

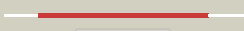





















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0422c_(thiD)_507761_508558
Date	Tue Jul 23 14:50:49 BST 2019
Unique Job ID	becbd476eb802d68

Detailed template information

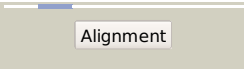
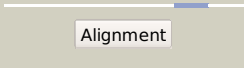
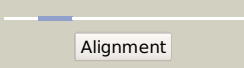
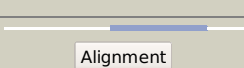
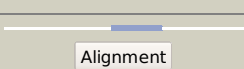
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3rm5B_</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB</b> <b>Molecule:</b> hydroxymethylpyrimidine/phosphomethylpyrimidine kinase <b>PDBTitle:</b> structure of trifunctional thi20 from yeast
2	<a href="#">d1ub0a_</a>	 Alignment		100.0	47	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
3	<a href="#">c2i5bC_</a>	 Alignment		100.0	35	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphomethylpyrimidine kinase; <b>PDBTitle:</b> the crystal structure of an adp complex of bacillus subtilis pyridoxal2 kinase provides evidence for the parralel emergence of enzyme3 activity during evolution
4	<a href="#">d1jxha_</a>	 Alignment		100.0	38	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
5	<a href="#">c4c5iC_</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphomethylpyrimidine kinase; <b>PDBTitle:</b> structure of the pyridoxal kinase from staphylococcus2 aureus in complex with pyridoxal
6	<a href="#">c3mbjA_</a>	 Alignment		100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphomethylpyrimidine kinase; <b>PDBTitle:</b> crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
7	<a href="#">c5b6aA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase pdxy; <b>PDBTitle:</b> structure of pyridoxal kinasefrom pseudomonas aeruginosa
8	<a href="#">d1vi9a_</a>	 Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
9	<a href="#">d1lhpa_</a>	 Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
10	<a href="#">c5zwbB_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridoxine/pyridoxal/pyridoxamine kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase (pdxk) from salmonella2 typhimurium in complex with adp, pl-linked to lys233 via a schiff3 base
11	<a href="#">c3ibqA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp

12	<a href="#">c4ijpB_</a>	Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphomethylpyrimidine kinase; <b>PDBTitle:</b> 2.06 angstrom resolution crystal structure of phosphomethylpyrimidine2 kinase (thid)from clostridium difficile 630
13	<a href="#">c3zs7A_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from trypanosoma brucei
14	<a href="#">c5trwA_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase pdxy; <b>PDBTitle:</b> crystal structure of pyridoxamine kinase pdxy from burkholderia2 xenovorans
15	<a href="#">c2ddmA_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from the escherichia coli pdxk2 gene at 2.1 a resolution
16	<a href="#">c4s1hA_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> pyridoxal kinase of entamoeba histolytica with adp
17	<a href="#">c4yI5A_</a>	Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphomethylpyrimidine kinase; <b>PDBTitle:</b> structure of a putative phosphomethylpyrimidine kinase from2 acinetobacter baumannii
18	<a href="#">d1kyha_</a>	Alignment		100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
19	<a href="#">c2r3bA_</a>	Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> yjef-related protein; <b>PDBTitle:</b> crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
20	<a href="#">d2ax3a1</a>	Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
21	<a href="#">c2ax3A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0922; <b>PDBTitle:</b> crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
22	<a href="#">c3bgkA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the crystal structure of hypothetic protein smu.573 from streptococcus2 mutans
23	<a href="#">c6efwA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent (s)-nad(p)h-hydrate dehydratase; <b>PDBTitle:</b> crystal structure of a yjef family protein from cryptococcus2 neoformans var. grubii serotype a
24	<a href="#">c3k5wA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate kinase; <b>PDBTitle:</b> crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
25	<a href="#">c3kzhA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> crystal structure of a putative sugar kinase from2 clostridium perfringens
26	<a href="#">c6jyyC_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> hydroxyethylthiazole kinase; <b>PDBTitle:</b> crystal structure of the 5-(hydroxyethyl)-methylthiazole kinase thim2 from klebsiella pneumonia
27	<a href="#">d2abqa1</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
28	<a href="#">c2jg5B_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructose 1-phosphate kinase; <b>PDBTitle:</b> crystal structure of a putative phosphofructokinase from2 staphylococcus aureus

