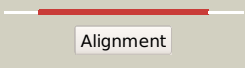

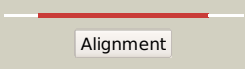

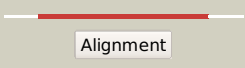

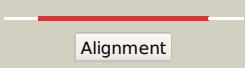

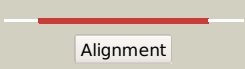

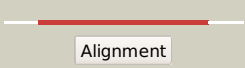

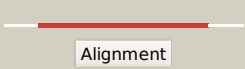

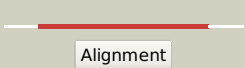

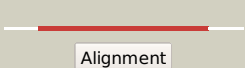

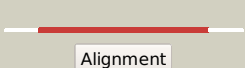

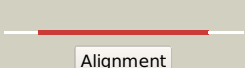












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0409_(ackA)_493854_495011
Date	Tue Jul 23 14:50:48 BST 2019
Unique Job ID	f1eff4c6df2ac90e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ioyD_</a>			100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis acetate kinase
2	<a href="#">c4ijnB_</a>			100.0	67	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of an acetate kinase from mycobacterium smegmatis2 bound to amp and sulfate
3	<a href="#">c2iirj_</a>			100.0	47	<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
4	<a href="#">c1tuuA_</a>			100.0	44	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> acetate kinase crystallized with atpgs
5	<a href="#">c3p4iA_</a>			100.0	77	<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
6	<a href="#">c1x3nA_</a>			100.0	40	<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
7	<a href="#">c3slcA_</a>			100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of apo form of acetate kinase (acka) from salmonella2 typhimurium
8	<a href="#">c3khyA_</a>			100.0	41	<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
9	<a href="#">c4h0pB_</a>			100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from cryptococcus neoformans
10	<a href="#">c4h0oB_</a>			100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> acetate kinase; <b>PDBTitle:</b> crystal structure of acetate kinase from entamoeba histolytica
11	<a href="#">c1sazA_</a>			100.0	22	<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

12	<a href="#">d2e1za2</a>	Alignment		100.0	40	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
13	<a href="#">d1g99a2</a>	Alignment		100.0	45	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
14	<a href="#">d1sa2a2</a>	Alignment		100.0	29	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
15	<a href="#">d1g99a1</a>	Alignment		100.0	45	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
16	<a href="#">d2e1za1</a>	Alignment		100.0	39	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
17	<a href="#">d1sa2a1</a>	Alignment		100.0	17	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Acetokinase-like
18	<a href="#">c2qm1D</a>	Alignment		99.0	14	<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="#">c3eo3B</a>	Alignment		98.8	15	<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
20	<a href="#">d2aa4a2</a>	Alignment		98.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
21	<a href="#">c4htiA</a>	Alignment	not modelled	98.6	14	<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
22	<a href="#">c5f7rA</a>	Alignment	not modelled	98.6	14	<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
23	<a href="#">d2ap1a1</a>	Alignment	not modelled	98.6	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
24	<a href="#">c4db3A</a>	Alignment	not modelled	98.5	17	<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.
25	<a href="#">c3vovC</a>	Alignment	not modelled	98.5	15	<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
26	<a href="#">c4ijaA</a>	Alignment	not modelled	98.4	13	<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 mecR2
27	<a href="#">d1z6ra3</a>	Alignment	not modelled	98.4	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
28	<a href="#">c2aa4B</a>	Alignment	not modelled	98.4	14	<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

