

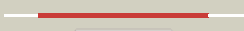






























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2aa4B_</a>	 Alignment		100.0	100	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylmannosamine kinase; <b>PDBTitle:</b> crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
2	<a href="#">c1z6rC_</a>	 Alignment		100.0	22	<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
3	<a href="#">c1z05A_</a>	 Alignment		100.0	24	<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.
4	<a href="#">c2ap1A_</a>	 Alignment		100.0	26	<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
5	<a href="#">c3mcpA_</a>	 Alignment		100.0	18	<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
6	<a href="#">c3r8eA_</a>	 Alignment		100.0	22	<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
7	<a href="#">c3vgkB_</a>	 Alignment		100.0	37	<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
8	<a href="#">c2hoeA_</a>	 Alignment		100.0	21	<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
9	<a href="#">c2qm1D_</a>	 Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
10	<a href="#">c2gupA_</a>	 Alignment		100.0	23	<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
11	<a href="#">c3eo3B_</a>	 Alignment		100.0	27	<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

12	<a href="#">c1xc3A_</a>	Alignment		100.0	24	<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
13	<a href="#">c3htvA_</a>	Alignment		100.0	19	<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
14	<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
15	<a href="#">c1woqB_</a>	Alignment		100.0	26	<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
16	<a href="#">c2e2pA_</a>	Alignment		100.0	19	<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
17	<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
18	<a href="#">c2ch5D_</a>	Alignment		100.0	17	<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="#">d2aa4a2</a>	Alignment		100.0	100	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
20	<a href="#">c3lm2B_</a>	Alignment		100.0	20	<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
21	<a href="#">c1zc6A_</a>	Alignment	not modelled	100.0	18	<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.
22	<a href="#">d1z05a2</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
23	<a href="#">d1z6ra3</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="#">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
25	<a href="#">d2gupa2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
26	<a href="#">d2hoea2</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
27	<a href="#">d1xc3a2</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
28	<a href="#">d2aa4a1</a>	Alignment	not modelled	99.9	100	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
						<b>Fold:</b> Ribonuclease H-like motif

29	<a href="#">dlq18a2</a>	Alignment	not modelled	99.9	14	<b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
30	<a href="#">dlhuxa</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
31	<a href="#">d2ews1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
32	<a href="#">clzbsA</a>	Alignment	not modelled	99.8	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
33	<a href="#">d2hoea3</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
34	<a href="#">dlz6ra2</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
35	<a href="#">dlwoqa2</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
36	<a href="#">dlwoqa1</a>	Alignment	not modelled	99.8	31	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
37	<a href="#">d2ap1a2</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
38	<a href="#">clzxoB</a>	Alignment	not modelled	99.8	15	<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.
39	<a href="#">dlz05a3</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
40	<a href="#">d2gup1</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
41	<a href="#">d2ch5a1</a>	Alignment	not modelled	99.7	20	<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="#">dlxc3a1</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
43	<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
44	<a href="#">clbdgA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> hexokinase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> hexokinase from schistosoma mansonii complexed with glucose
45	<a href="#">clv4sA</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase isoform 2; <b>PDBTitle:</b> crystal structure of human glucokinase
46	<a href="#">clig8A</a>	Alignment	not modelled	99.6	20	<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
47	<a href="#">dlq18a1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
48	<a href="#">clqhaA</a>	Alignment	not modelled	99.5	17	<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
49	<a href="#">dlzc6a1</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
50	<a href="#">clsazA</a>	Alignment	not modelled	99.3	17	<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
51	<a href="#">d2ch5a2</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
52	<a href="#">c3h1qB</a>	Alignment	not modelled	99.2	13	<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 carboxydotherrmus hydrogenofomans
53	<a href="#">c2ivoC</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
54	<a href="#">c3enoB</a>	Alignment	not modelled	99.1	14	<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
						<b>PDB header:</b> transferase

55	<a href="#">c2iirJ_</a>	Alignment	not modelled	99.1	15	<b>Chain:</b> J: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase from a hypothermophile thermotoga maritima
56	<a href="#">c3p4iA_</a>	Alignment	not modelled	99.0	17	<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
57	<a href="#">c1tuuA_</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
58	<a href="#">d1zc6a2</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
59	<a href="#">c3hz6A_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
60	<a href="#">c1x3nA_</a>	Alignment	not modelled	98.7	16	<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
61	<a href="#">c3en9B_</a>	Alignment	not modelled	98.6	12	<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
62	<a href="#">c2nlxA_</a>	Alignment	not modelled	98.6	24	<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
63	<a href="#">d1saza2</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
64	<a href="#">c1jcgA_</a>	Alignment	not modelled	98.4	12	<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="#">c3khyA_</a>	Alignment	not modelled	98.4	16	<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
66	<a href="#">c2ychA_</a>	Alignment	not modelled	98.2	15	<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
67	<a href="#">c3gbtA_</a>	Alignment	not modelled	98.2	20	<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
68	<a href="#">c2w40C_</a>	Alignment	not modelled	98.2	16	<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
69	<a href="#">c3gg4B_</a>	Alignment	not modelled	98.0	17	<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
70	<a href="#">c3ifrB_</a>	Alignment	not modelled	98.0	25	<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
71	<a href="#">c2zf5O_</a>	Alignment	not modelled	98.0	19	<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
72	<a href="#">d2p3ra1</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
73	<a href="#">d1bdga1</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
74	<a href="#">d1czan2</a>	Alignment	not modelled	98.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
75	<a href="#">d1g99a2</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
76	<a href="#">d1bg3a3</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
77	<a href="#">c2dnpB_</a>	Alignment	not modelled	97.9	16	<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
78	<a href="#">c2d4wA_</a>	Alignment	not modelled	97.9	18	<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
79	<a href="#">c3i8bA_</a>	Alignment	not modelled	97.9	14	<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
80	<a href="#">c1glbG_</a>	Alignment	not modelled	97.9	17	<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 iiiglc with2 glycerol kinase
81	<a href="#">c3n25B_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase;

81	<a href="#">c3g23B</a>	Alignment	not modelled	97.8	20	<b>PDBTitle:</b> 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol. <b>PDB header:</b> transferase
82	<a href="#">c3flcX</a>	Alignment	not modelled	97.8	15	<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
83	<a href="#">d2e1za2</a>	Alignment	not modelled	97.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
84	<a href="#">d3bzka5</a>	Alignment	not modelled	97.8	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
85	<a href="#">c3ezwD</a>	Alignment	not modelled	97.8	17	<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
86	<a href="#">d1v4sa1</a>	Alignment	not modelled	97.8	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
87	<a href="#">c3h6eB</a>	Alignment	not modelled	97.7	23	<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
88	<a href="#">d1czan3</a>	Alignment	not modelled	97.7	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
89	<a href="#">c2cgkB</a>	Alignment	not modelled	97.7	13	<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.
90	<a href="#">c1xupO</a>	Alignment	not modelled	97.7	14	<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
91	<a href="#">d1ig8a1</a>	Alignment	not modelled	97.7	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
92	<a href="#">c3smpA</a>	Alignment	not modelled	97.6	18	<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
93	<a href="#">c1o1f4</a>	Alignment	not modelled	97.6	14	<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
94	<a href="#">d1czan1</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
95	<a href="#">d1bg3a4</a>	Alignment	not modelled	97.6	20	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
96	<a href="#">d1bg3a1</a>	Alignment	not modelled	97.5	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
97	<a href="#">d1bdga2</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
98	<a href="#">d1v4sa2</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
99	<a href="#">c3jvpA</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
100	<a href="#">d1bg3a2</a>	Alignment	not modelled	97.4	22	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
101	<a href="#">c2i7pA</a>	Alignment	not modelled	97.3	19	<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
102	<a href="#">c3tsuA</a>	Alignment	not modelled	97.3	20	<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
103	<a href="#">d1zbsa1</a>	Alignment	not modelled	97.3	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
104	<a href="#">d1czan4</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
105	<a href="#">d1ig8a2</a>	Alignment	not modelled	97.2	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
106	<a href="#">c2v7yA</a>	Alignment	not modelled	97.1	16	<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
107	<a href="#">d3bexa1</a>	Alignment	not modelled	96.9	27	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
						<b>PDB header:</b> chaperone

108	<a href="#">c2khoA</a>	Alignment	not modelled	96.8	18	<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
109	<a href="#">d1r59o1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
110	<a href="#">c3cetA</a>	Alignment	not modelled	96.7	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> crystal structure of the pantheonate kinase-like protein2 q6m145 at the resolution 1.8 a. northeast structural3 genomics consortium target mrr63
111	<a href="#">d1vhxa</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
112	<a href="#">c2oceA</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pa5201; <b>PDBTitle:</b> crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
113	<a href="#">c3dwlB</a>	Alignment	not modelled	96.6	11	<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
114	<a href="#">c3iucC</a>	Alignment	not modelled	96.6	17	<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
115	<a href="#">d2e8aa2</a>	Alignment	not modelled	96.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
116	<a href="#">d1bupa2</a>	Alignment	not modelled	96.5	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
117	<a href="#">d1jcea2</a>	Alignment	not modelled	96.5	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
118	<a href="#">c1hpmA</a>	Alignment	not modelled	96.5	17	<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
119	<a href="#">d1iv0a</a>	Alignment	not modelled	96.4	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
120	<a href="#">d1zxoA2</a>	Alignment	not modelled	96.4	10	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like