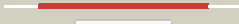



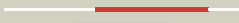

























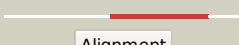















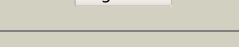


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3433c (-) _3851972_3853393
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	2c99e01b747692d2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ax3A_</a>	 Alignment		100.0	29	<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
2	<a href="#">c3k5wA_</a>	 Alignment		100.0	26	<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
3	<a href="#">c6efwA_</a>	 Alignment		100.0	27	<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
4	<a href="#">c2r3bA_</a>	 Alignment		100.0	23	<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
5	<a href="#">c3bgkA_</a>	 Alignment		100.0	22	<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
6	<a href="#">d2ax3a1</a>	 Alignment		100.0	30	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
7	<a href="#">d1kyha_</a>	 Alignment		100.0	30	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
8	<a href="#">c2dg2D_</a>	 Alignment		100.0	22	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> apolipoprotein a-i binding protein; <b>PDBTitle:</b> crystal structure of mouse apolipoprotein a-i binding protein
9	<a href="#">d1jzta_</a>	 Alignment		100.0	22	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
10	<a href="#">d2ax3a2</a>	 Alignment		100.0	28	<b>Fold:</b> YjeF N-terminal domain-like <b>Superfamily:</b> YjeF N-terminal domain-like <b>Family:</b> YjeF N-terminal domain-like
11	<a href="#">c3d3kD_</a>	 Alignment		100.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p

12	<a href="#">c3d3jA_</a>	 Alignment		100.0	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of human edc3p
13	<a href="#">d1ekqa_</a>	 Alignment		100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
14	<a href="#">c3rm5B_</a>	 Alignment		100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxymethylpyrimidine/phosphomethylpyrimidine kinase <b>PDBTitle:</b> structure of trifunctional thi20 from yeast
15	<a href="#">c6jyyC_</a>	 Alignment		100.0	23	<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
16	<a href="#">d1v8aa_</a>	 Alignment		100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
17	<a href="#">c5cgaC_</a>	 Alignment		100.0	18	<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-y)ethanol
18	<a href="#">c4yl5A_</a>	 Alignment		100.0	19	<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
19	<a href="#">c4c51C_</a>	 Alignment		100.0	18	<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
20	<a href="#">c3dzvB_</a>	 Alignment		99.9	17	<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
21	<a href="#">c4jjpB_</a>	 Alignment	not modelled	99.9	19	<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
22	<a href="#">d1jxha_</a>	 Alignment	not modelled	99.9	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
23	<a href="#">c3nm3D_</a>	 Alignment	not modelled	99.9	14	<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
24	<a href="#">d1ub0a_</a>	 Alignment	not modelled	99.9	26	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
25	<a href="#">c2i5bC_</a>	 Alignment	not modelled	99.9	19	<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
26	<a href="#">c3mbjA_</a>	 Alignment	not modelled	99.9	16	<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)
27	<a href="#">c3ibqA_</a>	 Alignment	not modelled	99.8	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
28	<a href="#">c5zwbB_</a>	 Alignment	not modelled	99.7	19	<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
29	<a href="#">d1vi9a_</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
30	<a href="#">d1lhpa_</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
31	<a href="#">c5b6aA_</a>	Alignment	not modelled	99.6	16	<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
32	<a href="#">c5trwA_</a>	Alignment	not modelled	99.6	16	<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
33	<a href="#">c2ddmA_</a>	Alignment	not modelled	99.5	17	<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
34	<a href="#">c4s1hA_</a>	Alignment	not modelled	99.5	15	<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
35	<a href="#">c3zs7A_</a>	Alignment	not modelled	99.4	14	<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
36	<a href="#">d2f02a1</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
37	<a href="#">d1vk4a_</a>	Alignment	not modelled	98.7	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
38	<a href="#">d2abqa1</a>	Alignment	not modelled	98.7	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
39	<a href="#">c3cqdB_</a>	Alignment	not modelled	98.7	20	<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
40	<a href="#">c2jg5B_</a>	Alignment	not modelled	98.6	22	<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
41	<a href="#">c2jg1C_</a>	Alignment	not modelled	98.6	17	<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
42	<a href="#">c3kzhA_</a>	Alignment	not modelled	98.6	14	<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
43	<a href="#">c4x8fD_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> vibrio cholerae o395 ribokinase in apo form
44	<a href="#">c2pkkA_</a>	Alignment	not modelled	98.6	14	<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
45	<a href="#">c6ilsB_</a>	Alignment	not modelled	98.5	18	<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
46	<a href="#">c3b1qD_</a>	Alignment	not modelled	98.5	16	<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
47	<a href="#">c3pl2D_</a>	Alignment	not modelled	98.5	15	<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
48	<a href="#">c5zwyB_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> ribokinase from leishmania donovani
49	<a href="#">c3in1A_</a>	Alignment	not modelled	98.4	15	<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
50	<a href="#">c2qcVA_</a>	Alignment	not modelled	98.4	20	<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
51	<a href="#">c2c49A_</a>	Alignment	not modelled	98.4	11	<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
52	<a href="#">d1vm7a_</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
53	<a href="#">c2rbcA_</a>	Alignment	not modelled	98.3	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
						<b>PDB header:</b> transferase

54	<a href="#">c3uq6B_</a>	Alignment	not modelled	98.3	14	<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
55	<a href="#">c4e8wA_</a>	Alignment	not modelled	98.3	20	<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
56	<a href="#">d1rkda_</a>	Alignment	not modelled	98.3	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
57	<a href="#">d2ajra1</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
58	<a href="#">c4ebuA_</a>	Alignment	not modelled	98.2	18	<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
59	<a href="#">c3iq0B_</a>	Alignment	not modelled	98.2	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
60	<a href="#">c6cw5A_</a>	Alignment	not modelled	98.2	18	<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
61	<a href="#">c2qhpA_</a>	Alignment	not modelled	98.1	19	<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
62	<a href="#">c3ktnA_</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> carbohydrate kinase, pfkf family; <b>PDBTitle:</b> crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
63	<a href="#">c4gm6C_</a>	Alignment	not modelled	98.1	12	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pfkf family carbohydrate kinase; <b>PDBTitle:</b> crystal structure of pfkf family carbohydrate kinase(target efi-5021462 from listeria grayi dsm 20601
64	<a href="#">d2afba1</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
65	<a href="#">d1bx4a_</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
66	<a href="#">c3kd6B_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, pfkf family; <b>PDBTitle:</b> crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
67	<a href="#">c2xtbA_</a>	Alignment	not modelled	98.0	15	<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
68	<a href="#">d2dcna1</a>	Alignment	not modelled	98.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
69	<a href="#">c3looC_</a>	Alignment	not modelled	98.0	14	<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
70	<a href="#">c2nwhA_</a>	Alignment	not modelled	97.9	17	<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
71	<a href="#">c4e3aB_</a>	Alignment	not modelled	97.9	13	<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
72	<a href="#">c3ry7A_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> crystal structure of sa239
73	<a href="#">c3jua_</a>	Alignment	not modelled	97.8	20	<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
74	<a href="#">c5eynA_</a>	Alignment	not modelled	97.8	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
75	<a href="#">c3lhxA_</a>	Alignment	not modelled	97.8	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
76	<a href="#">c2varB_</a>	Alignment	not modelled	97.8	14	<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
77	<a href="#">d1v19a_</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
78	<a href="#">d2absa1</a>	Alignment	not modelled	97.7	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
79	<a href="#">c2absA_</a>	Alignment	not modelled	97.7	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
80	<a href="#">c3no6B_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ribokinase rbsk;

