







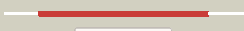
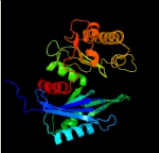














# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2702_(ppgK)_3016868_3017665
Date	Wed Aug 7 12:50:35 BST 2019
Unique Job ID	bc72dab469714693

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1woqB_</a>	 Alignment		100.0	50	<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
2	<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
3	<a href="#">c2hoeA_</a>	 Alignment		100.0	18	<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
4	<a href="#">c1z05A_</a>	 Alignment		100.0	21	<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.
5	<a href="#">c1z6rC_</a>	 Alignment		100.0	21	<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
6	<a href="#">c5f7pA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes
7	<a href="#">c4ijaA_</a>	 Alignment		100.0	16	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> xylr protein; <b>PDBTitle:</b> structure of s. aureus methicillin resistance factor mecrc2
8	<a href="#">c1xc3A_</a>	 Alignment		100.0	22	<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
9	<a href="#">c4htIA_</a>	 Alignment		100.0	23	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-glucoside kinase; <b>PDBTitle:</b> lmo2764 protein, a putative n-acetylmannosamine kinase, from listeria2 monocytogenes
10	<a href="#">c3r8eA_</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical sugar kinase; <b>PDBTitle:</b> crystal structure of a putative sugar kinase (chu_1875) from cytophaga2 hutchinsonii atcc 33406 at 1.65 a resolution
11	<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

12	<a href="#">c3htvA_</a>	Alignment		100.0	18	<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
13	<a href="#">c5f7rA_</a>	Alignment		100.0	19	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes bound to inducer
14	<a href="#">c3lm2B_</a>	Alignment		100.0	24	<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
15	<a href="#">c5nckA_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylmannosamine kinase; <b>PDBTitle:</b> the crystal structure of n-acetylmannosamine kinase in fusobacterium2 nucleatum
16	<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
17	<a href="#">c4db3A_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-d-glucosamine kinase; <b>PDBTitle:</b> 1.95 angstrom resolution crystal structure of n-acetyl-d-glucosamine2 kinase from vibrio vulnificus.
18	<a href="#">c2qm1D_</a>	Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from enterococcus faecalis
19	<a href="#">c2aa4B_</a>	Alignment		100.0	21	<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
20	<a href="#">c2gupA_</a>	Alignment		100.0	21	<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
21	<a href="#">c6ediA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of leishmania braziliensis glucokinase
22	<a href="#">c3vovC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of rok hexokinase from thermus thermophilus
23	<a href="#">d1sz2a1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
24	<a href="#">c3eo3B_</a>	Alignment	not modelled	100.0	26	<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
25	<a href="#">c6da0A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase (nfhk) from naegleria fowleri
26	<a href="#">c3vpzA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of glucokinase from antarctic psychrotroph at 1.69a
27	<a href="#">c2q2rA_</a>	Alignment	not modelled	100.0	22	<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
28	<a href="#">c2e2pA_</a>	Alignment	not modelled	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

29	<a href="#">c2ch5D</a>	Alignment	not modelled	100.0	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 kinase in2 complex with n-acetylglucosamine
30	<a href="#">c1zc6A</a>	Alignment	not modelled	99.9	15	<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.
31	<a href="#">d1woqa2</a>	Alignment	not modelled	99.9	45	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
32	<a href="#">d1woqa1</a>	Alignment	not modelled	99.9	56	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
33	<a href="#">d1z6ra3</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
34	<a href="#">d1z05a2</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
35	<a href="#">d2h0ea3</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
36	<a href="#">d1z05a3</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
37	<a href="#">d1z6ra2</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
38	<a href="#">d2ap1a2</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
39	<a href="#">d2aa4a2</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
40	<a href="#">d2ap1a1</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
41	<a href="#">d1xc3a2</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
42	<a href="#">d2h0ea2</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
43	<a href="#">d2gupa2</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
44	<a href="#">d2aa4a1</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
45	<a href="#">d1xc3a1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
46	<a href="#">d1huxa</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
47	<a href="#">d2ewsa1</a>	Alignment	not modelled	99.8	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
48	<a href="#">d2gupa1</a>	Alignment	not modelled	99.7	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
49	<a href="#">d1q18a2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
50	<a href="#">d1q18a1</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
51	<a href="#">c4ehtA</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> activator of 2-hydroxyisocaproyl-coa dehydratase; <b>PDBTitle:</b> activator of the 2-hydroxyisocaproyl-coa dehydratase from clostridium2 difficile with bound adp
52	<a href="#">d1zc6a1</a>	Alignment	not modelled	99.3	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
53	<a href="#">c1ig8A</a>	Alignment	not modelled	99.3	18	<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
54	<a href="#">c1bdgA</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> hexokinase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> hexokinase from schistosoma mansonii complexed with glucose
55	<a href="#">c5zqtA</a>	Alignment	not modelled	99.2	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase-6; <b>PDBTitle:</b> crystal structure of oryza sativa hexokinase 6

