	not modelled	99.3	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
58	d1yaga2	Alignment	not modelled	99.2	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
59	c3enoB_	Alignment	not modelled	99.2	13	PDB header: hydrolase/unknown function Chain: B: PDB Molecule: putative o-sialoglycoprotein endopeptidase; PDBTitle: crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
60	c3eo3B_	Alignment	not modelled	99.2	15	PDB header: isomerase, transferase Chain: B: PDB Molecule: bifunctional udp-n-acetylglucosamine 2-epimerase/n- PDBTitle: crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
61	c3htvA_	Alignment	not modelled	99.2	17	PDB header: transferase Chain: A: PDB Molecule: d-allose kinase; PDBTitle: crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
62	c1t6dB_	Alignment	not modelled	99.2	19	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
63	d2e8aa1	Alignment	not modelled	99.2	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
64	d1bupa1	Alignment	not modelled	99.2	25	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
65	c1nbwA_	Alignment	not modelled	99.2	27	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
66	c1z6rC_	Alignment	not modelled	99.1	15	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
67	c1zc6A_	Alignment	not modelled	99.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable n-acetylglucosamine kinase; PDBTitle: crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
68	c3vgkB_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
69	c2gupA_	Alignment	not modelled	99.1	18	PDB header: transferase Chain: A: PDB Molecule: rok family protein; PDBTitle: structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
70	d1k8ka2	Alignment	not modelled	99.1	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
71	d1dkgd1	Alignment	not modelled	99.1	28	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
72	c2cgkB_	Alignment	not modelled	99.1	16	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
73	c2floA_	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
74	c3r8eA_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: A: PDB Molecule: hypothetical sugar kinase; PDBTitle: crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
75	c1xupO_	Alignment	not modelled	99.1	15	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
76	c3mdqA_	Alignment	not modelled	99.1	12	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
77	c3en9B_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
78	c3cetA_	Alignment	not modelled	99.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: crystal structure of the pantheonate kinase-like protein2 q6m145 at the resolution 1.8 a. northeast structural 3 genomics consortium target mrr63
79	d1k8kb1	Alignment	not modelled	99.0	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain

						Family: Actin/HSP70
80	c3cerD_	Alignment	not modelled	98.9	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: possible exopolyphosphatase-like protein; PDBTitle: crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
81	c2hoeA_	Alignment	not modelled	98.9	12	PDB header: transferase Chain: A: PDB Molecule: n-acetylglucosamine kinase; PDBTitle: crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
82	c1xc3A_	Alignment	not modelled	98.9	15	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
83	c2q2rA_	Alignment	not modelled	98.7	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
84	c3h6eB_	Alignment	not modelled	98.6	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
85	d2d0oa3	Alignment	not modelled	98.6	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
86	d1nbwa3	Alignment	not modelled	98.5	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
87	c3mcpA_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
88	c3cqyA_	Alignment	not modelled	98.4	15	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
89	c2i7pA_	Alignment	not modelled	98.4	20	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 3; PDBTitle: crystal structure of human pank3 in complex with accoa
90	c1zbsA_	Alignment	not modelled	98.3	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein pg1100; PDBTitle: crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
91	d2p3ra1	Alignment	not modelled	98.3	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
92	d2ch5a2	Alignment	not modelled	98.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
93	c1woqB_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: B: PDB Molecule: inorganic polyphosphate/atp-glucomannokinase; PDBTitle: crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
94	d1zc6a1	Alignment	not modelled	98.1	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
95	c3qbwA_	Alignment	not modelled	98.1	19	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acteylmuramic acid kinase (anmk) bound to adenosine diphosphate
96	d1u6za3	Alignment	not modelled	98.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
97	d1sz2a1	Alignment	not modelled	98.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
98	d2p3ra2	Alignment	not modelled	97.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
99	d1t6ca2	Alignment	not modelled	97.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
100	d1r59o2	Alignment	not modelled	97.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
101	c3smpA_	Alignment	not modelled	97.7	20	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 1; PDBTitle: monoclinic crystal structure of human pantothenate kinase 1 alpha
102	d2ap1a2	Alignment	not modelled	97.4	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
103	d1q18a1	Alignment	not modelled	97.4	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
104	c1sazA_	Alignment	not modelled	97.4	17	PDB header: transferase Chain: A: PDB Molecule: probable butyrate kinase 2; PDBTitle: membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima

105	d1r59o1	Alignment	not modelled	97.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
106	d2aa4a2	Alignment	not modelled	97.0	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
107	c3tsuA	Alignment	not modelled	97.0	15	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
108	d2i7na2	Alignment	not modelled	96.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
109	d2gupa1	Alignment	not modelled	96.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
110	d2i7pa1	Alignment	not modelled	96.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
111	d2hoea3	Alignment	not modelled	96.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
112	c1zxoB	Alignment	not modelled	96.7	14	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical protein q8a1p1; PDBTitle: x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
113	d1z05a2	Alignment	not modelled	96.7	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
114	d2aa4a1	Alignment	not modelled	96.7	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
115	c3lm2B	Alignment	not modelled	96.7	13	PDB header: transferase Chain: B: PDB Molecule: putative kinase; PDBTitle: crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
116	d1z6ra2	Alignment	not modelled	96.7	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
117	c2h3gX	Alignment	not modelled	96.3	14	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
118	d1nbwa2	Alignment	not modelled	96.3	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
119	d1xc3a1	Alignment	not modelled	96.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
120	d1yaga1	Alignment	not modelled	96.2	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70