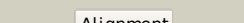
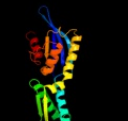


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2khoA_	 Alignment		100.0	100	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 70; PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
2	c3d2fC_	 Alignment		100.0	24	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
3	c2v7yA_	 Alignment		100.0	67	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
4	c1dkgD_	 Alignment		100.0	99	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
5	c3iucC_	 Alignment		100.0	54	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
6	c1hpmA_	 Alignment		100.0	51	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
7	c2v7zA_	 Alignment		100.0	50	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	c1jcgA_	 Alignment		100.0	25	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
9	c3h1qB_	 Alignment		100.0	29	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutJ; PDBTitle: crystal structure of ethanolamine utilization protein eutJ from2 carboxydotherrus hydrogenoformans
10	d1dkgd2	 Alignment		100.0	99	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
11	d1dkgd1	 Alignment		100.0	100	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70

12	c1e4gT_	Alignment		100.0	13	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
13	d2e8aa1	Alignment		100.0	56	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
14	d1bupa2	Alignment		100.0	47	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
15	c1u00A_	Alignment		100.0	37	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein hsca; PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkih
16	d2e8aa2	Alignment		100.0	49	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
17	d1bupa1	Alignment		100.0	54	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
18	c1o1f4_	Alignment		100.0	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
19	c2d0oA_	Alignment		100.0	18	PDB header: chaperone Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
20	c3dpqE_	Alignment		100.0	100	PDB header: chaperone, peptide binding protein Chain: E: PDB Molecule: chaperone protein dnak; PDBTitle: crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrolicocin-derived3 inhibitor peptide (form b)
21	c3dwlB_	Alignment	not modelled	99.9	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
22	c2p9lA_	Alignment	not modelled	99.9	16	PDB header: structural protein Chain: A: PDB Molecule: actin-like protein 3; PDBTitle: crystal structure of bovine arp2/3 complex
23	d1jcea2	Alignment	not modelled	99.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
24	c1mwmA_	Alignment	not modelled	99.9	17	PDB header: structural protein Chain: A: PDB Molecule: parm; PDBTitle: parm from plasmid r1 adp form
25	d1jcea1	Alignment	not modelled	99.9	34	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
26	c2fsnB_	Alignment	not modelled	99.9	20	PDB header: structural protein Chain: B: PDB Molecule: hypothetical protein ta0583; PDBTitle: crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
27	c3n8eA_	Alignment	not modelled	99.9	63	PDB header: chaperone Chain: A: PDB Molecule: stress-70 protein, mitochondrial; PDBTitle: substrate binding domain of the human heat shock 70kda protein 92 (mortalin)
28	c1bprA_	Alignment	not modelled	99.9	98	PDB header: molecular chaperone Chain: A: PDB Molecule: dnak; PDBTitle: nmr structure of the substrate binding domain of dnak,2 minimized average structure
						PDB header: structural protein

29	c3qb0C_	Alignment	not modelled	99.8	18	Chain: C: PDB Molecule: actin-related protein 4; PDBTitle: crystal structure of actin-related protein arp4 from s. cerevisiae2 complexed with atp
30	c2ychA_	Alignment	not modelled	99.8	19	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilm; PDBTitle: pilm-pilm type iv pilus biogenesis complex
31	c3js6A_	Alignment	not modelled	99.8	21	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized parm protein; PDBTitle: crystal structure of apo psk41 parm protein
32	d1yuwa1	Alignment	not modelled	99.8	58	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
33	c2op6A_	Alignment	not modelled	99.8	56	PDB header: peptide binding protein Chain: A: PDB Molecule: heat shock 70 kda protein d; PDBTitle: peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans
34	d1e4ft2	Alignment	not modelled	99.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
35	d1u00a2	Alignment	not modelled	99.7	50	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
36	c3dggC_	Alignment	not modelled	99.7	64	PDB header: chaperone Chain: C: PDB Molecule: heat shock 70 kda protein f; PDBTitle: peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.
37	d1dkza2	Alignment	not modelled	99.7	99	Fold: Heat shock protein 70kD (HSP70), peptide-binding domain Superfamily: Heat shock protein 70kD (HSP70), peptide-binding domain Family: Heat shock protein 70kD (HSP70), peptide-binding domain
38	d2zgya2	Alignment	not modelled	99.6	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
39	d1huxa_	Alignment	not modelled	99.6	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
40	d2fsja1	Alignment	not modelled	99.4	23	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
41	d1dkza1	Alignment	not modelled	99.3	100	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
42	d1u00a1	Alignment	not modelled	99.3	23	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
43	d1nm1a2	Alignment	not modelled	99.2	21	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
44	d2hf3a2	Alignment	not modelled	99.1	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
45	d1dkyb1	Alignment	not modelled	99.1	100	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
46	d2fxua2	Alignment	not modelled	99.1	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
47	d1ud0a_	Alignment	not modelled	99.0	14	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Heat shock protein 70kD (HSP70), C-terminal subdomain Family: Heat shock protein 70kD (HSP70), C-terminal subdomain
48	c3loff_	Alignment	not modelled	99.0	17	PDB header: chaperone Chain: F: PDB Molecule: heat shock 70 kda protein 1; PDBTitle: c-terminal domain of human heat shock 70kda protein 1b.
49	c2p32B_	Alignment	not modelled	98.9	16	PDB header: chaperone Chain: B: PDB Molecule: heat shock 70 kda protein a; PDBTitle: crystal structure of the c-terminal 10 kda subdomain from c. elegans2 hsp70
50	d1yaga2	Alignment	not modelled	98.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
51	d1k8ka2	Alignment	not modelled	98.9	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
52	c2e2pA_	Alignment	not modelled	98.8	13	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
53	c1ud0B_	Alignment	not modelled	98.8	14	PDB header: chaperone Chain: B: PDB Molecule: 70 kda heat-shock-like protein; PDBTitle: crystal structure of the c-terminal 10-kda subdomain of hsc70
54	c2p9kB_	Alignment	not modelled	98.7	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
55	d1k8kb1	Alignment	not modelled	98.7	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70