80	<a href="#">c3g0bB</a>	Alignment	not modelled	97.8	20	<b>PDBTitle:</b> crystal structure of m. tuberculosis ribokinase (rv2436) in complex2 with ribose and amp-prp
81	<a href="#">d1tyya</a>	Alignment	not modelled	97.6	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
82	<a href="#">d2fv7a1</a>	Alignment	not modelled	97.5	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
83	<a href="#">c3bf5A</a>	Alignment	not modelled	97.4	13	<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
84	<a href="#">c3hj6B</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> structure of halothermothrix orenii fructokinase (frk)
85	<a href="#">c4u7xA</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase:carbohydrate kinase, pfbk; <b>PDBTitle:</b> crystal structure of fructokinase from brucella abortus 2308
86	<a href="#">c4du5B</a>	Alignment	not modelled	97.3	20	<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
87	<a href="#">c1tz6B</a>	Alignment	not modelled	97.3	19	<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
88	<a href="#">c3b31C</a>	Alignment	not modelled	97.2	15	<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
89	<a href="#">c3i3yB</a>	Alignment	not modelled	97.1	17	<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
90	<a href="#">c3w4sB</a>	Alignment	not modelled	96.7	23	<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
91	<a href="#">c3lkiA</a>	Alignment	not modelled	96.1	13	<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
92	<a href="#">c3gbuD</a>	Alignment	not modelled	95.6	12	<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
93	<a href="#">d1qvwa</a>	Alignment	not modelled	93.4	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/Pfpl
94	<a href="#">d1uh5a</a>	Alignment	not modelled	92.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
95	<a href="#">c1gpiA</a>	Alignment	not modelled	91.5	19	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
96	<a href="#">d1j6ua1</a>	Alignment	not modelled	91.3	14	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
97	<a href="#">c5i01B</a>	Alignment	not modelled	90.5	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of phosphoheptose isomerase gmha from neisseria gonorrhoeae
98	<a href="#">c2hkoA</a>	Alignment	not modelled	90.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1
99	<a href="#">c3d4oA</a>	Alignment	not modelled	90.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
100	<a href="#">c4da9C</a>	Alignment	not modelled	89.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of putative short-chain dehydrogenase/reductase from2 sinorhizobium meliloti 1021
101	<a href="#">c2foiB</a>	Alignment	not modelled	89.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> synthesis, biological activity, and x-ray crystal structural analysis2 of diaryl ether inhibitors of malarial enoyl acp reductase.
102	<a href="#">c2nq8B</a>	Alignment	not modelled	89.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> malarial enoyl acyl acp reductase bound with inh-nad adduct
103	<a href="#">d1p3da1</a>	Alignment	not modelled	89.4	15	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
104	<a href="#">c3kk1A</a>	Alignment	not modelled	89.3	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable chaperone protein hsp33; <b>PDBTitle:</b> crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
105	<a href="#">d1a4ia1</a>	Alignment	not modelled	89.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
106	<a href="#">c4e08B</a>	Alignment	not modelled	89.0	15	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dj-1 beta; <b>PDBTitle:</b> crystal structure of drosophila melanogaster dj-1beta

107	<a href="#">c1f8sA_</a>	Alignment	not modelled	88.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
108	<a href="#">d1u9ca_</a>	Alignment	not modelled	87.8	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Class I glutamine amidotransferase-like <b>Family:</b> DJ-1/PfpI
109	<a href="#">c3d1B_</a>	Alignment	not modelled	87.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadp oxidoreductase bf3122; <b>PDBTitle:</b> crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
110	<a href="#">c5by2A_</a>	Alignment	not modelled	87.6	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> sedoheptulose 7-phosphate isomerase from colwellia psychrerythraea2 strain 34h
111	<a href="#">d1luaa1</a>	Alignment	not modelled	87.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
112	<a href="#">c3trjC_</a>	Alignment	not modelled	87.4	23	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> phosphoheptose isomerase; <b>PDBTitle:</b> structure of a phosphoheptose isomerase from francisella tularensis
113	<a href="#">c4a26B_</a>	Alignment	not modelled	87.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
114	<a href="#">c2e1mA_</a>	Alignment	not modelled	86.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-glutamate oxidase; <b>PDBTitle:</b> crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
115	<a href="#">c2xagA_</a>	Alignment	not modelled	86.5	26	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
116	<a href="#">d1pjca1</a>	Alignment	not modelled	86.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
117	<a href="#">c2v1dA_</a>	Alignment	not modelled	86.4	26	<b>PDB header:</b> oxidoreductase/repressor <b>Chain:</b> A: <b>PDB Molecule:</b> lysine-specific histone demethylase 1; <b>PDBTitle:</b> structural basis of lsd1-corest selectivity in histone h32 recognition
118	<a href="#">d1g0oa_</a>	Alignment	not modelled	86.3	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
119	<a href="#">c3cneD_</a>	Alignment	not modelled	86.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> putative protease i; <b>PDBTitle:</b> crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
120	<a href="#">c4k6fD_</a>	Alignment	not modelled	85.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative acetoacetyl-coa reductase; <b>PDBTitle:</b> x-ray crystal structure of a putative acetoacetyl-coa reductase from2 burkholderia cenocepacia bound to the co-factor nadp