









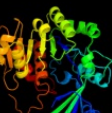








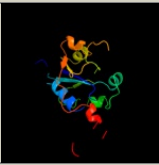
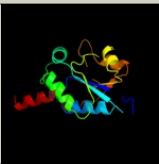



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kzhA_</a>	 Alignment		100.0	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> crystal structure of a putative sugar kinase from2 clostridium perfringens
2	<a href="#">d1rkda_</a>	 Alignment		100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
3	<a href="#">c3pl2D_</a>	 Alignment		100.0	23	<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
4	<a href="#">c2qcvA_</a>	 Alignment		100.0	16	<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
5	<a href="#">d1bx4a_</a>	 Alignment		100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
6	<a href="#">c2xtbA_</a>	 Alignment		100.0	18	<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
7	<a href="#">d2afba1</a>	 Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
8	<a href="#">c2pkkA_</a>	 Alignment		100.0	22	<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
9	<a href="#">c3looc_</a>	 Alignment		100.0	18	<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
10	<a href="#">c2rbca_</a>	 Alignment		100.0	19	<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
11	<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

12	<a href="#">c2nwhA_</a>	Alignment		100.0	21	<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
13	<a href="#">d2f02a1</a>	Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
14	<a href="#">d1v19a_</a>	Alignment		100.0	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
15	<a href="#">c2jg1C_</a>	Alignment		100.0	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
16	<a href="#">c3ktnA_</a>	Alignment		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
17	<a href="#">c3in1A_</a>	Alignment		100.0	19	<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
18	<a href="#">c3iq0B_</a>	Alignment		100.0	18	<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
19	<a href="#">c3go6B_</a>	Alignment		100.0	23	<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
20	<a href="#">d2abqa1</a>	Alignment		100.0	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
21	<a href="#">d2absa1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
22	<a href="#">c2absA_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">d2fv7a1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
24	<a href="#">c3b1qD_</a>	Alignment	not modelled	100.0	21	<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
25	<a href="#">d1vm7a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
26	<a href="#">c2jg5B_</a>	Alignment	not modelled	100.0	15	<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
27	<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 sulfobolus solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
28	<a href="#">c3i3yB_</a>	Alignment	not modelled	100.0	23	<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
						<b>PDB header:</b> transferase

29	<a href="#">c2c49A</a>	Alignment	not modelled	100.0	19	<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
30	<a href="#">d2dcna1</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
31	<a href="#">d2ajra1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
32	<a href="#">c3lhxA</a>	Alignment	not modelled	100.0	17	<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
33	<a href="#">d1tyya</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
34	<a href="#">c3lkiA</a>	Alignment	not modelled	100.0	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
35	<a href="#">c3gbuD</a>	Alignment	not modelled	100.0	20	<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
36	<a href="#">c2qhPA</a>	Alignment	not modelled	100.0	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
37	<a href="#">c3julA</a>	Alignment	not modelled	100.0	19	<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
38	<a href="#">c3kd6B</a>	Alignment	not modelled	100.0	18	<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
39	<a href="#">c3b3lC</a>	Alignment	not modelled	100.0	18	<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
40	<a href="#">c1tz6B</a>	Alignment	not modelled	100.0	25	<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
41	<a href="#">c3elbA</a>	Alignment		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ethanolamine-phosphate cytidylyltransferase; <b>PDBTitle:</b> human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
42	<a href="#">d1vk4a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
43	<a href="#">c3bf5A</a>	Alignment	not modelled	100.0	18	<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
44	<a href="#">c3hj6B</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> structure of halothermothrix orenii fructokinase (frk)
45	<a href="#">c3hl4B</a>	Alignment		100.0	28	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> choline-phosphate cytidylyltransferase a; <b>PDBTitle:</b> crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
46	<a href="#">c3glvB</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide core biosynthesis protein; <b>PDBTitle:</b> crystal structure of the lipopolysaccharide core biosynthesis protein2 from thermoplasma volcanium gss1
47	<a href="#">d1coza</a>	Alignment	not modelled	99.9	32	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Cytidylyltransferase
48	<a href="#">c2b7lD</a>	Alignment	not modelled	99.9	31	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> glycerol-3-phosphate cytidylyltransferase; <b>PDBTitle:</b> crystal structure of ctp:glycerol-3-phosphate2 cytidylyltransferase from staphylococcus aureus
49	<a href="#">c2ddmA</a>	Alignment	not modelled	99.9	22	<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
50	<a href="#">d1mrza2</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Adenylyltransferase
51	<a href="#">c1t6zB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin kinase/fmn adenylyltransferase; <b>PDBTitle:</b> crystal structure of riboflavin bound tm379
52	<a href="#">c3op1A</a>	Alignment	not modelled	99.8	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrolide-efflux protein; <b>PDBTitle:</b> crystal structure of macrolide-efflux protein sp_1110