56	<a href="#">c3hm8D_</a>	Alignment	not modelled	99.2	21	<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
57	<a href="#">c1v4sA_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase isoform 2; <b>PDBTitle:</b> crystal structure of human glucokinase
58	<a href="#">d2ch5a1</a>	Alignment	not modelled	99.1	25	<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="#">d2ch5a2</a>	Alignment	not modelled	99.1	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
60	<a href="#">c1qhaA_</a>	Alignment	not modelled	99.0	20	<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
61	<a href="#">c5hg1A_</a>	Alignment	not modelled	99.0	22	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase-2; <b>PDBTitle:</b> crystal structure of human hexokinase 2 with cmpd 1, a c-2-substituted2 glucosamine
62	<a href="#">c1zbsA_</a>	Alignment	not modelled	99.0	12	<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
63	<a href="#">c4qs9A_</a>	Alignment	not modelled	99.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase-1; <b>PDBTitle:</b> arabidopsis hexokinase 1 (athxk1) mutant s177a structure in glucose-2 bound form
64	<a href="#">c3h1qB_</a>	Alignment	not modelled	99.0	15	<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 hydrogenoformans
65	<a href="#">c3hz6A_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
66	<a href="#">c1zxoB_</a>	Alignment	not modelled	98.6	11	<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.
67	<a href="#">c5ya2A_</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> autoinducer-2 kinase; <b>PDBTitle:</b> crystal structure of lsrk-hpr complex with adp
68	<a href="#">c2ychA_</a>	Alignment	not modelled	98.0	20	<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
69	<a href="#">d1v4sa1</a>	Alignment	not modelled	98.0	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
70	<a href="#">c4e1jA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of glycerol kinase in complex with glycerol from2 sinorhizobium meliloti 1021
71	<a href="#">c3ezwD_</a>	Alignment	not modelled	97.9	15	<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
72	<a href="#">c3g25B_</a>	Alignment	not modelled	97.9	15	<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.
73	<a href="#">d2p3ra1</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
74	<a href="#">d1bdga1</a>	Alignment	not modelled	97.9	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
75	<a href="#">c5hv7A_</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> putative sugar kinases from synechococcus elongatus pcc7942 in complex2 with d-ribulose
76	<a href="#">d1czan3</a>	Alignment	not modelled	97.9	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
77	<a href="#">c3flcX_</a>	Alignment	not modelled	97.9	18	<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
78	<a href="#">c3gbtA_</a>	Alignment	not modelled	97.9	19	<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
79	<a href="#">c3gg4B_</a>	Alignment	not modelled	97.9	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
80	<a href="#">c3ifrB_</a>	Alignment	not modelled	97.9	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
81	<a href="#">c2dpnB_</a>	Alignment	not modelled	97.8	15	<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
82	<a href="#">c2zf5O_</a>	Alignment	not modelled	97.8	13 <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
83	<a href="#">d1ig8a1</a>	Alignment	not modelled	97.8	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
84	<a href="#">d1bg3a3</a>	Alignment	not modelled	97.8	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
85	<a href="#">c1hkgA_</a>	Alignment	not modelled	97.8	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase a; <b>PDBTitle:</b> structural dynamics of yeast hexokinase during catalysis
86	<a href="#">c3wxiB_</a>	Alignment	not modelled	97.8	16 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol kinase; <b>PDBTitle:</b> crystal structure of trypanosoma brucei gambiense glycerol kinase2 (ligand-free form)
87	<a href="#">c1glbG_</a>	Alignment	not modelled	97.8	15 <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
88	<a href="#">c2d4wA_</a>	Alignment	not modelled	97.8	13 <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
89	<a href="#">c5htxA_</a>	Alignment	not modelled	97.8	12 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylulose kinase; <b>PDBTitle:</b> putative sugar kinases from arabidopsis thaliana in complex with adp
90	<a href="#">c2w40C_</a>	Alignment	not modelled	97.6	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
91	<a href="#">c3i8bA_</a>	Alignment	not modelled	97.6	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
92	<a href="#">c2cgkB_</a>	Alignment	not modelled	97.6	15 <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 escherichia coli in an2 open uncomplexed conformation.
93	<a href="#">c4bc2A_</a>	Alignment	not modelled	97.6	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulose kinase; <b>PDBTitle:</b> crystal structure of human d-xylulokinase in complex with d-2 xylulose and adenosine diphosphate
94	<a href="#">d1czan1</a>	Alignment	not modelled	97.6	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
95	<a href="#">c3h6eB_</a>	Alignment	not modelled	97.5	14 <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
96	<a href="#">d1bg3a1</a>	Alignment	not modelled	97.5	14 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Hexokinase
97	<a href="#">c5vm1A_</a>	Alignment	not modelled	97.5	23 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of a xylolyose kinase from brucella ovis
98	<a href="#">c2nlxA_</a>	Alignment	not modelled	97.5	19 <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
99	<a href="#">c3jvpA_</a>	Alignment	not modelled	97.5	13 <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="#">c1sazA_</a>	Alignment	not modelled	97.5	18 <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
101	<a href="#">c1xupO_</a>	Alignment	not modelled	97.4	17 <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
102	<a href="#">d1saza2</a>	Alignment	not modelled	97.4	24 <b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
103	<a href="#">c6fpeG_</a>	Alignment	not modelled	97.2	13 <b>PDB header:</b> rna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> trna n6-adenosine threonylcarbamoyltransferase; <b>PDBTitle:</b> bacterial protein complex
104	<a href="#">c3wqtB_</a>	Alignment	not modelled	97.1	14 <b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsa; <b>PDBTitle:</b> staphylococcus aureus ftsa complexed with amppnp
105	<a href="#">c3p4iA_</a>	Alignment	not modelled	97.1	14 <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
106	<a href="#">c5tkyA_</a>	Alignment	not modelled	97.0	20 <b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation
107	<a href="#">c4c23A_</a>	Alignment	not modelled	97.0	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> l-fuculose kinase fuck; <b>PDBTitle:</b> l-fuculose kinase

