







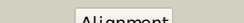

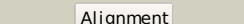

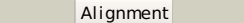

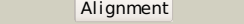

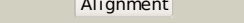
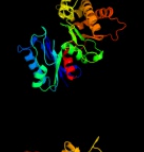
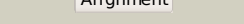

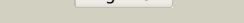
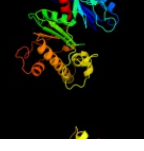
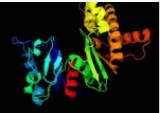







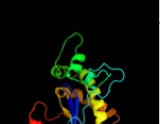


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1z6rC_</a>	 Alignment		100.0	17	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> mlc protein; <b>PDBTitle:</b> crystal structure of mlc from escherichia coli
2	<a href="#">c1z05A_</a>	 Alignment		100.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, rok family; <b>PDBTitle:</b> crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
3	<a href="#">c3htvA_</a>	 Alignment		100.0	96	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allose kinase; <b>PDBTitle:</b> crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
4	<a href="#">c3mcpA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
5	<a href="#">c2hoeA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
6	<a href="#">c3vgkB_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of a rok family glucokinase from streptomyces2 griseus
7	<a href="#">c2ap1A_</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative regulator protein; <b>PDBTitle:</b> crystal structure of the putative regulatory protein
8	<a href="#">c2qm1D_</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
9	<a href="#">c3r8eA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical sugar kinase; <b>PDBTitle:</b> crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
10	<a href="#">c2aa4B_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine kinase; <b>PDBTitle:</b> crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
11	<a href="#">c1xc3A_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative fructokinase; <b>PDBTitle:</b> structure of a putative fructokinase from bacillus subtilis

12	<a href="#">c2gupA</a>	Alignment		100.0	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rok family protein; <b>PDBTitle:</b> structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
13	<a href="#">c3eo3B</a>	Alignment		100.0	20	<b>PDB header:</b> isomerase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional udp-n-acetylglucosamine 2-epimerase/n- <b>PDBTitle:</b> crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
14	<a href="#">c1woqB</a>	Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> inorganic polyphosphate/atp-glucomannokinase; <b>PDBTitle:</b> crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
15	<a href="#">d1sz2a1</a>	Alignment		100.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
16	<a href="#">c2q2rA</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase 1, putative; <b>PDBTitle:</b> trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
17	<a href="#">c3lm2B</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
18	<a href="#">c2ch5D</a>	Alignment		100.0	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nagk protein; <b>PDBTitle:</b> crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
19	<a href="#">c2e2pA</a>	Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
20	<a href="#">d1z05a2</a>	Alignment		100.0	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
21	<a href="#">d1z6ra3</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
22	<a href="#">c1zc6A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> probable n-acetylglucosamine kinase; <b>PDBTitle:</b> crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
23	<a href="#">d2aa4a2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
24	<a href="#">d2hoea2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
25	<a href="#">d2ap1a1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
26	<a href="#">d2gupa2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
27	<a href="#">d1xc3a2</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
28	<a href="#">d1q18a2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
29	<a href="#">d2hoea3</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK

30	<a href="#">dlz6ra2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
31	<a href="#">dlz05a3</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
32	<a href="#">d2ap1a2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
33	<a href="#">d2aa4a1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
34	<a href="#">d1woqa2</a>	Alignment	not modelled	99.8	28	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
35	<a href="#">d1woqa1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
36	<a href="#">d2ews1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
37	<a href="#">d1huxa</a>	Alignment	not modelled	99.8	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
38	<a href="#">d2gupa1</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
39	<a href="#">d1xc3a1</a>	Alignment	not modelled	99.8	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
40	<a href="#">c1ig8A</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase pii; <b>PDBTitle:</b> crystal structure of yeast hexokinase pii with the correct2 amino acid sequence
41	<a href="#">c1bdgA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> hexokinase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> hexokinase from schistosoma mansonii complexed with glucose
42	<a href="#">c3hm8D</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hexokinase-3; <b>PDBTitle:</b> crystal structure of the c-terminal hexokinase domain of human hk3
43	<a href="#">c1v4sA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase isoform 2; <b>PDBTitle:</b> crystal structure of human glucokinase
44	<a href="#">c1zbsA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pg1100; <b>PDBTitle:</b> crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
45	<a href="#">d1zc6a1</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
46	<a href="#">c1qhaA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hexokinase); <b>PDBTitle:</b> human hexokinase type i complexed with atp analogue amp-pnp
47	<a href="#">d1q18a1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
48	<a href="#">d2ch5a2</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
49	<a href="#">c1zxoB</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> conserved hypothetical protein q8a1p1; <b>PDBTitle:</b> x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
50	<a href="#">d2ch5a1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
51	<a href="#">c3h1qB</a>	Alignment	not modelled	99.3	14	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> ethanolamine utilization protein eutj; <b>PDBTitle:</b> crystal structure of ethanolamine utilization protein eutj from2 carboxydotherrhus hydrogenofmans
52	<a href="#">c3hz6A</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
53	<a href="#">c3flcX</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> transferase <b>Chain:</b> X: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
54	<a href="#">d2p3ra1</a>	Alignment	not modelled	98.8	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
55	<a href="#">c3gbtA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gluconate kinase; <b>PDBTitle:</b> crystal structure of gluconate kinase from lactobacillus acidophilus
						<b>PDB header:</b> transferase

56	<a href="#">c3g25B</a>	Alignment	not modelled	98.8	15	<b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
57	<a href="#">c2dnpB</a>	Alignment	not modelled	98.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of the glycerol kinase from thermus2 thermophilus hb8
58	<a href="#">c1glbG</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> phosphotransferase <b>Chain:</b> G: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> structure of the regulatory complex of escherichia coli iiglc with2 glycerol kinase
59	<a href="#">c3ezwD</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
60	<a href="#">c2d4wA</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
61	<a href="#">d1v4sa1</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
62	<a href="#">d1bdga1</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
63	<a href="#">c2nlxA</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of the apo e. coli xylulose kinase
64	<a href="#">d1bg3a3</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
65	<a href="#">c3ifrB</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, fggy; <b>PDBTitle:</b> the crystal structure of xylulose kinase from rhodospirillum rubrum
66	<a href="#">c3enoB</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> hydrolase/unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative o-sialoglycoprotein endopeptidase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
67	<a href="#">d1czan3</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
68	<a href="#">d1czan1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
69	<a href="#">d1bg3a1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
70	<a href="#">c2w40C</a>	Alignment	not modelled	98.6	10	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerol kinase, putative; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
71	<a href="#">c3gg4B</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
72	<a href="#">c2zf5O</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
73	<a href="#">c2ivoC</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
74	<a href="#">d1ig8a1</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
75	<a href="#">c3jvpA</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
76	<a href="#">c3en9B</a>	Alignment	not modelled	98.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> o-sialoglycoprotein endopeptidase/protein kinase; <b>PDBTitle:</b> structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
77	<a href="#">c2cgkB</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> l-rhamnulose kinase; <b>PDBTitle:</b> crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
78	<a href="#">c1xupO</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> transferase <b>Chain:</b> O: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> enterococcus casseliflavus glycerol kinase complexed with glycerol
79	<a href="#">c1sazA</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable butyrate kinase 2; <b>PDBTitle:</b> membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
80	<a href="#">c3h6eB</a>	Alignment	not modelled	98.2	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, fggy; <b>PDBTitle:</b> the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
81	<a href="#">d1zc6a2</a>	Alignment	not modelled	98.1	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain

					<b>Family:</b> BadF/BadG/BcrA/BcrD-like
82	<a href="#">c3i8bA_</a>	Alignment	not modelled	98.1	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
83	<a href="#">d1r59o1</a>	Alignment	not modelled	98.1	17 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
84	<a href="#">c3p4iA_</a>	Alignment	not modelled	97.8	11 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from mycobacterium avium
85	<a href="#">c2khoA_</a>	Alignment	not modelled	97.7	18 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 70; <b>PDBTitle:</b> nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
86	<a href="#">c1hpmA_</a>	Alignment	not modelled	97.7	13 <b>PDB header:</b> hydrolase (acting on acid anhydrides) <b>Chain:</b> A: <b>PDB Molecule:</b> 44k atpase fragment (n-terminal) of 7o kd heat- <b>PDBTitle:</b> how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
87	<a href="#">c1jcgA_</a>	Alignment	not modelled	97.7	18 <b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> mreB from thermotoga maritima, amppnp
88	<a href="#">c3iucC_</a>	Alignment	not modelled	97.6	15 <b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock 70kda protein 5 (glucose-regulated <b>PDBTitle:</b> crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
89	<a href="#">c1x3nA_</a>	Alignment	not modelled	97.6	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> propionate kinase; <b>PDBTitle:</b> crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
90	<a href="#">c3khyA_</a>	Alignment	not modelled	97.5	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> propionate kinase; <b>PDBTitle:</b> crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
91	<a href="#">c2ychA_</a>	Alignment	not modelled	97.3	16 <b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> competence protein pilM; <b>PDBTitle:</b> pilM-pilN type iv pilus biogenesis complex
92	<a href="#">c3d2fC_</a>	Alignment	not modelled	97.2	16 <b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein homolog sse1; <b>PDBTitle:</b> crystal structure of a complex of sse1p and hsp70
93	<a href="#">d1saza2</a>	Alignment	not modelled	97.2	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
94	<a href="#">c1tuuA_</a>	Alignment	not modelled	97.1	9 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
95	<a href="#">d1e4ft1</a>	Alignment	not modelled	97.1	19 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
96	<a href="#">c2v7yA_</a>	Alignment	not modelled	97.0	15 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein dnak; <b>PDBTitle:</b> crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state
97	<a href="#">d1bdga2</a>	Alignment	not modelled	96.9	22 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
98	<a href="#">d1bg3a4</a>	Alignment	not modelled	96.9	18 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
99	<a href="#">c2liirJ_</a>	Alignment	not modelled	96.8	13 <b>PDB header:</b> transferase <b>Chain:</b> J: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase from a hypothermophile thermotoga maritima
100	<a href="#">d1ig8a2</a>	Alignment	not modelled	96.8	12 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
101	<a href="#">d1czan2</a>	Alignment	not modelled	96.7	19 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
102	<a href="#">d1bg3a2</a>	Alignment	not modelled	96.6	16 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
103	<a href="#">d3bzka5</a>	Alignment	not modelled	96.6	12 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
104	<a href="#">d1v4sa2</a>	Alignment	not modelled	96.6	25 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
105	<a href="#">c1o1f4_</a>	Alignment	not modelled	96.5	13 <b>PDB header:</b> contractile protein <b>Chain:</b> 4: <b>PDB Molecule:</b> skeletal muscle actin; <b>PDBTitle:</b> molecular models of averaged rigor crossbridges from2 tomograms of insect flight muscle
106	<a href="#">d1g99a2</a>	Alignment	not modelled	96.4	11 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
107	<a href="#">d1czan4</a>	Alignment	not modelled	96.3	18 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase

108	<a href="#">d1nu0a_</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
109	<a href="#">d1iv0a_</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
110	<a href="#">c2i7pA_</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 3; <b>PDBTitle:</b> crystal structure of human pank3 in complex with accoa
111	<a href="#">d1hjra_</a>	Alignment	not modelled	95.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> RuvC resolvase
112	<a href="#">d2e1za2</a>	Alignment	not modelled	95.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
113	<a href="#">d1vhxa_</a>	Alignment	not modelled	95.7	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
114	<a href="#">c3tsuA_</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
115	<a href="#">d3bexa1</a>	Alignment	not modelled	95.2	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
116	<a href="#">c3cqyA_</a>	Alignment	not modelled	94.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
117	<a href="#">d2e8aa2</a>	Alignment	not modelled	94.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
118	<a href="#">d1bupa2</a>	Alignment	not modelled	94.6	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
119	<a href="#">c3dw1B_</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> actin-related protein 3; <b>PDBTitle:</b> crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
120	<a href="#">c2h3gX_</a>	Alignment	not modelled	94.4	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> X: <b>PDB Molecule:</b> biosynthetic protein; <b>PDBTitle:</b> structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis