



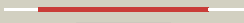

















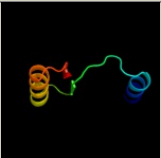
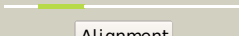
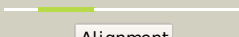
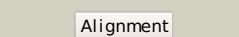



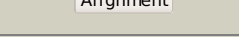


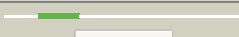


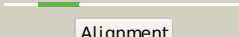
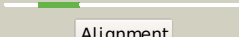
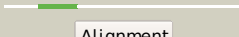





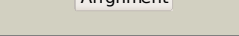
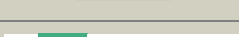
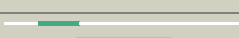



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rkda_	 Alignment		100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
2	c3pl2D_	 Alignment		100.0	18	PDB header: transferase Chain: D: PDB Molecule: sugar kinase, ribokinase family; PDBTitle: crystal structure of a 5-keto-2-deoxygluconokinase (ncgl0155, cgl0158)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.89 a3 resolution
3	d1vm7a_	 Alignment		100.0	21	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
4	c3go6B_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: ribokinase rbsk; PDBTitle: crystal structure of m. tuberculosis ribokinase (rv2436) in2 complex with ribose and amp-pnp
5	c3kzhA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: probable sugar kinase; PDBTitle: crystal structure of a putative sugar kinase from2 clostridium perfringens
6	c2rbca_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: sugar kinase; PDBTitle: crystal structure of a putative ribokinase from agrobacterium2 tumefaciens
7	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
8	c2c49A_	 Alignment		100.0	20	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
9	d1v19a_	 Alignment		100.0	25	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
10	c3iq0B_	 Alignment		100.0	17	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
11	d2abqa1	 Alignment		100.0	20	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like

12	c2qcvA_	Alignment		100.0	20	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
13	c2pkkA_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of m tuberculosis adenosine kinase complexed with 2-2 fluoro adenosine
14	c3cqdB_	Alignment		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
15	c2jg1C_	Alignment		100.0	12	PDB header: transferase Chain: C: PDB Molecule: tagatose-6-phosphate kinase; PDBTitle: structure of staphylococcus aureus d-tagatose-6-phosphate2 kinase with cofactor and substrate
16	c3b1qD_	Alignment		100.0	23	PDB header: transferase Chain: D: PDB Molecule: ribokinase, putative; PDBTitle: structure of burkholderia thailandensis nucleoside kinase (bthnk) in2 complex with inosine
17	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
18	d1bx4a_	Alignment		100.0	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
19	c2nwhA_	Alignment		100.0	19	PDB header: signaling protein,transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: carbohydrate kinase from agrobacterium tumefaciens
20	d2f02a1	Alignment		100.0	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
21	c2varB_	Alignment	not modelled	100.0	17	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
22	d2fv7a1	Alignment	not modelled	100.0	21	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
23	d2absa1	Alignment	not modelled	100.0	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
24	c2absA_	Alignment	not modelled	100.0	19	PDB header: signaling protein,transferase Chain: A: PDB Molecule: adenosine kinase; PDBTitle: crystal structure of t. gondii adenosine kinase complexed2 with amp-pcp
25	c3i3yB_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: B: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of ribokinase in complex with d-ribose from2 klebsiella pneumoniae
26	d2dcna1	Alignment	not modelled	100.0	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
27	c2jg5B_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: fructose 1-phosphate kinase; PDBTitle: crystal structure of a putative phosphofructokinase from2 staphylococcus aureus
28	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
						PDB header: transferase