108	<a href="#">c3c7nB_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> chaperone/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> heat shock cognate; <b>PDBTitle:</b> structure of the hsp110:hsc70 nucleotide exchange complex
109	<a href="#">c5eoxB_</a>	Alignment	not modelled	96.9	16	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> type 4 fimbrial biogenesis protein pilm; <b>PDBTitle:</b> pseudomonas aeruginosa pilm bound to adp
110	<a href="#">c4czeA_</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> rod shape-determining protein mreB; <b>PDBTitle:</b> c. crescentus mreB, double filament, empty
111	<a href="#">c2i7pA_</a>	Alignment	not modelled	96.8	20	<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
112	<a href="#">c3enoB_</a>	Alignment	not modelled	96.7	17	<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
113	<a href="#">c3khyA_</a>	Alignment	not modelled	96.5	11	<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 francisella tularensis2 subsp. tularensis schu s4
114	<a href="#">c2v7yA_</a>	Alignment	not modelled	96.2	18	<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
115	<a href="#">c1tuuA_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
116	<a href="#">c5m45K_</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> acetone carboxylase beta subunit; <b>PDBTitle:</b> structure of acetone carboxylase purified from xanthobacter2 autotrophicus
117	<a href="#">c2v7zA_</a>	Alignment	not modelled	96.1	17	<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
118	<a href="#">c2ivoC_</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
119	<a href="#">d1r59o1</a>	Alignment	not modelled	96.0	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
120	<a href="#">c5mb9B_</a>	Alignment	not modelled	95.9	19	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair