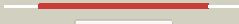



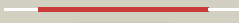




























# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P09099
Date	Wed Jan 25 15:20:14 GMT 2012
Unique Job ID	42b7ce6550b7e674

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2nlxA_</a>	 Alignment		100.0	100	<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
2	<a href="#">c3gbtA_</a>	 Alignment		100.0	24	<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
3	<a href="#">c3flcX_</a>	 Alignment		100.0	19	<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
4	<a href="#">c3ifrB_</a>	 Alignment		100.0	29	<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
5	<a href="#">c2zf5O_</a>	 Alignment		100.0	23	<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
6	<a href="#">c2d4wA_</a>	 Alignment		100.0	22	<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
7	<a href="#">c3hz6A_</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
8	<a href="#">c3jvpA_</a>	 Alignment		100.0	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
9	<a href="#">c3g25B_</a>	 Alignment		100.0	21	<b>PDB header:</b> transferase <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.
10	<a href="#">c3gg4B_</a>	 Alignment		100.0	21	<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
11	<a href="#">c1glbG_</a>	 Alignment		100.0	22	<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

12	<a href="#">c2dpnB</a>	Alignment		100.0	24	<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 thermophilus hb8
13	<a href="#">c2w40C</a>	Alignment		100.0	21	<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
14	<a href="#">c1xupO</a>	Alignment		100.0	20	<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
15	<a href="#">c3ezwD</a>	Alignment		100.0	23	<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
16	<a href="#">c3i8bA</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> the crystal structure of xylulose kinase from bifidobacterium adolescentis
17	<a href="#">c2cgkB</a>	Alignment		100.0	17	<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.
18	<a href="#">c3h6eB</a>	Alignment		100.0	16	<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
19	<a href="#">d2p3ra1</a>	Alignment		100.0	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
20	<a href="#">d1r59o1</a>	Alignment		100.0	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
21	<a href="#">d2p3ra2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
22	<a href="#">d1r59o2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
23	<a href="#">d1huxa</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
24	<a href="#">c3h1qB</a>	Alignment	not modelled	99.5	16	<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 carboxydotherrnus hydrogenoformans
25	<a href="#">d2ewsA1</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
26	<a href="#">c2e2pA</a>	Alignment	not modelled	99.0	14	<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
27	<a href="#">c2qm1D</a>	Alignment	not modelled	99.0	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
28	<a href="#">c2ap1A</a>	Alignment	not modelled	98.9	20	<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
						<b>PDB header:</b> isomerase, transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional udp-n-acetylglucosamine 2-

29	<a href="#">c3eo3B</a>	Alignment	not modelled	98.8	24	epimerase/n- <b>PDBTitle:</b> crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
30	<a href="#">c1e4gT</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> bacterial cell division <b>Chain:</b> T; <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> ftsa (atp-bound form) from thermotoga maritima
31	<a href="#">c3r8eA</a>	Alignment	not modelled	98.8	19	<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
32	<a href="#">c2ivoC</a>	Alignment	not modelled	98.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
33	<a href="#">c3enoB</a>	Alignment	not modelled	98.6	18	<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
34	<a href="#">d1zc6a1</a>	Alignment	not modelled	98.6	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
35	<a href="#">d1z05a3</a>	Alignment	not modelled	98.5	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
36	<a href="#">c3en9B</a>	Alignment	not modelled	98.4	18	<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
37	<a href="#">c1dkgD</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> complex (hsp24/hsp70) <b>Chain:</b> D; <b>PDB Molecule:</b> molecular chaperone dnak; <b>PDBTitle:</b> crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
38	<a href="#">d2ap1a2</a>	Alignment	not modelled	98.4	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
39	<a href="#">c2ch5D</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> nagk protein; <b>PDBTitle:</b> crystal structure of human n-acetylglucosamine in2 complex with n-acetylglucosamine
40	<a href="#">c2v7zA</a>	Alignment	not modelled	98.3	23	<b>PDB header:</b> chaperone <b>Chain:</b> A; <b>PDB Molecule:</b> heat shock cognate 71 kda protein; <b>PDBTitle:</b> crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
41	<a href="#">d2ch5a2</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
42	<a href="#">d1dkgd2</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
43	<a href="#">d2e8aa2</a>	Alignment	not modelled	98.1	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
44	<a href="#">c2v7yA</a>	Alignment	not modelled	98.1	19	<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
45	<a href="#">d1z6ra2</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
46	<a href="#">c1hpmA</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> hydrolase (acting on acid anhydrides) <b>Chain:</b> A; <b>PDB Molecule:</b> 44k atpase fragment (n-terminal) of 70 kd heat- <b>PDBTitle:</b> how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
47	<a href="#">c3d2fC</a>	Alignment	not modelled	98.1	23	<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
48	<a href="#">c1zc6A</a>	Alignment	not modelled	98.1	25	<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.
49	<a href="#">d2h0ea3</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
50	<a href="#">d1bupa2</a>	Alignment	not modelled	98.0	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
51	<a href="#">d1jcea2</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
52	<a href="#">c3iucC</a>	Alignment	not modelled	98.0	18	<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
53	<a href="#">d1woqa1</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
						<b>PDB header:</b> transferase

54	<a href="#">c3htvA</a>	Alignment	not modelled	97.9	13	<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
55	<a href="#">c1xc3A</a>	Alignment	not modelled	97.9	14	<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
56	<a href="#">c1z05A</a>	Alignment	not modelled	97.8	16	<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.
57	<a href="#">c1z6rC</a>	Alignment	not modelled	97.8	13	<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
58	<a href="#">d1xc3a1</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
59	<a href="#">c3vgkB</a>	Alignment	not modelled	97.8	26	<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
60	<a href="#">d2aa4a1</a>	Alignment	not modelled	97.7	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
61	<a href="#">c2aa4B</a>	Alignment	not modelled	97.7	22	<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
62	<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
63	<a href="#">c3cqyA</a>	Alignment	not modelled	97.7	19	<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
64	<a href="#">c1jcgA</a>	Alignment	not modelled	97.6	16	<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
65	<a href="#">d1e4ft2</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
66	<a href="#">d2gupA1</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
67	<a href="#">c2q2rA</a>	Alignment	not modelled	97.5	11	<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
68	<a href="#">c1woqB</a>	Alignment	not modelled	97.5	15	<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
69	<a href="#">d1q18a1</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
70	<a href="#">c2hoeA</a>	Alignment	not modelled	97.4	19	<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
71	<a href="#">c2gupA</a>	Alignment	not modelled	97.4	24	<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
72	<a href="#">d1sz2a1</a>	Alignment	not modelled	97.3	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
73	<a href="#">c3mcpA</a>	Alignment	not modelled	97.2	10	<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
74	<a href="#">d2i7na2</a>	Alignment	not modelled	97.1	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
75	<a href="#">d1e4ft1</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
76	<a href="#">d1bg3a3</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
77	<a href="#">c3qbwA</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> anhydro-n-acetylmuramic acid kinase; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 acetylmuramic acid kinase (anmk) bound to adenosine diphosphate
78	<a href="#">d2i7pa1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
79	<a href="#">d1bdga1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase

80	<a href="#">c3lm2B</a>	Alignment	not modelled	96.9	15	<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
81	<a href="#">d1v4sa1</a>	Alignment	not modelled	96.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
82	<a href="#">c2ychA</a>	Alignment	not modelled	96.6	24	<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
83	<a href="#">d3bexa1</a>	Alignment	not modelled	96.6	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
84	<a href="#">c1bdgA</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> hexokinase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> hexokinase from schistosoma mansoni complexed with glucose
85	<a href="#">d1ig8a1</a>	Alignment	not modelled	96.5	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
86	<a href="#">c2d0oA</a>	Alignment	not modelled	96.5	16	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> diol dehydratase-reactivating factor large <b>PDBTitle:</b> strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
87	<a href="#">c1v4sA</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase isoform 2; <b>PDBTitle:</b> crystal structure of human glucokinase
88	<a href="#">c1zbsA</a>	Alignment	not modelled	96.4	15	<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
89	<a href="#">d2zgya2</a>	Alignment	not modelled	96.4	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
90	<a href="#">c2i7pA</a>	Alignment	not modelled	96.4	16	<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
91	<a href="#">c3tsuA</a>	Alignment	not modelled	96.3	23	<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
92	<a href="#">d1czan1</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
93	<a href="#">d1bg3a1</a>	Alignment	not modelled	96.1	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
94	<a href="#">c1ig8A</a>	Alignment	not modelled	96.0	25	<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
95	<a href="#">d1czan3</a>	Alignment	not modelled	96.0	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
96	<a href="#">c2h3gX</a>	Alignment	not modelled	96.0	16	<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
97	<a href="#">c3smpA</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 1; <b>PDBTitle:</b> monoclinic crystal structure of human pantothenate kinase 1 alpha
98	<a href="#">c3hm8D</a>	Alignment	not modelled	95.8	15	<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
99	<a href="#">c3t69A</a>	Alignment	not modelled	95.7	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2-dehydro-3-deoxygalactonokinase; <b>PDBTitle:</b> crystal structure of a putative 2-dehydro-3-deoxygalactonokinase2 protein from sinorhizobium meliloti
100	<a href="#">c1mwmA</a>	Alignment	not modelled	95.5	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> parm; <b>PDBTitle:</b> parm from plasmid r1 adp form
101	<a href="#">d2e1za1</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
102	<a href="#">c3khyA</a>	Alignment	not modelled	95.3	18	<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
103	<a href="#">c1qhaA</a>	Alignment	not modelled	95.3	12	<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
104	<a href="#">d1u6za2</a>	Alignment	not modelled	95.2	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
105	<a href="#">d2aa4a2</a>	Alignment	not modelled	95.2	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK

106	<a href="#">c3bf1C</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> type iii pantothenate kinase; <b>PDBTitle:</b> type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp
107	<a href="#">d1t6ca1</a>	Alignment	not modelled	94.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Ppx/GppA phosphatase
108	<a href="#">c3djca</a>	Alignment	not modelled	94.5	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type iii pantothenate kinase; <b>PDBTitle:</b> crystal structure of pantothenate kinase from legionella pneumophila
109	<a href="#">c1tuuA</a>	Alignment	not modelled	94.4	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
110	<a href="#">c2floA</a>	Alignment	not modelled	94.2	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
111	<a href="#">c3mdqA</a>	Alignment	not modelled	93.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
112	<a href="#">c1zxoB</a>	Alignment	not modelled	93.8	12	<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.
113	<a href="#">c3hi0B</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative exopolyphosphatase; <b>PDBTitle:</b> crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
114	<a href="#">c1t6dB</a>	Alignment	not modelled	93.7	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> exopolyphosphatase; <b>PDBTitle:</b> miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
115	<a href="#">c3nuwC</a>	Alignment	not modelled	93.4	24	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxo-3-deoxygalactonate kinase; <b>PDBTitle:</b> crystal structure of 2-oxo-3-deoxygalactonate kinase from klebsiella2 pneumoniae
116	<a href="#">d3bzka5</a>	Alignment	not modelled	93.4	31	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
117	<a href="#">d1g99a1</a>	Alignment	not modelled	93.3	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
118	<a href="#">d2ap1a1</a>	Alignment	not modelled	92.4	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
119	<a href="#">c3cerD</a>	Alignment	not modelled	92.4	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> possible exopolyphosphatase-like protein; <b>PDBTitle:</b> crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
120	<a href="#">c1o1f4</a>	Alignment	not modelled	91.4	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