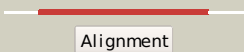

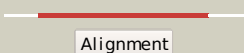

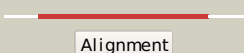
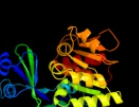
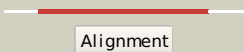

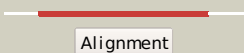

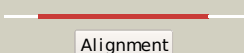

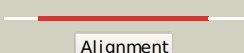

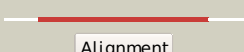

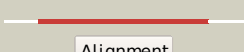

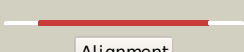

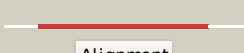



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1bx4a_	 Alignment		100.0	22	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
2	c2xtbA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of trypanosoma brucei rhodesiense2 adenosine kinase complexed with activator
3	c3looc_	 Alignment		100.0	18	PDB header: transferase Chain: C: PDB Molecule: anopheles gambiae adenosine kinase; PDBTitle: crystal structure of anopheles gambiae adenosine kinase in complex2 with p1,p4-di(adenosine-5) tetrphosphate
4	d2absa1	 Alignment		100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
5	c2absA_	 Alignment		100.0	23	PDB header: signaling protein,transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
6	c2pkkA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
7	c2qcvA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: putative 5-dehydro-2-deoxygluconokinase; PDBTitle: crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
8	c3pl2D_	 Alignment		100.0	20	PDB header: transferase Chain: D: PDB Molecule: sugar kinase, ribokinase family; PDBTitle: crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
9	c2rbca_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: sugar kinase; PDBTitle: crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
10	d2dcna1	 Alignment		100.0	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
11	c3iq0B_	 Alignment		100.0	18	PDB header: transferase Chain: B: PDB Molecule: putative ribokinase ii; PDBTitle: crystal structure of a putative ribokinase ii in complex2 with atp and mg+2 from e.coli

12	c2varB_	Alignment		100.0	19	PDB header: transferase Chain: B: PDB Molecule: fructokinase; PDBTitle: crystal structure of sulfolobus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
13	c3in1A_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: uncharacterized sugar kinase ydjh; PDBTitle: crystal structure of a putative ribokinase in complex with2 adp from e.coli
14	d1v19a_	Alignment		100.0	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
15	d1vm7a_	Alignment		100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
16	d1rkda_	Alignment		100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
17	c3b1qD_	Alignment		100.0	15	PDB header: transferase Chain: D: PDB Molecule: ribokinase, putative; PDBTitle: structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
18	c3kzhA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: crystal structure of a putative sugar kinase from2 clostridium perfringens
19	c3go6B_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: ribokinase rbsk; PDBTitle: crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
20	c3lhxA_	Alignment		100.0	15	PDB header: transferase Chain: A: PDB Molecule: ketodeoxygluconokinase; PDBTitle: crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
21	d2fv7a1	Alignment	not modelled	100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
22	c3ktnA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
23	c2nwhA_	Alignment	not modelled	100.0	15	PDB header: signaling protein,transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: carbohydrate kinase from agrobacterium tumefaciens
24	c2jg1C_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: C: PDB Molecule: tagatose-6-phosphate kinase; PDBTitle: structure of the tetrameric inhibited form of2 phosphate2 kinase with cofactor and substrate
25	c2c49A_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: sugar kinase mj0406; PDBTitle: crystal structure of methanocaldococcus jannaschii2 nucleoside kinase - an archaeal member of the ribokinase3 family
26	c3cqdB_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase isozyme 2; PDBTitle: structure of the tetrameric inhibited form of2 phosphofructokinase-2 from escherichia coli
27	d2afb1	Alignment	not modelled	100.0	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
28	d2f02a1	Alignment	not modelled	100.0	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
						Fold: Ribokinase-like

29	d1tyya_	Alignment	not modelled	100.0	20	Superfamily: Ribokinase-like Family: Ribokinase-like
30	c3kd6B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of nucleoside kinase from chlorobium tepidum in2 complex with amp
31	d2abqa1	Alignment	not modelled	100.0	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
32	c3jula_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: lin2199 protein; PDBTitle: crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
33	c3lkiA_	Alignment	not modelled	100.0	15	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase with bound atp from2 xylella fastidiosa
34	c1tz6B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: crystal structure of aminoimidazole riboside kinase from2 salmonella enterica complexed with aminoimidazole riboside3 and atp analog
35	c3gbuD_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: D: PDB Molecule: uncharacterized sugar kinase ph1459; PDBTitle: crystal structure of an uncharacterized sugar kinase ph1459 from2 pyrococcus horikoshii in complex with atp
36	c3i3yB_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
37	c2jg5B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: fructose 1-phosphate kinase; PDBTitle: crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
38	c3b3lC_	Alignment	not modelled	100.0	13	PDB header: transferase Chain: C: PDB Molecule: ketoheokinase; PDBTitle: crystal structures of alternatively-spliced isoforms of human2 ketoheokinase
39	c2qhpA_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase (np_810670.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.80 a resolution
40	c3bf5A_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: A: PDB Molecule: ribokinase related protein; PDBTitle: crystal structure of putative ribokinase (10640157) from thermoplasma2 acidophilum at 1.91 a resolution
41	c3hj6B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: fructokinase; PDBTitle: structure of halothermothrix orenii fructokinase (frk)
42	d2ajra1	Alignment	not modelled	100.0	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
43	d1vk4a_	Alignment	not modelled	100.0	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
44	c2ddmA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: pyridoxine kinase; PDBTitle: crystal structure of pyridoxal kinase from the escherichia2 coli pdxk gene at 2.1 a resolution
45	c3mbjA_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: crystal structure of a putative phosphomethylpyrimidine kinase2 (bt_4458) from bacteroides thetaiotaomicron vpi-5482 at 2.10 a3 resolution (rhombohedral form)
46	d1vi9a_	Alignment	not modelled	99.6	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
47	d1lhpa_	Alignment	not modelled	99.6	22	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
48	c3ibqA_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
49	d1ub0a_	Alignment	not modelled	99.5	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
50	c2i5bC_	Alignment	not modelled	99.5	20	PDB header: transferase Chain: C: PDB Molecule: phosphomethylpyrimidine kinase; PDBTitle: the crystal structure of an adp complex of bacillus2 subtilis pyridoxal kinase provides evidence for the3 parralel emergence of enzyme activity during evolution
51	c3dzvB_	Alignment	not modelled	99.5	16	PDB header: transferase Chain: B: PDB Molecule: 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; PDBTitle: crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
52	d1jxha_	Alignment	not modelled	99.4	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
53	d1v8aa_	Alignment	not modelled	99.2	18	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
						PDB header: transferase

54	c3rm5B_	Alignment	not modelled	99.2	16	Chain: B: PDB Molecule: hydroxymethylpyrimidine/phosphomethylpyrimidine kinase PDBTitle: structure of trifunctional thi20 from yeast
55	d1gc5a_	Alignment	not modelled	98.9	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
56	c3drwA_	Alignment	not modelled	98.9	13	PDB header: transferase Chain: A: PDB Molecule: adp-specific phosphofructokinase; PDBTitle: crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
57	d1u2xa_	Alignment	not modelled	98.8	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
58	d1l2la_	Alignment	not modelled	98.8	9	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
59	d1ekqa_	Alignment	not modelled	98.8	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
60	c3nm3D_	Alignment	not modelled	98.7	15	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
61	d1kyha_	Alignment	not modelled	98.6	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
62	d1ua4a_	Alignment	not modelled	98.5	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
63	d2ax3a1	Alignment	not modelled	98.0	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
64	c2r3bA_	Alignment	not modelled	97.9	10	PDB header: transferase Chain: A: PDB Molecule: yjef-related protein; PDBTitle: crystal structure of a ribokinase-like superfamily protein (ef1790)2 from enterococcus faecalis v583 at 1.80 a resolution
65	c2ax3A_	Alignment	not modelled	97.4	12	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tm0922; PDBTitle: crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
66	c3bgkA_	Alignment	not modelled	96.0	15	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
67	c3k5wA_	Alignment	not modelled	95.9	17	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of a carbohydrate kinase (yjef family)from2 helicobacter pylori
68	d1xw8a_	Alignment	not modelled	51.4	9	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
69	d1q6oa_	Alignment	not modelled	40.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
70	c3npgD_	Alignment	not modelled	39.8	7	PDB header: unknown function Chain: D: PDB Molecule: uncharacterized duf364 family protein; PDBTitle: crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
71	c3p6lA_	Alignment	not modelled	35.7	10	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
72	c3ndnC_	Alignment	not modelled	33.0	14	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulphydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulphydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
73	d2h1qa1	Alignment	not modelled	27.2	12	Fold: PLP-dependent transferase-like Superfamily: Dhaf3308-like Family: Dhaf3308-like
74	c3iraA_	Alignment	not modelled	26.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: the crystal structure of one domain of the conserved protein from2 methanosarcina mazei go1
75	d1c4ka2	Alignment	not modelled	21.2	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Ornithine decarboxylase major domain
76	d1t15a2	Alignment	not modelled	17.9	9	Fold: BRCT domain Superfamily: BRCT domain Family: BRCT domain
77	c2fjaC_	Alignment	not modelled	17.2	23	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with2 substrate
78	c3n0lA_	Alignment	not modelled	15.3	12	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
						Fold: DNA/RNA-binding 3-helical bundle

79	d1ucra_	Alignment	not modelled	14.3	56	Superfamily: "Winged helix" DNA-binding domain Family: Dissimilatory sulfite reductase DsvD
80	c2d6fa_	Alignment	not modelled	14.0	22	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
81	d1tqxa_	Alignment	not modelled	13.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
82	d2ctza1	Alignment	not modelled	13.6	15	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
83	d1wbha1	Alignment	not modelled	13.6	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
84	d1v0wa1	Alignment	not modelled	13.6	12	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Phospholipase D
85	d2q02a1	Alignment	not modelled	13.3	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
86	d1a3xa2	Alignment	not modelled	13.2	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
87	c2e85B_	Alignment	not modelled	11.8	0	PDB header: hydrolase Chain: B: PDB Molecule: hydrogenase 3 maturation protease; PDBTitle: crystal structure of the hydrogenase 3 maturation protease
88	d1sgva1	Alignment	not modelled	11.8	35	Fold: PUA domain-like Superfamily: PUA domain-like Family: PUA domain
89	c2jwlB_	Alignment	not modelled	11.3	13	PDB header: membrane protein Chain: B: PDB Molecule: protein tolR; PDBTitle: solution structure of periplasmic domain of tolR from h.2 influenzae with saxes data
90	d1vmia_	Alignment	not modelled	10.8	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
91	c1vmiA_	Alignment	not modelled	10.8	16	PDB header: transferase Chain: A: PDB Molecule: putative phosphate acetyltransferase; PDBTitle: crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
92	c3exsB_	Alignment	not modelled	10.6	12	PDB header: lyase Chain: B: PDB Molecule: rmpp (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
93	c2zdsB_	Alignment	not modelled	10.6	11	PDB header: dna binding protein Chain: B: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor2 a3(2)
94	d1cfza_	Alignment	not modelled	10.5	33	Fold: Phosphorylase/hydrolase-like Superfamily: HybD-like Family: Hydrogenase maturing endopeptidase HybD
95	d1t4ba1	Alignment	not modelled	10.3	7	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d2d6fa2	Alignment	not modelled	10.3	22	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
97	c3pu6A_	Alignment	not modelled	10.1	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of an uncharacterized protein from wolinetla2 succinogenes
98	d1mxsa_	Alignment	not modelled	9.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c2xsba_	Alignment	not modelled	9.8	13	PDB header: hydrolase Chain: A: PDB Molecule: hyaluronoglucosaminidase; PDBTitle: ogoga pugnac complex