56	c3gg4B_	Alignment	not modelled	98.6	13	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
57	d2hf3a1	Alignment	not modelled	98.2	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
58	d1c0fa1	Alignment	not modelled	98.1	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
59	c3hz6A_	Alignment	not modelled	98.1	12	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
60	c3ifrB_	Alignment	not modelled	98.1	19	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
61	d1yaga1	Alignment	not modelled	98.0	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
62	c2nlxA_	Alignment	not modelled	98.0	18	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
63	d2fxua1	Alignment	not modelled	97.9	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
64	d1k8ka1	Alignment	not modelled	97.9	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
65	d2p3ra2	Alignment	not modelled	97.8	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
66	c2zf5O_	Alignment	not modelled	97.8	18	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
67	d1r59o2	Alignment	not modelled	97.8	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
68	c3gbtA_	Alignment	not modelled	97.8	13	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
69	c1t6dB_	Alignment	not modelled	97.8	21	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
70	c2dpmB_	Alignment	not modelled	97.8	17	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8
71	d1e4ft1	Alignment	not modelled	97.7	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
72	c3hi0B_	Alignment	not modelled	97.7	21	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
73	c3flcX_	Alignment	not modelled	97.7	23	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
74	c1glbG_	Alignment	not modelled	97.7	14	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
75	c1nbwA_	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: A: PDB Molecule: glycerol dehydratase reactivase alpha subunit; PDBTitle: glycerol dehydratase reactivase
76	c3g25B_	Alignment	not modelled	97.7	18	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.
77	c1xupO_	Alignment	not modelled	97.7	22	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
78	c2aa4B_	Alignment	not modelled	97.7	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
79	c3i8bA_	Alignment	not modelled	97.7	22	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
80	c3jvpA_	Alignment	not modelled	97.7	15	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
81	c2d4wA_	Alignment	not modelled	97.6	16	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060

82	c2cgkB	Alignment	not modelled	97.6	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.
83	c3htvA	Alignment	not modelled	97.6	20	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
84	c3ezwD	Alignment	not modelled	97.5	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
85	d2d0oa3	Alignment	not modelled	97.5	27	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
86	c2w40C	Alignment	not modelled	97.4	14	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
87	d1nbwa3	Alignment	not modelled	97.4	27	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
88	c3cerD	Alignment	not modelled	97.2	15	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
89	c2floA	Alignment	not modelled	97.1	16	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
90	c3eo3B	Alignment	not modelled	97.0	20	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
91	c1zc6A	Alignment	not modelled	96.8	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	c2ap1A	Alignment	not modelled	96.7	17	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
93	c1z6rC	Alignment	not modelled	96.7	14	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
94	c2ivoC	Alignment	not modelled	96.7	18	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
95	c3enoB	Alignment	not modelled	96.4	17	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
96	c3r8eA	Alignment	not modelled	96.3	19	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
97	c2qm1D	Alignment	not modelled	96.0	21	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
98	c3h6eB	Alignment	not modelled	95.8	13	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
99	c2ch5D	Alignment	not modelled	95.8	15	PDB header: transferase Chain: D: PDB Molecule: nakg protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
100	d2ewsal	Alignment	not modelled	95.7	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
101	c1woqB	Alignment	not modelled	94.9	21	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
102	c3mdqA	Alignment	not modelled	94.0	14	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
103	c1z05A	Alignment	not modelled	93.9	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.
104	d1zc6a1	Alignment	not modelled	93.5	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
105	d2p3ra1	Alignment	not modelled	93.4	35	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
						PDB header: structural genomics, unknown function

106	c3cetA	Alignment	not modelled	92.8	22	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
107	d1sz2a1	Alignment	not modelled	91.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
108	d1vhxa	Alignment	not modelled	91.7	41	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
109	d2apia1	Alignment	not modelled	91.4	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
110	c3tsuA	Alignment	not modelled	91.1	12	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
111	d1nu0a	Alignment	not modelled	90.9	32	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
112	d2fsja2	Alignment	not modelled	90.7	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ta0583-like
113	d1iv0a	Alignment	not modelled	90.4	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Putative Holliday junction resolvase RuvX
114	d2aa4a2	Alignment	not modelled	90.0	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
115	d2ch5a2	Alignment	not modelled	89.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
116	d2i7na2	Alignment	not modelled	89.7	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
117	c3aapA	Alignment	not modelled	89.6	22	PDB header: hydrolase Chain: A: PDB Molecule: ectonucleoside triphosphate diphosphohydrolase i; PDBTitle: crystal structure of Ip1ntpdase from Legionella pneumophila
118	c3cqyA	Alignment	not modelled	89.5	14	PDB header: transferase Chain: A: PDB Molecule: anhydro-n-acetyl muramic acid kinase; PDBTitle: crystal structure of a functionally unknown protein (so_1313) from Shewanella oneidensis mr-1
119	d1u6za3	Alignment	not modelled	88.7	24	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
120	d1z05a2	Alignment	not modelled	88.6	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK