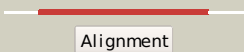

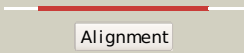







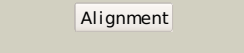

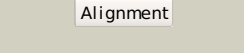

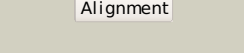



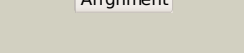

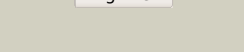












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kzhA_</a>	 Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable sugar kinase; <b>PDBTitle:</b> crystal structure of a putative sugar kinase from2 clostridium perfringens
2	<a href="#">d1rkda_</a>	 Alignment		100.0	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
3	<a href="#">c2nwhA_</a>	 Alignment		100.0	27	<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
4	<a href="#">c2c49A_</a>	 Alignment		100.0	18	<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
5	<a href="#">c3pl2D_</a>	 Alignment		100.0	18	<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
6	<a href="#">c2rbca_</a>	 Alignment		100.0	15	<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
7	<a href="#">c2pkkA_</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 m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
8	<a href="#">d2fv7a1</a>	 Alignment		100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
9	<a href="#">c3in1A_</a>	 Alignment		100.0	22	<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
10	<a href="#">c2qcvA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 5-dehydro-2-deoxygluconokinase; <b>PDBTitle:</b> crystal structure of a putative 5-dehydro-2-deoxygluconokinase (iolc)2 from bacillus halodurans c-125 at 1.90 a resolution
11	<a href="#">c3b1qD_</a>	 Alignment		100.0	19	<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

12	<a href="#">d1vm7a_</a>	Alignment		100.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
13	<a href="#">c3cqdB_</a>	Alignment		100.0	19	<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
14	<a href="#">c3go6B_</a>	Alignment		100.0	19	<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
15	<a href="#">c3iq0B_</a>	Alignment		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
16	<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
17	<a href="#">d2f02a1</a>	Alignment		100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
18	<a href="#">d1v19a_</a>	Alignment		100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
19	<a href="#">c2varB_</a>	Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fructokinase; <b>PDBTitle:</b> crystal structure of anopheles solfataricus 2-keto-3-2 deoxygluconate kinase complexed with 2-keto-3-3 deoxygluconate
20	<a href="#">c3loqC_</a>	Alignment		100.0	15	<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
21	<a href="#">c3i3yB_</a>	Alignment	not modelled	100.0	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
22	<a href="#">d2abqa1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
23	<a href="#">d1bx4a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
24	<a href="#">c2jg5B_</a>	Alignment	not modelled	100.0	18	<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
25	<a href="#">c2xtbA_</a>	Alignment	not modelled	100.0	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
26	<a href="#">d2dcna1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
27	<a href="#">c3b3lC_</a>	Alignment	not modelled	100.0	15	<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
28	<a href="#">d2afba1</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
						<b>PDB header:</b> transferase

29	<a href="#">c3ktnA_</a>	Alignment	not modelled	100.0	15	<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
30	<a href="#">d2ajra1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
31	<a href="#">d2absa1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
32	<a href="#">c2absA_</a>	Alignment	not modelled	100.0	18	<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
33	<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
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="#">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
36	<a href="#">d1tyya_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
37	<a href="#">c3lhxA_</a>	Alignment	not modelled	100.0	18	<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
38	<a href="#">c2qhpa_</a>	Alignment	not modelled	100.0	18	<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
39	<a href="#">c3julA_</a>	Alignment	not modelled	100.0	18	<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
40	<a href="#">c3lkiA_</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 with bound atp from2 xylella fastidiosa
41	<a href="#">c1tz6B_</a>	Alignment	not modelled	100.0	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
42	<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)
43	<a href="#">d1vk4a_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Ribokinase-like
44	<a href="#">c2ddmA_</a>	Alignment	not modelled	99.9	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 escherichia2 coli pdxk gene at 2.1 a resolution
45	<a href="#">c3mbjA_</a>	Alignment	not modelled	99.8	15	<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)
46	<a href="#">c2i5bC_</a>	Alignment	not modelled	99.7	21	<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
47	<a href="#">d1vi9a_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
48	<a href="#">c3ibqA_</a>	Alignment	not modelled	99.7	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 lactobacillus2 plantarum in complex with atp
49	<a href="#">d1ub0a_</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
50	<a href="#">d1lhpa_</a>	Alignment	not modelled	99.6	21	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> PfkB-like kinase
51	<a href="#">c3rm5B_</a>	Alignment	not modelled	99.5	16	<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
52	<a href="#">d1jxha_</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
53	<a href="#">c3dzvB_</a>	Alignment	not modelled	99.2	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)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution

54	<a href="#">d1v8aa_</a>	Alignment	not modelled	99.0	20	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
55	<a href="#">d2ax3a1</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
56	<a href="#">d1kyha_</a>	Alignment	not modelled	98.9	11	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> YjeF C-terminal domain-like
57	<a href="#">c2ax3A_</a>	Alignment	not modelled	98.7	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
58	<a href="#">c2r3bA_</a>	Alignment	not modelled	98.6	11	<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
59	<a href="#">d1ekqa_</a>	Alignment	not modelled	98.6	17	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> Thiamin biosynthesis kinases
60	<a href="#">c3k5wA_</a>	Alignment	not modelled	98.5	16	<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
61	<a href="#">c3bgkA_</a>	Alignment	not modelled	98.3	13	<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
62	<a href="#">c3nm3D_</a>	Alignment	not modelled	98.2	15	<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
63	<a href="#">d1l2la_</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
64	<a href="#">d1gc5a_</a>	Alignment	not modelled	97.8	13	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
65	<a href="#">d1u2xa_</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
66	<a href="#">c3drwA_</a>	Alignment	not modelled	97.3	17	<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
67	<a href="#">d1ua4a_</a>	Alignment	not modelled	97.1	10	<b>Fold:</b> Ribokinase-like <b>Superfamily:</b> Ribokinase-like <b>Family:</b> ADP-specific Phosphofructokinase/Glucokinase
68	<a href="#">c3kljA_</a>	Alignment	not modelled	68.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-dependent dehydrogenase, nirb-family (n-terminal <b>PDBTitle:</b> crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
69	<a href="#">c3lzxB_</a>	Alignment	not modelled	63.7	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase 2; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
70	<a href="#">c2hkoA_</a>	Alignment	not modelled	61.5	41	<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
71	<a href="#">c1c0iA_</a>	Alignment	not modelled	59.3	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-amino acid oxidase; <b>PDBTitle:</b> crystal structure of d-amino acid oxidase in complex with2 two anthranilate molecules
72	<a href="#">c2v1dA_</a>	Alignment	not modelled	54.4	41	<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
73	<a href="#">c2xagA_</a>	Alignment	not modelled	54.4	41	<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
74	<a href="#">c3crcB_</a>	Alignment	not modelled	52.7	9	<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
75	<a href="#">d1p3da1</a>	Alignment	not modelled	51.4	33	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
76	<a href="#">d2dw4a2</a>	Alignment	not modelled	48.4	39	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
77	<a href="#">c1v59B_</a>	Alignment	not modelled	41.1	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
78	<a href="#">d1gega_</a>	Alignment	not modelled	40.7	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
79	<a href="#">d1c0pa1</a>	Alignment	not modelled	35.9	39	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> D-aminoacid oxidase, N-terminal domain

80	<a href="#">d1trba2</a>	Alignment	not modelled	35.7	19	<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
81	<a href="#">c1ps9A</a>	Alignment	not modelled	35.5	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
82	<a href="#">c1djnb</a>	Alignment	not modelled	35.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
83	<a href="#">d1xgka</a>	Alignment	not modelled	34.6	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
84	<a href="#">c3k5iB</a>	Alignment	not modelled	34.1	29	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoribosyl-aminimidazole carboxylase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimidazole ribonucleotide
85	<a href="#">c3a1iA</a>	Alignment	not modelled	33.7	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; <b>PDBTitle:</b> crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
86	<a href="#">c3gucB</a>	Alignment	not modelled	33.2	45	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme 5; <b>PDBTitle:</b> human ubiquitin-activating enzyme 5 in complex with amppnp
87	<a href="#">c2f00A</a>	Alignment	not modelled	33.1	33	<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
88	<a href="#">c1vdcA</a>	Alignment	not modelled	32.2	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dependent thioredoxin reductase; <b>PDBTitle:</b> structure of nadph dependent thioredoxin reductase
89	<a href="#">d1nyta1</a>	Alignment	not modelled	31.0	22	<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
90	<a href="#">c2e1mA</a>	Alignment	not modelled	30.8	28	<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
91	<a href="#">c3enkB</a>	Alignment	not modelled	30.7	32	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei
92	<a href="#">d1ml4a2</a>	Alignment	not modelled	30.5	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
93	<a href="#">d1q5qa</a>	Alignment	not modelled	30.4	12	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Proteasome subunits
94	<a href="#">c2ppvA</a>	Alignment	not modelled	27.9	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
95	<a href="#">d1pzga1</a>	Alignment	not modelled	26.2	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
96	<a href="#">d2hzba1</a>	Alignment	not modelled	25.9	33	<b>Fold:</b> CofD-like <b>Superfamily:</b> CofD-like <b>Family:</b> CofD-like
97	<a href="#">d1hdoa</a>	Alignment	not modelled	25.2	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
98	<a href="#">c3d8xB</a>	Alignment	not modelled	25.2	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
99	<a href="#">d1v59a1</a>	Alignment	not modelled	24.9	39	<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
100	<a href="#">c1f8sA</a>	Alignment	not modelled	24.8	44	<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 callioselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
101	<a href="#">c2b9yA</a>	Alignment	not modelled	24.6	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aminooxidase; <b>PDBTitle:</b> crystal structure of cla-producing fatty acid isomerase2 from p. acnes
102	<a href="#">d1uz5a3</a>	Alignment	not modelled	24.5	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
103	<a href="#">d1seza1</a>	Alignment	not modelled	24.3	38	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
104	<a href="#">c3d3jA</a>	Alignment	not modelled	24.1	15	<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



105	<a href="#">c3nlcA_</a>	Alignment	not modelled	24.1	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956; <b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
106	<a href="#">c3lxdA_</a>	Alignment	not modelled	24.1	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
107	<a href="#">c2fu3A_</a>	Alignment	not modelled	23.8	15	<b>PDB header:</b> biosynthetic protein/structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> gephyrin; <b>PDBTitle:</b> crystal structure of gephyrin e-domain
108	<a href="#">d1djqa3</a>	Alignment	not modelled	23.2	41	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
109	<a href="#">c1y56B_</a>	Alignment	not modelled	22.7	45	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sarcosine oxidase; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
110	<a href="#">c3rhaA_</a>	Alignment	not modelled	22.4	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putrescine oxidase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from arthrobacter aurescens
111	<a href="#">c2nqqa_</a>	Alignment	not modelled	22.2	16	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> molybdopterin biosynthesis protein moea; <b>PDBTitle:</b> moea r137q
112	<a href="#">c1q5rD_</a>	Alignment	not modelled	22.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> proteasome alpha-type subunit 1; <b>PDBTitle:</b> the rhodococcus 20s proteasome with unprocessed pro-peptides
113	<a href="#">c3pl5A_</a>	Alignment	not modelled	21.7	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> fatty acid binding protein
114	<a href="#">c1w7pD_</a>	Alignment	not modelled	21.3	12	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> vps36p, ylr417w; <b>PDBTitle:</b> the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
115	<a href="#">d1j6ua1</a>	Alignment	not modelled	21.1	16	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
116	<a href="#">c2wfbA_</a>	Alignment	not modelled	20.8	33	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein orp; <b>PDBTitle:</b> high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
117	<a href="#">d1wu2a3</a>	Alignment	not modelled	20.7	10	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
118	<a href="#">d1trba1</a>	Alignment	not modelled	20.6	35	<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
119	<a href="#">d2ftsaa3</a>	Alignment	not modelled	20.5	17	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MoeA central domain-like
120	<a href="#">c2vdcl_</a>	Alignment	not modelled	20.4	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadh] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.