












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pc3A_</a>	 Alignment		100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cg1753, isoform a; <b>PDBTitle:</b> full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
2	<a href="#">d2bhsa1</a>	 Alignment		100.0	100	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
3	<a href="#">d1jbqa_</a>	 Alignment		100.0	37	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
4	<a href="#">c1jbqD_</a>	 Alignment		100.0	37	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> cystathionine beta-synthase; <b>PDBTitle:</b> structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent heme protein
5	<a href="#">c3dwgA_</a>	 Alignment		100.0	41	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase b; <b>PDBTitle:</b> crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
6	<a href="#">d1z7wa1</a>	 Alignment		100.0	45	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
7	<a href="#">d1ve1a1</a>	 Alignment		100.0	46	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
8	<a href="#">c2pqmA_</a>	 Alignment		100.0	40	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
9	<a href="#">c2eguA_</a>	 Alignment		100.0	47	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase; <b>PDBTitle:</b> crystal structure of o-acetylserine sulphydrase from geobacillus2 kaustophilus hta426
10	<a href="#">d1y7la1</a>	 Alignment		100.0	42	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
11	<a href="#">d1wkva1</a>	 Alignment		100.0	30	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes

12	<a href="#">c2q3bA</a>	Alignment		100.0	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase a; <b>PDBTitle:</b> 1.8 a resolution crystal structure of o-acetylserine sulphydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
13	<a href="#">d1o58a</a>	Alignment		100.0	46	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
14	<a href="#">c1tdjA</a>	Alignment		100.0	19	<b>PDB header:</b> allostery <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic threonine deaminase; <b>PDBTitle:</b> threonine deaminase (biosynthetic) from e. coli
15	<a href="#">d1fcja</a>	Alignment		100.0	42	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
16	<a href="#">c3l6cA</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
17	<a href="#">c2d1fA</a>	Alignment		100.0	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> structure of mycobacterium tuberculosis threonine synthase
18	<a href="#">d1pwha</a>	Alignment		100.0	21	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
19	<a href="#">d1tdja1</a>	Alignment		100.0	18	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	<a href="#">d1v71a1</a>	Alignment		100.0	20	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
21	<a href="#">c3iauA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine deaminase; <b>PDBTitle:</b> the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
22	<a href="#">c2gn0A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> threonine dehydratase catabolic; <b>PDBTitle:</b> crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
23	<a href="#">c1x1qA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
24	<a href="#">d1v7ca</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
25	<a href="#">d1p5ja</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Family:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	<a href="#">c1p5jA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure analysis of human serine dehydratase
27	<a href="#">d1qopb</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes <b>Superfamily:</b> Tryptophan synthase beta subunit-like PLP-dependent enzymes

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49	<a href="#">d1ml4a2</a>	Alignment	not modelled	81.5	17	<b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
50	<a href="#">c3krtC_</a>	Alignment	not modelled	80.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> crotonyl coa reductase; <b>PDBTitle:</b> crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
51	<a href="#">c3eywA_</a>	Alignment	not modelled	76.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
52	<a href="#">d1tt7a2</a>	Alignment	not modelled	76.2	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
53	<a href="#">d1l7da1</a>	Alignment	not modelled	74.5	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
54	<a href="#">d1xa0a2</a>	Alignment	not modelled	71.3	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
55	<a href="#">d1hyua1</a>	Alignment	not modelled	71.0	37	<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
56	<a href="#">c1ml4A_</a>	Alignment	not modelled	70.8	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate transcarbamoylase; <b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
57	<a href="#">d1fl2a1</a>	Alignment	not modelled	70.6	37	<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
58	<a href="#">c3p2yA_</a>	Alignment	not modelled	68.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
59	<a href="#">c2vq3B_</a>	Alignment	not modelled	68.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> metalloreductase steap3; <b>PDBTitle:</b> crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
60	<a href="#">d1trba1</a>	Alignment	not modelled	67.9	25	<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
61	<a href="#">c3s8mA_</a>	Alignment	not modelled	67.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> enoyl-acp reductase; <b>PDBTitle:</b> the crystal structure of fabv
62	<a href="#">d1llua2</a>	Alignment	not modelled	67.4	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
63	<a href="#">d1ekxa2</a>	Alignment	not modelled	66.9	21	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
64	<a href="#">c3orgA_</a>	Alignment	not modelled	66.2	21	<b>PDB header:</b> ligase,biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide synthetase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
65	<a href="#">c3grkE_</a>	Alignment	not modelled	65.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> enoyl-(acyl-carrier-protein) reductase (nadh); <b>PDBTitle:</b> crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
66	<a href="#">c2bryA_</a>	Alignment	not modelled	64.9	24	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> nedd9 interacting protein with calponin homology <b>PDBTitle:</b> crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
67	<a href="#">c2rgwD_</a>	Alignment	not modelled	64.6	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
68	<a href="#">d1cdoa2</a>	Alignment	not modelled	64.4	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
69	<a href="#">c1m67A_</a>	Alignment	not modelled	63.7	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
70	<a href="#">c3o82A_</a>	Alignment	not modelled	63.6	11	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine
71	<a href="#">d1vdca1</a>	Alignment	not modelled	62.6	22	<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
72	<a href="#">d1bgva1</a>	Alignment	not modelled	60.8	16	<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
73	<a href="#">d1otha2</a>	Alignment	not modelled	60.6	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase

74	<a href="#">dlreoa1</a>	Alignment	not modelled	59.2	14	<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
75	<a href="#">c2rirA</a>	Alignment	not modelled	58.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
76	<a href="#">d2i0za1</a>	Alignment	not modelled	58.0	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
77	<a href="#">d1ykfa2</a>	Alignment	not modelled	57.8	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
78	<a href="#">d1p0fa2</a>	Alignment	not modelled	57.8	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
79	<a href="#">d1mv8a2</a>	Alignment	not modelled	56.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
80	<a href="#">d3lada1</a>	Alignment	not modelled	56.0	26	<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="#">d1t57a</a>	Alignment	not modelled	55.5	18	<b>Fold:</b> Pyruvate kinase C-terminal domain-like <b>Superfamily:</b> PK C-terminal domain-like <b>Family:</b> MTH1675-like
82	<a href="#">c2bruB</a>	Alignment	not modelled	54.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
83	<a href="#">c2ywlA</a>	Alignment	not modelled	54.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase related protein; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
84	<a href="#">c3allA</a>	Alignment	not modelled	54.0	19	<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
85	<a href="#">d1v9la1</a>	Alignment	not modelled	54.0	19	<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
86	<a href="#">d1pg5a2</a>	Alignment	not modelled	53.2	15	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
87	<a href="#">c3r3sD</a>	Alignment	not modelled	52.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> structure of the ygha oxidoreductase from salmonella enterica
88	<a href="#">d1ebda1</a>	Alignment	not modelled	52.8	22	<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
89	<a href="#">d2cula1</a>	Alignment	not modelled	52.6	33	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GidA-like
90	<a href="#">c2vhyB</a>	Alignment	not modelled	52.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
91	<a href="#">c3pduF</a>	Alignment	not modelled	52.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase family protein; <b>PDBTitle:</b> crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
92	<a href="#">c2rghA</a>	Alignment	not modelled	52.1	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
93	<a href="#">d1rjwa2</a>	Alignment	not modelled	52.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
94	<a href="#">d1tuga1</a>	Alignment	not modelled	51.7	22	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
95	<a href="#">c2dplA</a>	Alignment	not modelled	51.6	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing] subunit b; <b>PDBTitle:</b> crystal structure of the gmp synthase from pyrococcus horikoshii ot3
96	<a href="#">d1seza1</a>	Alignment	not modelled	50.4	17	<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
97	<a href="#">d1ryia1</a>	Alignment	not modelled	50.4	22	<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
98	<a href="#">c3a11D</a>	Alignment	not modelled	50.1	19	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> translation initiation factor eif-2b, delta <b>PDBTitle:</b> crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
						<b>Fold:</b> FAD/NAD(P)-binding domain



99	<a href="#">d1lvla1</a>	Alignment	not modelled	49.7	26	<b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
100	<a href="#">c3tqiB</a>	Alignment	not modelled	49.6	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> gmp synthase [glutamine-hydrolyzing]; <b>PDBTitle:</b> structure of the gmp synthase (guaa) from coxiella burnetii
101	<a href="#">d2gf3a1</a>	Alignment	not modelled	49.6	26	<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
102	<a href="#">c2jb1B</a>	Alignment	not modelled	49.2	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine
103	<a href="#">d1pvva2</a>	Alignment	not modelled	48.7	16	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
104	<a href="#">d1d1ta2</a>	Alignment	not modelled	48.7	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
105	<a href="#">c1hyuA</a>	Alignment	not modelled	48.2	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
106	<a href="#">d1dxla1</a>	Alignment	not modelled	48.0	22	<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
107	<a href="#">c3cumA</a>	Alignment	not modelled	47.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
108	<a href="#">d1neka2</a>	Alignment	not modelled	47.5	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
109	<a href="#">c3ezsB</a>	Alignment	not modelled	47.3	16	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminotransferase aspb; <b>PDBTitle:</b> crystal structure of aminotransferase aspb (np 207418.1) from2 helicobacter pylori 26695 at 2.19 a resolution
110	<a href="#">c2q2qG</a>	Alignment	not modelled	47.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> beta-d-hydroxybutyrate dehydrogenase; <b>PDBTitle:</b> structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
111	<a href="#">d1ojta1</a>	Alignment	not modelled	46.9	22	<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
112	<a href="#">d1u3wa2</a>	Alignment	not modelled	46.8	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
113	<a href="#">c4a10A</a>	Alignment	not modelled	46.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> octenoyl-coa reductase/carboxylase; <b>PDBTitle:</b> apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
114	<a href="#">c1m6yA</a>	Alignment	not modelled	46.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-methyltransferase mraw; <b>PDBTitle:</b> crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
115	<a href="#">c3nrnA</a>	Alignment	not modelled	45.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pf1083; <b>PDBTitle:</b> crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
116	<a href="#">d1lpfa1</a>	Alignment	not modelled	45.2	22	<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
117	<a href="#">c2qx7A</a>	Alignment	not modelled	45.1	15	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
118	<a href="#">c3ijrF</a>	Alignment	not modelled	44.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase, short chain dehydrogenase/reductase family; <b>PDBTitle:</b> 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
119	<a href="#">d1e3ia2</a>	Alignment	not modelled	44.8	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Alcohol dehydrogenase-like, C-terminal domain
120	<a href="#">c3o82B</a>	Alignment	not modelled	44.6	11	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide arylation enzyme; <b>PDBTitle:</b> structure of base n-terminal domain from acinetobacter baumannii bound2 to 5'-o-[n-(2,3-dihydroxybenzoyl)sulfamoyl] adenosine