29	c3ktnA_	Alignment	not modelled	100.0	14	Chain: A: PDB Molecule: carbohydrate kinase, pfkb family; PDBTitle: crystal structure of a putative 2-keto-3-deoxygluconate2 kinase from enterococcus faecalis
30	c3looc_	Alignment	not modelled	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) tetraphosphate
31	d2afba1	Alignment	not modelled	100.0	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
32	c2qhpA_	Alignment	not modelled	100.0	15	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
33	d1tyya_	Alignment	not modelled	100.0	23	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
34	c3b3lC_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: C: PDB Molecule: ketohehexokinase; PDBTitle: crystal structures of alternatively-spliced isoforms of human2 ketohehexokinase
35	c3bf5A_	Alignment	not modelled	100.0	18	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
36	c1tz6B_	Alignment	not modelled	100.0	23	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
37	c3lkiA_	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: fructokinase; PDBTitle: crystal structure of fructokinase with bound atp from2 xylella fastidiosa
38	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
39	c3julA_	Alignment	not modelled	100.0	14	PDB header: transferase Chain: A: PDB Molecule: lin2199 protein; PDBTitle: crystal structure of listeria innocua d-tagatose-6-phosphate2 kinase bound with substrate
40	d2ajra1	Alignment	not modelled	100.0	12	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
41	c3lhxA_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: ketodeoxygluconokinase; PDBTitle: crystal structure of a ketodeoxygluconokinase (kdgk) from2 shigella flexneri
42	d1vk4a_	Alignment	not modelled	100.0	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
43	c3hj6B_	Alignment	not modelled	100.0	18	PDB header: transferase Chain: B: PDB Molecule: fructokinase; PDBTitle: structure of halothermothrix orenii fructokinase (frk)
44	c2ddmA_	Alignment	not modelled	99.9	25	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	c2i5bC_	Alignment	not modelled	99.8	18	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 parrallel emergence of enzyme activity during evolution
46	c3mbjA_	Alignment	not modelled	99.8	13	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)
47	d1ub0a_	Alignment	not modelled	99.7	20	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
48	d1lhpA_	Alignment	not modelled	99.7	19	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
49	c3ibqA_	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: pyridoxal kinase; PDBTitle: crystal structure of pyridoxal kinase from lactobacillus2 plantarum in complex with atp
50	d1vi9a_	Alignment	not modelled	99.7	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: PfkB-like kinase
51	d1jxha_	Alignment	not modelled	99.5	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
52	c3rm5B_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: B: PDB Molecule: hydroxymethylpyrimidine/phosphomethylpyrimidine kinase PDBTitle: structure of trifunctional thi20 from yeast
53	c3dzvB_	Alignment	not modelled	99.2	14	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

54	d1kyha_	Alignment	not modelled	99.1	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
55	d1v8aa_	Alignment	not modelled	99.1	11	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
56	d2ax3a1	Alignment	not modelled	98.9	12	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: YjeF C-terminal domain-like
57	d1gc5a_	Alignment	not modelled	98.8	15	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
58	d1ekqa_	Alignment	not modelled	98.6	14	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
59	d1ua4a_	Alignment	not modelled	98.6	16	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
60	d1l2la_	Alignment	not modelled	98.6	17	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
61	c2r3bA_	Alignment	not modelled	98.5	13	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
62	c2ax3A_	Alignment	not modelled	98.4	9	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
63	c3drwA_	Alignment	not modelled	98.3	20	PDB header: transferase Chain: A: PDB Molecule: adp-specific phosphofructokinase; PDBTitle: crystal structure of a phosphofructokinase from pyrococcus2 horikoshii ot3 with amp
64	c3k5wA_	Alignment	not modelled	98.2	14	PDB header: transferase Chain: A: PDB Molecule: carbohydrate kinase; PDBTitle: crystal structure of a carbohydrate kinase (yjeF family)from2 helicobacter pylori
65	d1u2xa_	Alignment	not modelled	98.2	20	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: ADP-specific Phosphofructokinase/Glucokinase
66	c3nm3D_	Alignment	not modelled	98.2	12	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
67	c3bgkA_	Alignment	not modelled	98.1	8	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of hypothetic protein smu.573 from2 streptococcus mutans
68	c1qo8A_	Alignment		85.1	31	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
69	c1d4cB_	Alignment	not modelled	83.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1
70	c2f00A_	Alignment	not modelled	82.6	28	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
71	c1c0iA_	Alignment	not modelled	81.3	30	PDB header: oxidoreductase Chain: A: PDB Molecule: d-amino acid oxidase; PDBTitle: crystal structure of d-amino acid oxidase in complex with2 two anthranilate molecules
72	c1jrxA_	Alignment	not modelled	78.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
73	d1p3da1	Alignment	not modelled	73.7	30	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
74	c2elmA_	Alignment	not modelled	69.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: l- glutamate oxidase; PDBTitle: crystal structure of l- glutamate oxidase from streptomyces sp. x-119-6
75	d1v59a1	Alignment	not modelled	69.0	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
76	d1d4ca2	Alignment	not modelled	67.6	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
77	c1v59B_	Alignment	not modelled	67.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
78	d1c0pa1	Alignment	not modelled	65.4	30	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: D-aminoacid oxidase, N-terminal domain

79	c1yq4A	 Alignment	not modelled	65.4	39	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
80	d1trba2	 Alignment	not modelled	64.5	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
81	d1reoa1	 Alignment	not modelled	64.5	42	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
82	d1dxa1	 Alignment	not modelled	61.6	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
83	c3da1A	 Alignment	not modelled	61.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
84	d1ryia1	 Alignment	not modelled	60.6	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
85	d1x94a	 Alignment	not modelled	58.9	12	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
86	d3lada1	 Alignment	not modelled	58.7	38	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
87	d1h6va2	 Alignment	not modelled	57.9	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
88	d2iida1	 Alignment	not modelled	55.8	39	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
89	c1ps9A	 Alignment	not modelled	55.2	38	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
90	c1f8sA	 Alignment	not modelled	54.4	41	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
91	c2zxiC	 Alignment	not modelled	53.0	27	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
92	d1trba1	 Alignment	not modelled	52.6	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
93	c3kljA	 Alignment	not modelled	52.3	29	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal) PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
94	c3v76A	 Alignment	not modelled	51.7	38	PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti
95	d1d7ya2	 Alignment	not modelled	51.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
96	d1lpfa1	 Alignment	not modelled	50.5	38	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
97	c3nlcA	 Alignment	not modelled	50.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
98	c1vdca	 Alignment	not modelled	50.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
99	d1vdca1	 Alignment	not modelled	50.0	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
100	d1qo8a2	 Alignment	not modelled	49.6	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
101	d1ps9a3	 Alignment	not modelled	49.3	38	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: N-terminal domain of adrenodoxin reductase-like
102	d1y0pa2	 Alignment	not modelled	49.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
103	c2hkoA	Alignment	not modelled	49.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1

104	d1d5ta1	Alignment	not modelled	48.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain
105	c3g05B	Alignment	not modelled	48.6	24	PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
106	c1f6mF	Alignment	not modelled	47.6	22	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
107	c2rghA	Alignment	not modelled	46.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
108	c3i3IA	Alignment	not modelled	46.3	27	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
109	c2gqfA	Alignment	not modelled	45.5	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
110	c3lzxB	Alignment	not modelled	45.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
111	d3grsa2	Alignment	not modelled	44.5	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
112	c2v1dA	Alignment	not modelled	44.5	25	PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition
113	c2xagA	Alignment	not modelled	44.5	25	PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine
114	d2dw4a2	Alignment	not modelled	43.7	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
115	d2ftsa3	Alignment	not modelled	43.4	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
116	c1v0jB	Alignment	not modelled	43.1	33	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
117	c3k30B	Alignment	not modelled	42.4	50	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioes simplex
118	c3k5iB	Alignment	not modelled	42.2	24	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimidazole ribonucleotide
119	c1tytA	Alignment	not modelled	42.1	30	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase, oxidized form; PDBTitle: crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
120	c2v6oA	Alignment	not modelled	41.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansonii thioredoxin-gluthathione2 reductase (smtgr)