

























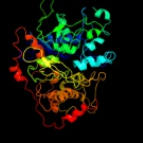

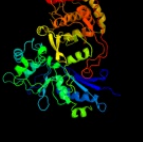




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cgkB_	 Alignment		100.0	98	PDB header: transferase Chain: B: PDB Molecule: l-rhamnulose kinase; PDBTitle: crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
2	c3gbtA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: gluconate kinase; PDBTitle: crystal structure of gluconate kinase from lactobacillus acidophilus
3	c3flcX_	 Alignment		100.0	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
4	c2zf5O_	 Alignment		100.0	18	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
5	c2d4wA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
6	c3hz6A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: xylulokinase; PDBTitle: crystal structure of xylulokinase from chromobacterium violaceum
7	c3lfrB_	 Alignment		100.0	16	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of xylulose kinase from rhodospirillum rubrum
8	c3jvpA_	 Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: ribulokinase; PDBTitle: crystal structure of ribulokinase from bacillus halodurans
9	c3g25B_	 Alignment		100.0	17	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.
10	c2w40C_	 Alignment		100.0	15	PDB header: transferase Chain: C: PDB Molecule: glycerol kinase, putative; PDBTitle: crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
11	c2dpnB_	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: crystal structure of the glycerol kinase from thermus2 thermophilus hb8

12	c2nlxA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: crystal structure of the apo e. coli xylulose kinase
13	c1glbG_	Alignment		100.0	17	PDB header: phosphotransferase Chain: G: PDB Molecule: glycerol kinase; PDBTitle: structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
14	c3ezwD_	Alignment		100.0	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
15	c3gg4B_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: glycerol kinase; PDBTitle: the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
16	c1xupO_	Alignment		100.0	17	PDB header: transferase Chain: O: PDB Molecule: glycerol kinase; PDBTitle: enterococcus casseliflavus glycerol kinase complexed with glycerol
17	c3i8bA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: xylulose kinase; PDBTitle: the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
18	c3h6eB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, fggy; PDBTitle: the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
19	d2p3ra1	Alignment		100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
20	d1r59o1	Alignment		100.0	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
21	d2p3ra2	Alignment	not modelled	100.0	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
22	d1r59o2	Alignment	not modelled	100.0	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glycerol kinase
23	d1huxa_	Alignment	not modelled	99.4	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
24	c3h1qB_	Alignment	not modelled	99.2	18	PDB header: structural protein Chain: B: PDB Molecule: ethanolamine utilization protein eutj; PDBTitle: crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrus hydrogenoformans
25	c2e2pA_	Alignment	not modelled	99.2	15	PDB header: transferase Chain: A: PDB Molecule: hexokinase; PDBTitle: crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
26	d1zc6a1	Alignment	not modelled	98.8	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
27	c3enoB_	Alignment	not modelled	98.7	14	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
28	c3eo3B_	Alignment	not modelled	98.6	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 qne protein

29	c2ivoC	Alignment	not modelled	98.6	18	PDB header: hydrolase Chain: C: PDB Molecule: up1; PDBTitle: structure of up1 protein
30	d2ews1	Alignment	not modelled	98.6	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
31	c1zc6A	Alignment	not modelled	98.4	11	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.
32	d1z6ra2	Alignment	not modelled	98.3	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
33	c2ap1A	Alignment	not modelled	98.2	12	PDB header: transferase Chain: A: PDB Molecule: putative regulator protein; PDBTitle: crystal structure of the putative regulatory protein
34	d1z05a3	Alignment	not modelled	98.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
35	c1z6rC	Alignment	not modelled	98.1	17	PDB header: transcription Chain: C: PDB Molecule: mlc protein; PDBTitle: crystal structure of mlc from escherichia coli
36	c2qm1D	Alignment	not modelled	98.1	18	PDB header: transferase Chain: D: PDB Molecule: glucokinase; PDBTitle: crystal structure of glucokinase from enterococcus faecalis
37	d2hoea3	Alignment	not modelled	98.1	6	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
38	c2ch5D	Alignment	not modelled	98.0	16	PDB header: transferase Chain: D: PDB Molecule: nagk protein; PDBTitle: crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
39	c3en9B	Alignment	not modelled	97.9	13	PDB header: hydrolase Chain: B: PDB Molecule: o-sialoglycoprotein endopeptidase/protein kinase; PDBTitle: structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
40	c1dkgD	Alignment	not modelled	97.9	19	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
41	c2aa4B	Alignment	not modelled	97.9	14	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
42	d2ap1a2	Alignment	not modelled	97.9	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
43	d2ch5a2	Alignment	not modelled	97.9	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
44	d2aa4a1	Alignment	not modelled	97.9	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
45	d1woqa1	Alignment	not modelled	97.8	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
46	c1z05A	Alignment	not modelled	97.8	21	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.
47	d1dkgd2	Alignment	not modelled	97.7	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
48	c3r8eA	Alignment	not modelled	97.7	17	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
49	c2v7zA	Alignment	not modelled	97.7	19	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
50	c3htvA	Alignment	not modelled	97.6	18	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
51	c3d2fC	Alignment	not modelled	97.6	16	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein homolog sse1; PDBTitle: crystal structure of a complex of sse1p and hsp70
52	d2gupa1	Alignment	not modelled	97.6	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
53	d1q18a1	Alignment	not modelled	97.6	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
54	c2v7yA	Alignment	not modelled	97.5	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
55	d1sz2a1	Alignment	not modelled	97.5	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Glucokinase
56	c3vgkB	Alignment	not modelled	97.5	17	PDB header: transferase Chain: B: PDB Molecule: glucokinase; PDBTitle: crystal structure of a rok family glucokinase from streptomyces2 griseus
57	c1hpmA	Alignment	not modelled	97.5	20	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
58	c1xc3A	Alignment	not modelled	97.4	12	PDB header: transferase Chain: A: PDB Molecule: putative fructokinase; PDBTitle: structure of a putative fructokinase from bacillus subtilis
59	c3mcpA	Alignment	not modelled	97.4	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
60	c2hoeA	Alignment	not modelled	97.3	5	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
61	d2e8aa2	Alignment	not modelled	97.3	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
62	c3cqyA	Alignment	not modelled	97.3	21	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
63	d1bupa2	Alignment	not modelled	97.3	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
64	d1jcea2	Alignment	not modelled	97.3	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
65	c2gupA	Alignment	not modelled	97.2	15	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
66	c3iucC	Alignment	not modelled	97.2	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
67	d1xc3a1	Alignment	not modelled	97.2	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ROK
68	c2q2rA	Alignment	not modelled	97.1	11	PDB header: transferase Chain: A: PDB Molecule: glucokinase 1, putative; PDBTitle: trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
69	c1woqB	Alignment	not modelled	97.1	6	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
70	d1e4ft1	Alignment	not modelled	97.0	11	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
71	c1jcgA	Alignment	not modelled	97.0	21	PDB header: structural protein Chain: A: PDB Molecule: rod shape-determining protein mreB; PDBTitle: mreB from thermotoga maritima, amppnp
72	c1e4gT	Alignment	not modelled	96.9	17	PDB header: bacterial cell division Chain: T: PDB Molecule: cell division protein ftsa; PDBTitle: ftsa (atp-bound form) from thermotoga maritima
73	c2khoA	Alignment	not modelled	96.9	20	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
74	d1e4ft2	Alignment	not modelled	96.9	20	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
75	c2ychA	Alignment	not modelled	96.9	11	PDB header: cell cycle Chain: A: PDB Molecule: competence protein pilM; PDBTitle: pilM-pilN type iv pilus biogenesis complex
76	c1sazA	Alignment	not modelled	96.7	12	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
77	c3qbwA	Alignment	not modelled	96.6	18	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
78	c3lm2B	Alignment	not modelled	96.6	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
						PDB header: chaperone

