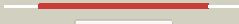



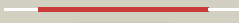



















# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A0B9
Date	Tue Jul 17 17:05:05 BST 2012
Unique Job ID	3c49d4e27d11b65f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2f02a1</a>	 Alignment		100.0	50	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
2	<a href="#">c2jg1C_</a>	 Alignment		100.0	99	<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
3	<a href="#">c2jg5B_</a>	 Alignment		100.0	31	<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
4	<a href="#">c3cqdB_</a>	 Alignment		100.0	23	<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 of2 phosphofructokinase-2 from escherichia coli
5	<a href="#">d2ajra1</a>	 Alignment		100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
6	<a href="#">d2abqa1</a>	 Alignment		100.0	31	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
7	<a href="#">c3julA_</a>	 Alignment		100.0	27	<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
8	<a href="#">c3kzhA_</a>	 Alignment		100.0	21	<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
9	<a href="#">d1vm7a_</a>	 Alignment		100.0	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
10	<a href="#">c2pkkA_</a>	 Alignment		100.0	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
11	<a href="#">d1rkda_</a>	 Alignment		100.0	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like

12	<a href="#">c3pl2D_</a>	Alignment		100.0	17	<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, cg10158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
13	<a href="#">c2rbca_</a>	Alignment		100.0	14	<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
14	<a href="#">c2xtbA_</a>	Alignment		100.0	17	<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
15	<a href="#">d1bx4a_</a>	Alignment		100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
16	<a href="#">c3i3yB_</a>	Alignment		100.0	16	<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
17	<a href="#">c3looc_</a>	Alignment		100.0	16	<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
18	<a href="#">c2nwhA_</a>	Alignment		100.0	15	<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
19	<a href="#">c3in1A_</a>	Alignment		100.0	18	<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
20	<a href="#">d1v19a_</a>	Alignment		100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
21	<a href="#">c2qcvA_</a>	Alignment	not modelled	100.0	15	<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
22	<a href="#">d2afba1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
23	<a href="#">c3b1qD_</a>	Alignment	not modelled	100.0	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
24	<a href="#">c2absA_</a>	Alignment	not modelled	100.0	16	<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 complexed2 with amp-pcp
25	<a href="#">d2absa1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
26	<a href="#">c2c49A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar kinase mj0406; <b>PDBTitle:</b> crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
27	<a href="#">c3go6B_</a>	Alignment	not modelled	100.0	16	<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) in2 complex with ribose and amp-pnp
28	<a href="#">c3ktnA_</a>	Alignment	not modelled	100.0	14	<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

29	<a href="#">d2fv7a1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
30	<a href="#">c2varB</a>	Alignment	not modelled	100.0	15	<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
31	<a href="#">c3iq0B</a>	Alignment	not modelled	100.0	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
32	<a href="#">c3ry7A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ribokinase; <b>PDBTitle:</b> crystal sructure of sa239
33	<a href="#">d2dcna1</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
34	<a href="#">c3gbuD</a>	Alignment	not modelled	100.0	18	<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
35	<a href="#">c4ebuA</a>	Alignment	not modelled	100.0	15	<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 granulosus, with bound amp/adp crystal form i
36	<a href="#">c3bf5A</a>	Alignment	not modelled	100.0	15	<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
37	<a href="#">d1byya</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
38	<a href="#">c4du5B</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pfkb; <b>PDBTitle:</b> crystal structure of pfkb protein from polaromonas sp. js666
39	<a href="#">c2qhpA</a>	Alignment	not modelled	100.0	17	<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
40	<a href="#">c3lhxA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ketodeoxygluconokinase; <b>PDBTitle:</b> crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
41	<a href="#">c1tz6B</a>	Alignment	not modelled	100.0	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
42	<a href="#">c3kd6B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> carbohydrate kinase, pfkb family; <b>PDBTitle:</b> crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
43	<a href="#">c3b3lC</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> ketoheokinase; <b>PDBTitle:</b> crystal structures of alternatively-spliced isoforms of human2 ketoheokinase
44	<a href="#">c3lkiA</a>	Alignment	not modelled	100.0	16	<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
45	<a href="#">d1vk4a</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
46	<a href="#">c3hj6B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> structure of halothermothrix orenii fructokinase (frk)
47	<a href="#">c2ddmA</a>	Alignment	not modelled	99.9	15	<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 escherichia2 coli pdxk gene at 2.1 a resolution
48	<a href="#">c3mbjA</a>	Alignment	not modelled	99.8	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)
49	<a href="#">c2i5bC</a>	Alignment	not modelled	99.8	15	<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 bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
50	<a href="#">c3ibqA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
51	<a href="#">d1vi9a</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Pfkb-like kinase
52	<a href="#">d1lhpa</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Pfkb-like kinase
53	<a href="#">c3zs7A</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from trypanosoma2 brucei
						<b>Fold:</b> Ribokinase-like