29	<a href="#">d2gupa2</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
30	<a href="#">d1z05a2</a>	Alignment	not modelled	98.3	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
31	<a href="#">c1z6rC</a>	Alignment	not modelled	98.2	10	<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
32	<a href="#">c2gupA</a>	Alignment	not modelled	98.2	20	<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
33	<a href="#">c5nckA</a>	Alignment	not modelled	98.1	13	<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
34	<a href="#">c1z05A</a>	Alignment	not modelled	98.0	10	<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.
35	<a href="#">c3vpzA</a>	Alignment	not modelled	98.0	16	<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
36	<a href="#">c3mcpA</a>	Alignment	not modelled	97.9	14	<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
37	<a href="#">c3r8eA</a>	Alignment	not modelled	97.9	15	<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
38	<a href="#">c2ap1A</a>	Alignment	not modelled	97.9	16	<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
39	<a href="#">d2ewsA1</a>	Alignment	not modelled	97.8	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
40	<a href="#">d1sz2a1</a>	Alignment	not modelled	97.8	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
41	<a href="#">c5eoxB</a>	Alignment	not modelled	97.7	13	<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
42	<a href="#">c3vgkB</a>	Alignment	not modelled	97.7	13	<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
43	<a href="#">d1huxa</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
44	<a href="#">c6ediA</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucokinase; <b>PDBTitle:</b> crystal structure of leishmania braziliensis glucokinase
45	<a href="#">c5f7pA</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0178 protein; <b>PDBTitle:</b> rok repressor lmo0178 from listeria monocytogenes
46	<a href="#">c1xc3A</a>	Alignment	not modelled	97.6	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
47	<a href="#">d2h0ea2</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
48	<a href="#">c3enoB</a>	Alignment	not modelled	97.6	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
49	<a href="#">c4ehtA</a>	Alignment	not modelled	97.4	11	<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
50	<a href="#">d1q18a2</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glucokinase
51	<a href="#">c6fpeG</a>	Alignment	not modelled	97.1	18	<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
52	<a href="#">c2hoeA</a>	Alignment	not modelled	97.1	11	<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
53	<a href="#">c5ya2A</a>	Alignment	not modelled	97.0	15	<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
54	<a href="#">c3jvpA</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribulokinase; <b>PDBTitle:</b> crystal structure of ribulokinase from bacillus halodurans
						<b>PDB header:</b> transferase

55	<a href="#">c2e2pA</a>	Alignment	not modelled	96.5	14	<b>Chain:</b> A: <b>PDB Molecule:</b> hexokinase; <b>PDBTitle:</b> crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
56	<a href="#">c2ch5D</a>	Alignment	not modelled	96.5	14	<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
57	<a href="#">c1zc6A</a>	Alignment	not modelled	96.3	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.
58	<a href="#">c6da0A</a>	Alignment	not modelled	96.2	15	<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
59	<a href="#">c6gwjK</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> rna binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> probable trna n6-adenosine threonylcarbamoyltransferase; <b>PDBTitle:</b> protein complex
60	<a href="#">c3htvA</a>	Alignment	not modelled	96.1	14	<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
61	<a href="#">d1xc3a2</a>	Alignment	not modelled	96.1	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> ROK
62	<a href="#">c2q2rA</a>	Alignment	not modelled	96.0	16	<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
63	<a href="#">c2ivoC</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
64	<a href="#">c3hz6A</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> xylulokinase; <b>PDBTitle:</b> crystal structure of xylulokinase from chromobacterium violaceum
65	<a href="#">c3zeuE</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> probable trna threonylcarbamoyladenosine biosynthesis <b>PDBTitle:</b> structure of a salmonella typhimurium yjgd-yeaz heterodimer bound to2 atpgammas
66	<a href="#">c1woqB</a>	Alignment	not modelled	95.3	18	<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
67	<a href="#">c3h1qB</a>	Alignment	not modelled	94.9	20	<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 carboxydotherrus hydrogenoformans
68	<a href="#">c3wxiB</a>	Alignment	not modelled	94.9	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)
69	<a href="#">d2ch5a1</a>	Alignment	not modelled	94.5	12	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
70	<a href="#">c3gg4B</a>	Alignment	not modelled	94.2	8	<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
71	<a href="#">c2zf5O</a>	Alignment	not modelled	94.2	10	<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="#">c3i8bA</a>	Alignment	not modelled	94.0	15	<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
73	<a href="#">c3h6eB</a>	Alignment	not modelled	93.5	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
74	<a href="#">c5htxA</a>	Alignment	not modelled	93.1	15	<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
75	<a href="#">c3en9B</a>	Alignment	not modelled	92.2	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
76	<a href="#">c4bc2A</a>	Alignment	not modelled	92.2	15	<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
77	<a href="#">c3ifrB</a>	Alignment	not modelled	90.8	15	<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
78	<a href="#">c2w40C</a>	Alignment	not modelled	90.5	15	<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
79	<a href="#">c5hv7A</a>	Alignment	not modelled	90.5	13	<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

80	<a href="#">c3ezwD</a>	Alignment	not modelled	89.8	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
81	<a href="#">d2i7pa1</a>	Alignment	not modelled	88.8	15	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
82	<a href="#">d2p3ra1</a>	Alignment	not modelled	88.6	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
83	<a href="#">c4k25A</a>	Alignment	not modelled	87.7	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable trna threonylcarbamoyladenose biosynthesis <b>PDBTitle:</b> crystal structure of yeast qri7 homodimer
84	<a href="#">c3vthA</a>	Alignment	not modelled	87.0	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate- and2 nucleotide-bound form
85	<a href="#">c1qlbG</a>	Alignment	not modelled	86.9	14	<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 iiiiglc with2 glycerol kinase
86	<a href="#">d2f9wa2</a>	Alignment	not modelled	85.5	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
87	<a href="#">c2d4wA</a>	Alignment	not modelled	85.3	14	<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
88	<a href="#">c4e1jA</a>	Alignment	not modelled	84.8	15	<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
89	<a href="#">c2dnpB</a>	Alignment	not modelled	84.7	14	<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
90	<a href="#">c3tsuA</a>	Alignment	not modelled	84.6	14	<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
91	<a href="#">c1xupO</a>	Alignment	not modelled	84.6	12	<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
92	<a href="#">c3lm2B</a>	Alignment	not modelled	84.3	18	<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
93	<a href="#">c3vthB</a>	Alignment	not modelled	84.0	10	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hydrogenase maturation factor; <b>PDBTitle:</b> crystal structure of full-length hypf in the phosphate- and2 nucleotide-bound form
94	<a href="#">c3flcX</a>	Alignment	not modelled	83.9	10	<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
95	<a href="#">d1zc6a1</a>	Alignment	not modelled	83.6	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
96	<a href="#">d1r59o2</a>	Alignment	not modelled	83.3	9	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
97	<a href="#">c3bf1C</a>	Alignment	not modelled	81.8	20	<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
98	<a href="#">c2ychA</a>	Alignment	not modelled	81.3	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> competence protein pilm; <b>PDBTitle:</b> pilm-pilm type iv pilus biogenesis complex
99	<a href="#">c1ydnA</a>	Alignment	not modelled	81.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
100	<a href="#">d2p3ra2</a>	Alignment	not modelled	80.0	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Glycerol kinase
101	<a href="#">c2i7pA</a>	Alignment	not modelled	80.0	12	<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="#">d1zc6a2</a>	Alignment	not modelled	79.2	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
103	<a href="#">c2cgbB</a>	Alignment	not modelled	77.9	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 escherichia coli in an2 open uncomplexed conformation.
104	<a href="#">d2i7na2</a>	Alignment	not modelled	77.1	14	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
105	<a href="#">c3js6A</a>	Alignment	not modelled	76.2	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized parm protein; <b>PDBTitle:</b> crystal structure of apo psk41 parm protein <b>PDB header:</b> transferase

106	<a href="#">c4bgaB_</a>	Alignment	not modelled	75.3	16	<b>Chain:</b> B: <b>PDB Molecule:</b> predicted molecular chaperone distantly related to <b>PDBTitle:</b> nucleotide-bound open form of a putative sugar kinase2 mk0840 from methanopyrus kandleri
107	<a href="#">d3bexa1</a>	Alignment	not modelled	74.5	19	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like
108	<a href="#">c3smpA_</a>	Alignment	not modelled	74.1	16	<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
109	<a href="#">d1bupa2</a>	Alignment	not modelled	74.0	5	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
110	<a href="#">d1zbsa1</a>	Alignment	not modelled	73.8	16	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like
111	<a href="#">c3gbtA_</a>	Alignment	not modelled	73.3	15	<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
112	<a href="#">c3g25B_</a>	Alignment	not modelled	73.2	13	<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.
113	<a href="#">c1t6dB_</a>	Alignment	not modelled	73.1	19	<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
114	<a href="#">c1zbsA_</a>	Alignment	not modelled	73.0	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
115	<a href="#">c2f9tB_</a>	Alignment	not modelled	71.4	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate kinase; <b>PDBTitle:</b> structure of the type iii coaa from pseudomonas aeruginosa
116	<a href="#">c2cw6B_</a>	Alignment	not modelled	71.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase, mitochondrial; <b>PDBTitle:</b> crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
117	<a href="#">c2fsnB_</a>	Alignment	not modelled	71.0	11	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ta0583; <b>PDBTitle:</b> crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
118	<a href="#">c3nvbA_</a>	Alignment	not modelled	69.6	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
119	<a href="#">c6gfaA_</a>	Alignment	not modelled	68.3	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 105 kda; <b>PDBTitle:</b> structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed
120	<a href="#">d2ch5a2</a>	Alignment	not modelled	66.1	11	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> BadF/BadG/BcrA/BcrD-like