29	<a href="#">c3dzvB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; <b>PDBTitle:</b> crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
30	<a href="#">c2jg1C_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> tagatose-6-phosphate kinase; <b>PDBTitle:</b> structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
31	<a href="#">c3cqdB_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructokinase isozyme 2; <b>PDBTitle:</b> structure of the tetrameric inhibited form of phosphofructokinase-22 from escherichia coli
32	<a href="#">c3uq6B_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosine kinase, putative; <b>PDBTitle:</b> adenosine kinase from schistosoma mansoni in complex with adenosine2 and amp
33	<a href="#">c4e8wA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> d-beta-d-heptose 7-phosphate kinase; <b>PDBTitle:</b> crystal structure of burkholderia cenocepacia hlda in complex with an2 atp-competitive inhibitor
34	<a href="#">c2qhpA_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
35	<a href="#">d1v8aa_</a>	Alignment	not modelled	99.8	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
36	<a href="#">d1rkda_</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
37	<a href="#">c5cgaC_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> hydroxyethylthiazole kinase; <b>PDBTitle:</b> structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
38	<a href="#">c2nwhA_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> signaling protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate kinase; <b>PDBTitle:</b> carbohydrate kinase from agrobacterium tumefaciens
39	<a href="#">c4x8fD_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> vibrio cholerae o395 ribokinase in apo form
40	<a href="#">c2qcva_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 5-dehydro-2-deoxygluconokinase; <b>PDBTitle:</b> crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
41	<a href="#">d2f02a1</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
42	<a href="#">c2xtbA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine kinase; <b>PDBTitle:</b> crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
43	<a href="#">c6ilsB_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> structure of arabidopsis thaliana ribokinase complexed with ribose and2 atp
44	<a href="#">c3looc_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> anopheles gambiae adenosine kinase; <b>PDBTitle:</b> crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetraphosphate
45	<a href="#">d1vm7a_</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
46	<a href="#">c3pl2D_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> sugar kinase, ribokinase family; <b>PDBTitle:</b> crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
47	<a href="#">c2pkkA_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine kinase; <b>PDBTitle:</b> crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
48	<a href="#">c4ebuA_</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxygluconokinase; <b>PDBTitle:</b> crystal structure of a sugar kinase (target efi-502312) from2 oceanicola granulosis, with bound amp/adp crystal form i
49	<a href="#">c2rbcA_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar kinase; <b>PDBTitle:</b> crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
50	<a href="#">c3ktnA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate kinase, pfkb family; <b>PDBTitle:</b> crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
51	<a href="#">d1ekqa_</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
52	<a href="#">c3ry7A_</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> crystal structure of sa239
53	<a href="#">d1bx4a_</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like

54	<a href="#">d1v19a_</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
55	<a href="#">c6cw5A_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> crystal structure of ribokinase from cryptococcus neoformans var.2 grubii serotype a
56	<a href="#">c5zwyB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> ribokinase from leishmania donovani
57	<a href="#">c3b1qD_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribokinase, putative; <b>PDBTitle:</b> structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
58	<a href="#">d2afba1</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
59	<a href="#">c3nm3D_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> thiamine biosynthetic bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
60	<a href="#">c3go6B_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribokinase rbsk; <b>PDBTitle:</b> crystal structure of m. tuberculosis ribokinase (rv2436) in complex2 with ribose and amp-pnp
61	<a href="#">c4gm6C_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pfkb family carbohydrate kinase; <b>PDBTitle:</b> crystal structure of pfkb family carbohydrate kinase(target efi-5021462 from listeria grayi dsm 20601
62	<a href="#">c2c49A_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar kinase mj0406; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii nucleoside kinase -2 an archaeal member of the ribokinase family
63	<a href="#">c3in1A_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized sugar kinase ydjh; <b>PDBTitle:</b> crystal structure of a putative ribokinase in complex with2 adp from e.coli
64	<a href="#">c3iq0B_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative ribokinase ii; <b>PDBTitle:</b> crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli
65	<a href="#">c4u7xA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase:carbohydrate kinase, pfkb; <b>PDBTitle:</b> crystal structure of fructokinase from brucella abortus 2308
66	<a href="#">c4e3aB_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar kinase protein; <b>PDBTitle:</b> crystal structure of probable sugar kinase protein from rhizobium etli2 cfn 42
67	<a href="#">c3lhxA_</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ketodeoxygluconokinase; <b>PDBTitle:</b> crystal structure of a ketodeoxygluconokinase (kdgk) from shigella2 flexneri
68	<a href="#">c2absA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> signaling protein,transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosine kinase; <b>PDBTitle:</b> crystal structure of t. gondii adenosine kinase complexed with amp-pcp
69	<a href="#">d2absa1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
70	<a href="#">c5eynA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of fructokinase from vibrio cholerae o395 in2 fructose, adp, beryllium trifluoride and calcium ion bound form
71	<a href="#">c2varB_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
72	<a href="#">c3julA_</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lin2199 protein; <b>PDBTitle:</b> crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
73	<a href="#">d1tyya_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
74	<a href="#">c3gbuD_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized sugar kinase ph1459; <b>PDBTitle:</b> crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
75	<a href="#">d2dcna1</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
76	<a href="#">d2fv7a1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
77	<a href="#">c3i3yB_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase; <b>PDBTitle:</b> crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
78	<a href="#">d2ajra1</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
79	<a href="#">d1vk4a_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
						<b>PDB header:</b> transferase

80	<a href="#">c3kd6B_</a>	Alignment	not modelled	99.5	19	<b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, pfbk family; <b>PDBTitle:</b> crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
81	<a href="#">c4du5B_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pfbk; <b>PDBTitle:</b> crystal structure of pfbk protein from polaromonas sp. js666
82	<a href="#">c3bf5A_</a>	Alignment	not modelled	99.5	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase related protein; <b>PDBTitle:</b> crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
83	<a href="#">c3b31C_</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ketohehexokinase; <b>PDBTitle:</b> crystal structures of alternatively-spliced isoforms of human2 ketohehexokinase
84	<a href="#">c1tz6B_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative sugar kinase; <b>PDBTitle:</b> crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog
85	<a href="#">c3w4sB_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate/pyrimidine kinase, pfbk family; <b>PDBTitle:</b> myo-inositol kinase from thermococcus kodakarensis
86	<a href="#">c3hj6B_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> structure of halothermothrix orenii fructokinase (frk)
87	<a href="#">c3lkiA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of fructokinase with bound atp from2 xylella fastidiosa
88	<a href="#">c5k27B_</a>	Alignment	not modelled	90.3	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ancmt; <b>PDBTitle:</b> crystal structure of ancestral protein ancmt of adp-dependent sugar2 kinases family.
89	<a href="#">d1u2xa_</a>	Alignment	not modelled	85.6	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
90	<a href="#">c3x0vA_</a>	Alignment	not modelled	69.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine oxidase; <b>PDBTitle:</b> structure of l-lysine oxidase
91	<a href="#">c5od2B_</a>	Alignment	not modelled	60.7	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional adp-specific glucokinase/phosphofructokinase; <b>PDBTitle:</b> crystal structure of adp-dependent glucokinase from methanocaldococcus2 jannaschii
92	<a href="#">d1a9xa4</a>	Alignment	not modelled	60.7	8	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
93	<a href="#">c2q62A_</a>	Alignment	not modelled	52.2	24	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
94	<a href="#">c1apzB_</a>	Alignment	not modelled	52.1	14	<b>PDB header:</b> complex (hydrolase/peptide) <b>Chain:</b> B: <b>PDB Molecule:</b> aspartylglucosaminidase; <b>PDBTitle:</b> human aspartylglucosaminidase complex with reaction product
95	<a href="#">d1a9xa3</a>	Alignment	not modelled	49.5	11	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
96	<a href="#">c5ccfA_</a>	Alignment	not modelled	47.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-dependent glucokinase; <b>PDBTitle:</b> structure of mouse adp-dependent glucokinase
97	<a href="#">d1gc5a_</a>	Alignment	not modelled	44.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
98	<a href="#">c3v3tA_</a>	Alignment	not modelled	43.4	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell division gtpase ftsz, diverged; <b>PDBTitle:</b> crystal structure of clostridium botulinum phage c-st tubz
99	<a href="#">c3i31A_</a>	Alignment	not modelled	40.8	41	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkylhalidase cmls; <b>PDBTitle:</b> crystal structure of cmls, a flavin-dependent halogenase
100	<a href="#">c6c8zA_</a>	Alignment	not modelled	35.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-dependent phosphofructokinase; <b>PDBTitle:</b> last common ancestor of adp-dependent phosphofructokinases from2 methanosarcinales
101	<a href="#">c2xdoC_</a>	Alignment	not modelled	29.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
102	<a href="#">c5tu1A_</a>	Alignment	not modelled	25.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline destructase tet(55); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(55)
103	<a href="#">d2nu7b1</a>	Alignment	not modelled	25.1	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
104	<a href="#">d1a2za_</a>	Alignment	not modelled	24.1	15	<b>Fold:</b> Phosphorylase/hydrolase-like <b>Superfamily:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) <b>Family:</b> Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase)
105	<a href="#">c3vteA_</a>	Alignment	not modelled	22.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetrahydrocannabinolic acid synthase; <b>PDBTitle:</b> crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa

106	<a href="#">d1reoa1</a>	 Alignment	not modelled	21.7	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
107	<a href="#">c2gacD</a>	 Alignment	not modelled	21.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> glycosylasparaginase; <b>PDBTitle:</b> t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
108	<a href="#">c2aczA</a>	 Alignment	not modelled	21.5	34	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
109	<a href="#">d1ua4a</a>	 Alignment	not modelled	21.3	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
110	<a href="#">c3drwA</a>	 Alignment	not modelled	21.2	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adp-specific phosphofructokinase; <b>PDBTitle:</b> crystal structure of a phosphofructokinase from pyrococcus horikoshii2 ot3 with amp