








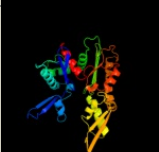









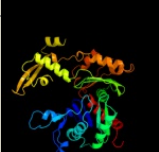





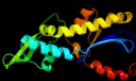




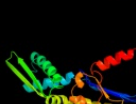


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1jcgA_	 Alignment		100.0	54	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
2	c2v7yA_	 Alignment		100.0	26	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein dnaK; PDBTitle: crystal structure of the molecular chaperone dnaK from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
3	c3d2fC_	 Alignment		100.0	19	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
4	c2khoA_	 Alignment		100.0	21	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnaK) chaperone2 (1-605) complexed with adp and substrate
5	c1dkgD_	 Alignment		100.0	24	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
6	c3iucC_	 Alignment		100.0	23	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
7	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 rattus norvegicus in post-atp hydrolysis state
8	c1hpmA_	 Alignment		100.0	22	PDB header: hydrolase (acting on acid anhydrides) Chain: A: PDB Molecule: 44k atpase fragment (n-terminal) of 70 kd heat- PDBTitle: how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
9	c1o1f4_	 Alignment		100.0	15	PDB header: contractile protein Chain: 4: PDB Molecule: skeletal muscle actin; PDBTitle: molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
10	c2p9lA_	 Alignment		100.0	18	PDB header: structural protein Chain: A: PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
11	c3dwlB_	 Alignment		100.0	18	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

12	c3h1qB_	Alignment		100.0	26	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from <i>2 carboxydotherrmus hydrogenoformans</i>
13	c3qb0C_	Alignment		100.0	19	PDB header: structural protein Chain: C: PDB Molecule: actin-related protein 4; PDBTitle: crystal structure of actin-related protein arp4 from <i>s. cerevisiae</i> 2 complexed with atp
14	c1e4gT_	Alignment		100.0	19	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from <i>thermotoga maritima</i>
15	d1jcea2	Alignment		100.0	53	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
16	c2d0oA_	Alignment		100.0	21	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
17	c2fsnB_	Alignment		100.0	19	PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
18	c1mwmA_	Alignment		100.0	12	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
19	d1bupa2	Alignment		100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
20	d1dkgd2	Alignment		100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
21	d2e8aa2	Alignment	not modelled	99.9	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
22	c2ychA_	Alignment	not modelled	99.9	23	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-piln type iv pilus biogenesis complex
23	c3js6A_	Alignment	not modelled	99.9	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
24	c2p9kB_	Alignment	not modelled	99.9	20	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
25	d1e4ft2	Alignment	not modelled	99.9	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
26	d1jcea1	Alignment	not modelled	99.9	53	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
27	d2hf3a2	Alignment	not modelled	99.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
28	d1nm1a2	Alignment	not modelled	99.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
29	d2fxua2	Alignment	not modelled	99.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain

					Family: Actin/HSP70
30	d1k8ka2	Alignment	not modelled	99.8	18 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
31	d1yaga2	Alignment	not modelled	99.8	17 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
32	d2gga2	Alignment	not modelled	99.8	14 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
33	d2e8aa1	Alignment	not modelled	99.7	29 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
34	d1bupa1	Alignment	not modelled	99.7	27 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
35	d1dkgd1	Alignment	not modelled	99.7	29 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
36	d2fsja1	Alignment	not modelled	99.7	21 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
37	d1huxa_	Alignment	not modelled	99.6	17 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
38	d1k8kb1	Alignment	not modelled	99.6	19 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
39	d1k8ka1	Alignment	not modelled	99.4	18 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
40	d1yaga1	Alignment	not modelled	99.3	15 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
41	d1c0fa1	Alignment	not modelled	99.2	16 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
42	d2fxua1	Alignment	not modelled	99.2	15 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
43	d2hf3a1	Alignment	not modelled	99.2	17 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
44	d2ews1	Alignment	not modelled	99.1	14 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
45	c2e2pA_	Alignment	not modelled	98.9	10 PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
46	c2aa4B_	Alignment	not modelled	98.4	17 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
47	c1nbwA_	Alignment	not modelled	98.4	20 PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
48	c3gg4B_	Alignment	not modelled	98.3	10 PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
49	c3ifrB_	Alignment	not modelled	98.3	15 PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
50	c3hz6A_	Alignment	not modelled	98.3	19 PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
51	d2d0oa3	Alignment	not modelled	98.3	21 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
52	d2p3ra2	Alignment	not modelled	98.2	16 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
53	c2ivoC_	Alignment	not modelled	98.2	15 PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
54	c2nlxA_	Alignment	not modelled	98.2	18 PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
55	d1nbwa3	Alignment	not modelled	98.2	22 Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
56	c2zf5O_	Alignment	not modelled	98.1	11 PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase

						from a2 hyperthermophilic archaeon
57	c2dnpB_	Alignment	not modelled	98.1	20	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
58	c1t6dB_	Alignment	not modelled	98.1	16	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
59	c3flcX_	Alignment	not modelled	98.1	16	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
60	c1xupO_	Alignment	not modelled	98.0	15	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
61	c2d4wA_	Alignment	not modelled	98.0	16	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
62	c3g25B_	Alignment	not modelled	98.0	12	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.
63	d1r59o2	Alignment	not modelled	98.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
64	c3hi0B_	Alignment	not modelled	98.0	18	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
65	c3gbtA_	Alignment	not modelled	98.0	14	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
66	c3jvpA_	Alignment	not modelled	97.9	14	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
67	c2cgkB_	Alignment	not modelled	97.9	18	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.
68	c1glbG_	Alignment	not modelled	97.9	19	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
69	c2floA_	Alignment	not modelled	97.9	16	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
70	c3i8bA_	Alignment	not modelled	97.9	23	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
71	c2ap1A_	Alignment	not modelled	97.9	16	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
72	c1z05A_	Alignment	not modelled	97.9	16	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.
73	c2w40C_	Alignment	not modelled	97.8	9	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
74	c3cetA_	Alignment	not modelled	97.8	15	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 structural3 genomics consortium target mrr63
75	c3htvA_	Alignment	not modelled	97.8	13	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
76	c3ezwD_	Alignment	not modelled	97.8	17	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
77	c3cqyA_	Alignment	not modelled	97.8	16	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
78	c3vgkB_	Alignment	not modelled	97.7	16	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
79	c3mdqA_	Alignment	not modelled	97.7	20	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
80	c1z6rC_	Alignment	not modelled	97.6	12	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
81	c2qm1D_	Alignment	not modelled	97.6	16	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis

82	c2ch5D	Alignment	not modelled	97.5	9	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
83	c3eo3B	Alignment	not modelled	97.5	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
84	c2h3gX	Alignment	not modelled	97.5	21	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
85	c3enoB	Alignment	not modelled	97.3	16	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
86	c3cerD	Alignment	not modelled	97.2	18	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
87	c3r8eA	Alignment	not modelled	97.2	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
88	d2i7pa1	Alignment	not modelled	96.8	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
89	c2hoeA	Alignment	not modelled	96.4	14	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
90	d2i7na2	Alignment	not modelled	96.4	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
91	c1zc6A	Alignment	not modelled	96.3	14	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.
92	d2zgya1	Alignment	not modelled	96.3	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
93	d2aa4a2	Alignment	not modelled	96.2	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
94	c1sazA	Alignment	not modelled	96.2	16	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
95	c2f9tB	Alignment	not modelled	96.1	16	PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the type iii coa from pseudomonas aeruginosa
96	c3qbwA	Alignment	not modelled	96.0	16	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetylmuramic acid kinase; PDBTitle: crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acetylmuramic acid kinase (anmk) bound to adenosine diphosphate
97	d1u6za3	Alignment	not modelled	95.9	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
98	d1z05a2	Alignment	not modelled	95.8	9	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
99	c2i7pA	Alignment	not modelled	95.8	14	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 3; PDBTitle: crystal structure of human pank3 in complex with accoa
100	d1t6ca2	Alignment	not modelled	95.8	31	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
101	c3tsuA	Alignment	not modelled	95.7	15	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
102	c2gupA	Alignment	not modelled	95.7	13	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
103	d2ap1a1	Alignment	not modelled	95.7	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
104	d2fsja2	Alignment	not modelled	95.1	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
105	c3h6eB	Alignment	not modelled	94.9	14	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
106	c3smnA	Alignment	not modelled	94.8	13	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase 1;

106	c3snpA	Alignment	not modelled	94.8	13	PDBTitle: monoclinic crystal structure of human pantothenate kinase 1 alpha PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
107	c3en9B	Alignment	not modelled	94.6	13	PDB header: transferase Chain: C: PDB Molecule: type iii pantothenate kinase; PDBTitle: type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
108	c3bf1C	Alignment	not modelled	94.6	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
109	d2hoea2	Alignment	not modelled	94.3	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
110	d2ch5a1	Alignment	not modelled	94.1	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
111	d1z6ra3	Alignment	not modelled	93.7	8	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
112	c3aapA	Alignment	not modelled	92.8	12	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleoside triphosphate diphosphohydrolase i; PDBTitle: crystal structure of Ip1ntpdase from legionella pneumophila
113	d2gupa2	Alignment	not modelled	91.6	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
114	d1xc3a2	Alignment	not modelled	91.1	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
115	d2p3ra1	Alignment	not modelled	90.9	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
116	c3djca	Alignment	not modelled	90.6	18	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
117	d1zc6a1	Alignment	not modelled	90.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
118	c3p4iA	Alignment	not modelled	89.8	15	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
119	d1saza2	Alignment	not modelled	89.3	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
120	c1zxoB	Alignment	not modelled	88.6	15	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.