79	c2d0aA	Alignment	not modelled	96.6	24	Chain: A: PDB Molecule: diol dehydratase-reactivating factor large PDBTitle: strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
80	d2e1za1	Alignment	not modelled	96.2	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
81	c1zbsA	Alignment	not modelled	96.1	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
82	d1g99a1	Alignment	not modelled	96.0	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
83	d2d0oa2	Alignment	not modelled	95.9	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: ATPase domain of dehydratase reactivase alpha subunit
84	d1bg3a3	Alignment	not modelled	95.8	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
85	d1bdga1	Alignment	not modelled	95.7	14	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
86	c3tsuA	Alignment	not modelled	95.4	25	PDB header: transferase Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
87	d1ig8a1	Alignment	not modelled	95.2	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
88	c2h3gX	Alignment	not modelled	95.2	16	PDB header: biosynthetic protein Chain: X: PDB Molecule: biosynthetic protein; PDBTitle: structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
89	c1bdgA	Alignment	not modelled	95.1	14	PDB header: hexokinase Chain: A: PDB Molecule: hexokinase; PDBTitle: hexokinase from schistosoma mansoni complexed with glucose
90	c3t69A	Alignment	not modelled	95.1	24	PDB header: transferase Chain: A: PDB Molecule: putative 2-dehydro-3-deoxygalactonokinase; PDBTitle: crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
91	d1v4sa1	Alignment	not modelled	95.0	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
92	c1ig8A	Alignment	not modelled	95.0	14	PDB header: transferase Chain: A: PDB Molecule: hexokinase pii; PDBTitle: crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
93	d1saza1	Alignment	not modelled	94.9	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
94	c1okjB	Alignment	not modelled	94.6	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protease yeaz; PDBTitle: crystal structure of the essential e. coli yeaz2 protein by mad method using the gadolinium complex3 "dotma"
95	c1tuuA	Alignment	not modelled	94.6	15	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: acetate kinase crystallized with atpgs
96	c1t6dB	Alignment	not modelled	94.4	10	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
97	d3bexa1	Alignment	not modelled	94.4	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
98	d1bg3a1	Alignment	not modelled	94.3	19	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
99	c1x3nA	Alignment	not modelled	94.2	19	PDB header: transferase Chain: A: PDB Molecule: propionate kinase; PDBTitle: crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
100	c1zxoB	Alignment	not modelled	94.2	9	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.
101	d1czan3	Alignment	not modelled	94.1	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
102	c3p4iA	Alignment	not modelled	94.1	16	PDB header: transferase Chain: A: PDB Molecule: acetate kinase; PDBTitle: crystal structure of acetate kinase from mycobacterium avium
103	c1v4sA	Alignment	not modelled	94.0	18	PDB header: transferase Chain: A: PDB Molecule: glucokinase isoform 2; PDBTitle: crystal structure of human glucokinase
104	d3bzka5	Alignment	not modelled	94.0	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like

105	d1t6ca1	Alignment	not modelled	93.9	12	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
106	c2iirj_	Alignment	not modelled	93.8	15	PDB header: transferase Chain: J: PDB Molecule: acetate kinase; PDBTitle: acetate kinase from a hypothermophile thermotoga maritima
107	c1mwmA_	Alignment	not modelled	93.6	7	PDB header: structural protein Chain: A: PDB Molecule: parM; PDBTitle: parM from plasmid r1 adp form
108	d2i7pa1	Alignment	not modelled	93.2	15	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
109	c3hm8D_	Alignment	not modelled	93.0	20	PDB header: transferase Chain: D: PDB Molecule: hexokinase-3; PDBTitle: crystal structure of the c-terminal hexokinase domain of human hk3
110	d1czan1	Alignment	not modelled	93.0	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
111	c3hi0B_	Alignment	not modelled	92.9	13	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
112	d2e8aa1	Alignment	not modelled	92.8	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
113	d2i7na2	Alignment	not modelled	92.7	13	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Fumble-like
114	d2a6aa1	Alignment	not modelled	92.6	16	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like
115	c3mdqA_	Alignment	not modelled	92.1	8	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
116	c3cerD_	Alignment	not modelled	92.0	12	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
117	c1qhaA_	Alignment	not modelled	91.8	21	PDB header: transferase Chain: A: PDB Molecule: protein (hexokinase); PDBTitle: human hexokinase type i complexed with atp analogue amp-pnp
118	d1bupa1	Alignment	not modelled	91.5	26	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
119	c3djca_	Alignment	not modelled	91.5	16	PDB header: transferase Chain: A: PDB Molecule: type iii pantothenate kinase; PDBTitle: crystal structure of pantothenate kinase from legionella pneumophila
120	c2a6aB_	Alignment	not modelled	91.3	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein tm0874; PDBTitle: crystal structure of glycoprotein endopeptidase (tm0874) from2 thermotoga maritima at 2.50 a resolution