					from2 streptococcus pneumoniae
53	<a href="#">c2x0kB_</a>	Alignment	not modelled	99.8	19 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribf; <b>PDBTitle:</b> crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
54	<a href="#">d1vi9a_</a>	Alignment	not modelled	99.8	21 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
55	<a href="#">c2i5bC_</a>	Alignment	not modelled	99.7	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 bacillus2 subtilis pyridoxal kinase provides evidence for the3 parrallel emergence of enzyme activity during evolution
56	<a href="#">c3mbjA_</a>	Alignment	not modelled	99.7	18 <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)
57	<a href="#">d1ub0a_</a>	Alignment	not modelled	99.7	24 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
58	<a href="#">c3rm5B_</a>	Alignment	not modelled	99.7	20 <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
59	<a href="#">d1lhpa_</a>	Alignment	not modelled	99.7	20 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
60	<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
61	<a href="#">c3do8B_</a>	Alignment	not modelled	99.6	20 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> the crystal structure of the protein with unknown function2 from archaeoglobus fulgidus
62	<a href="#">d1jxha_</a>	Alignment	not modelled	99.6	19 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
63	<a href="#">d1qjca_</a>	Alignment	not modelled	99.5	18 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenyltransferase
64	<a href="#">c3f3mA_</a>	Alignment	not modelled	99.5	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> six crystal structures of two phosphopantetheine2 adenyltransferases reveal an alternative ligand binding3 mode and an associated structural change
65	<a href="#">c3nd5D_</a>	Alignment	not modelled	99.5	18 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenyltransferase (ppat)2 from enterococcus faecalis
66	<a href="#">c3ikzA_</a>	Alignment	not modelled	99.5	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> crystal structure of phosphopantetheine adenyltransferase from2 burkholderia pseudomallei
67	<a href="#">c3nv7A_</a>	Alignment	not modelled	99.5	22 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantetheine adenyltransferase; <b>PDBTitle:</b> crystal structure of h.pylori phosphopantetheine adenyltransferase2 mutant i4v/n76y
68	<a href="#">d1od6a_</a>	Alignment	not modelled	99.5	22 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenyltransferase
69	<a href="#">c3dzvB_</a>	Alignment	not modelled	99.5	20 <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
70	<a href="#">d1tfua_</a>	Alignment	not modelled	99.5	13 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenyltransferase
71	<a href="#">d1o6ba_</a>	Alignment	not modelled	99.4	13 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenyltransferase
72	<a href="#">d1vlha_</a>	Alignment	not modelled	99.4	20 <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenyltransferase
73	<a href="#">c3guzB_</a>	Alignment	not modelled	99.4	21 <b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
74	<a href="#">d1v8aa_</a>	Alignment	not modelled	99.4	20 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
75	<a href="#">d1kyha_</a>	Alignment	not modelled	99.3	19 <b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
76	<a href="#">c3h05A_</a>	Alignment	not modelled	99.3	18 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vpa0413; <b>PDBTitle:</b> the crystal structure of a putative nicotinate-nucleotide2 adenyltransferase from vibrio parahaemolyticus

77	<a href="#">dl1w7a1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
78	<a href="#">c2qjoB</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional nm adenylyltransferase/nudix hydrolase; <b>PDBTitle:</b> crystal structure of a bifunctional nm adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
79	<a href="#">c2r5wA</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinamide-nucleotide adenylyltransferase; <b>PDBTitle:</b> crystal structure of a bifunctional nm2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
80	<a href="#">d1ej2a</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
81	<a href="#">d1f9aa</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
82	<a href="#">d2ax3a1</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
83	<a href="#">c2h29A</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
84	<a href="#">d1ekqa</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
85	<a href="#">c3e27B</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> nicotinate (nicotinamide) nucleotide <b>PDBTitle:</b> nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
86	<a href="#">c1yunB</a>	Alignment	not modelled	99.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable nicotinate-nucleotide <b>PDBTitle:</b> crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
87	<a href="#">c2r3bA</a>	Alignment	not modelled	99.0	18	<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
88	<a href="#">c1lw7A</a>	Alignment	not modelled	99.0	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator nadr; <b>PDBTitle:</b> nadr protein from haemophilus influenzae
89	<a href="#">c2ax3A</a>	Alignment	not modelled	98.9	13	<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
90	<a href="#">d1kama</a>	Alignment	not modelled	98.9	20	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
91	<a href="#">d1k4ma</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
92	<a href="#">c3nm3D</a>	Alignment	not modelled	98.7	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
93	<a href="#">d1kr2a</a>	Alignment	not modelled	98.7	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
94	<a href="#">d1nuua</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Adenylyltransferase
95	<a href="#">c3ag5A</a>	Alignment		98.6	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantothenate synthetase from staphylococcus2 aureus
96	<a href="#">d1gc5a</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
97	<a href="#">c2ejcA</a>	Alignment	not modelled	98.6	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantoate--beta-alanine ligase; <b>PDBTitle:</b> crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
98	<a href="#">d1ihoa</a>	Alignment	not modelled	98.5	25	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidylyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
99	<a href="#">c3gmiA</a>	Alignment	not modelled	98.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0348 protein mj0951; <b>PDBTitle:</b> crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
100	<a href="#">d1l2la</a>	Alignment	not modelled	98.4	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase



101	<a href="#">c3k5wA</a>	Alignment	not modelled	98.4	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
102	<a href="#">c3innB</a>	Alignment	not modelled	98.4	29	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
103	<a href="#">c3bgkA</a>	Alignment	not modelled	98.4	17	<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
104	<a href="#">d1ua4a</a>	Alignment	not modelled	98.3	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
105	<a href="#">d1u2xa</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
106	<a href="#">c3mxtA</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
107	<a href="#">d2a84a1</a>	Alignment	not modelled	98.3	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
108	<a href="#">c3drwA</a>	Alignment	not modelled	98.2	18	<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
109	<a href="#">c3n8hA</a>	Alignment	not modelled	98.2	26	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
110	<a href="#">c3uk2B</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pantothenate synthetase; <b>PDBTitle:</b> the structure of pantothenate synthetase from burkholderia2 thailandensis
111	<a href="#">d1v8fa</a>	Alignment	not modelled	98.0	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
112	<a href="#">c1r6uB</a>	Alignment	not modelled	91.8	12	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
113	<a href="#">c2f00A</a>	Alignment	not modelled	89.9	27	<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
114	<a href="#">d1r6ta2</a>	Alignment	not modelled	86.9	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> Class I aminoacyl-tRNA synthetases (RS), catalytic domain
115	<a href="#">d1v47a2</a>	Alignment	not modelled	83.9	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
116	<a href="#">d1jhda2</a>	Alignment	not modelled	83.8	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain
117	<a href="#">c3i3lA</a>	Alignment	not modelled	83.6	29	<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
118	<a href="#">c3i05B</a>	Alignment	not modelled	81.8	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from trypanosoma brucei
119	<a href="#">c3hv0A</a>	Alignment	not modelled	81.2	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophanyl-trna synthetase; <b>PDBTitle:</b> tryptophanyl-trna synthetase from cryptosporidium parvum
120	<a href="#">d1g8fa2</a>	Alignment	not modelled	79.5	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Nucleotidyl transferase <b>Family:</b> ATP sulfurylase catalytic domain