54	<a href="#">d1ub0a_</a>	Alignment	not modelled	99.7	14	<b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
55	<a href="#">c3rm5B_</a>	Alignment	not modelled	99.6	12	<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
56	<a href="#">d1jxha_</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
57	<a href="#">c3dzvB_</a>	Alignment	not modelled	99.5	16	<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)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
58	<a href="#">d1v8aa_</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
59	<a href="#">d1kyha_</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
60	<a href="#">d2ax3a1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
61	<a href="#">d1ekqa_</a>	Alignment	not modelled	99.1	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
62	<a href="#">c2ax3A_</a>	Alignment	not modelled	99.0	18	<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
63	<a href="#">c2r3bA_</a>	Alignment	not modelled	99.0	14	<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
64	<a href="#">d1u2xa_</a>	Alignment	not modelled	98.9	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
65	<a href="#">c3nm3D_</a>	Alignment	not modelled	98.8	17	<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
66	<a href="#">d1gc5a_</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
67	<a href="#">d1ua4a_</a>	Alignment	not modelled	98.8	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
68	<a href="#">c3k5wA_</a>	Alignment	not modelled	98.8	19	<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
69	<a href="#">c3bgkA_</a>	Alignment	not modelled	98.8	12	<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 from2 streptococcus mutans
70	<a href="#">d1l2la_</a>	Alignment	not modelled	98.6	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
71	<a href="#">c3drwA_</a>	Alignment	not modelled	98.6	15	<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 pyrococcus2 horikoshii ot3 with amp
72	<a href="#">c4e6eA_</a>	Alignment	not modelled	71.8	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution
73	<a href="#">c3crcB_</a>	Alignment	not modelled	71.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein mazg; <b>PDBTitle:</b> crystal structure of escherichia coli mazg, the regulator2 of nutritional stress response
74	<a href="#">d2vapa1</a>	Alignment	not modelled	70.2	16	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
75	<a href="#">d1rq2a1</a>	Alignment	not modelled	69.7	19	<b>Fold:</b> Tubulin nucleotide-binding domain-like <b>Superfamily:</b> Tubulin nucleotide-binding domain-like <b>Family:</b> Tubulin, GTPase domain
76	<a href="#">d1t4ba1</a>	Alignment	not modelled	65.5	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	<a href="#">c2f00A_</a>	Alignment	not modelled	61.2	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylmuramate--l-alanine ligase; <b>PDBTitle:</b> escherichia coli murc
78	<a href="#">d1mb4a1</a>	Alignment	not modelled	60.5	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	<a href="#">c3ndnC_</a>	Alignment	not modelled	56.4	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> o-succinylhomoserine sulfhydrylase; <b>PDBTitle:</b> crystal structure of o-succinylhomoserine sulfhydrylase

						from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
80	<a href="#">d1j6ua1</a>	Alignment	not modelled	56.4	19	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
81	<a href="#">d1p3da1</a>	Alignment	not modelled	55.4	30	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
82	<a href="#">d1djqa2</a>	Alignment	not modelled	35.8	13	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> C-terminal domain of adrenodoxin reductase-like
83	<a href="#">c1qp8A_</a>	Alignment	not modelled	30.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
84	<a href="#">c2e5vA_</a>	Alignment	not modelled	29.8	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate oxidase; <b>PDBTitle:</b> crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
85	<a href="#">c3aemD_</a>	Alignment	not modelled	29.5	13	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> methionine gamma-lyase; <b>PDBTitle:</b> reaction intermediate structure of entamoeba histolytica methionine2 gamma-lyase 1 containing michaelis complex and methionine imine-3 pyridoxamine-5'-phosphate
86	<a href="#">d2obba1</a>	Alignment	not modelled	29.2	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> BT0820-like
87	<a href="#">c2rhoB_</a>	Alignment	not modelled	26.9	17	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
88	<a href="#">c4dlpA_</a>	Alignment	not modelled	26.5	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> aminoacyl-trna synthetase, class i:aminoacyl-trna <b>PDBTitle:</b> crystal structure of methionyl-trna synthetase metrs from brucella2 melitensis bound to selenomethionine
89	<a href="#">d1pqua1</a>	Alignment	not modelled	25.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	<a href="#">c2x1lC_</a>	Alignment	not modelled	24.5	20	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> methionyl-trna synthetase; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
91	<a href="#">c2xhzC_</a>	Alignment	not modelled	23.6	12	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> arabinose 5-phosphate isomerase; <b>PDBTitle:</b> probing the active site of the sugar isomerase domain from e. coli2 arabinose-5-phosphate isomerase via x-ray crystallography
92	<a href="#">c3d3kD_</a>	Alignment	not modelled	23.5	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
93	<a href="#">d1y4ia1</a>	Alignment	not modelled	22.9	14	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> Cystathionine synthase-like
94	<a href="#">c2yxhB_</a>	Alignment	not modelled	22.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> mazg-related protein; <b>PDBTitle:</b> crystal structure of mazg-related protein from thermotoga maritima
95	<a href="#">d1d8wa_</a>	Alignment	not modelled	22.8	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> L-rhamnose isomerase
96	<a href="#">c3v3tA_</a>	Alignment	not modelled	22.1	15	<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
97	<a href="#">c2vavA_</a>	Alignment	not modelled	21.7	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsz; <b>PDBTitle:</b> ftsz pseudomonas aeruginosa gdp
98	<a href="#">c3d3jA_</a>	Alignment	not modelled	21.2	21	<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
99	<a href="#">d1nhpa2</a>	Alignment	not modelled	20.6	16	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains