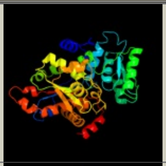
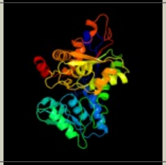
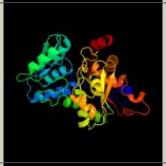
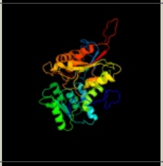
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P66899
Date	Thu Jan 5 12:10:21 GMT 2012
Unique Job ID	64e437e3879ae46e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1tdjA_	Alignment		100.0	23	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
2	c3r0zA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of apo d-serine deaminase from salmonella2 typhimurium
3	c3l6cA_	Alignment		100.0	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**serine racemase; **PDBTitle:** x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
4	c3iauA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine deaminase; **PDBTitle:** the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
5	d1v71a1	Alignment		100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
6	d1pwha_	Alignment		100.0	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
7	c2gn0A_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine dehydratase catabolic; **PDBTitle:** 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)
8	d1ve5a1	Alignment		100.0	25	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
9	d1p5ja_	Alignment		100.0	20	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
10	c1p5jA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
11	d1tdja1	Alignment		100.0	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes

12	c2rkbE_	Alignment		100.0	22	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
13	c1x1qA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
14	d1v8za1	Alignment		100.0	22	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
15	d1qopb_	Alignment		100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
16	c1jbqD_	Alignment		100.0	20	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cystathionine beta-synthase; **PDBTitle:** structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
17	d1jbqa_	Alignment		100.0	20	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
18	d1e5xa_	Alignment		100.0	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
19	c3pc3A_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
20	c2d1fA_	Alignment		100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** structure of mycobacterium tuberculosis threonine synthase
21	d1v7ca_	Alignment	not modelled	100.0	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
22	c2zsjB_	Alignment	not modelled	100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase from aquifex aeolicus vf5
23	d1wkva1	Alignment	not modelled	100.0	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
24	d1ve1a1	Alignment	not modelled	100.0	22	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
25	d1y7la1	Alignment	not modelled	100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	c2pqmA_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution

27	d1z7wa1	Alignment	not modelled	100.0	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
28	d2bhsa1	Alignment	not modelled	100.0	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
29	d1fcja_	Alignment	not modelled	100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	c3dwgA_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase b; **PDBTitle:** crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
31	c2o2jA_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
32	d1o58a_	Alignment	not modelled	100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
33	c2q3bA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase a; **PDBTitle:** 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
34	d1f2da_	Alignment	not modelled	100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
35	c2eguA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
36	d1tyza_	Alignment	not modelled	100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
37	d1j0aa_	Alignment	not modelled	100.0	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
38	d1vb3a1	Alignment	not modelled	100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
39	c3v7nA_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
40	d1kl7a_	Alignment	not modelled	100.0	12	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
41	d1vp8a_	Alignment	not modelled	89.9	13	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
42	c3iupB_	Alignment	not modelled	89.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadph:quinone oxidoreductase; **PDBTitle:** crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
43	d1c1da1	Alignment	not modelled	89.4	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
44	d1l7da1	Alignment	not modelled	88.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
45	c3dzbA_	Alignment	not modelled	85.9	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
46	d1o8ca2	Alignment	not modelled	85.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
47	d1ml4a2	Alignment	not modelled	84.6	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase

48	c3k96B_	Alignment	not modelled	82.8	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
49	c2csuB_	Alignment	not modelled	81.6	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
50	d1o89a2	Alignment	not modelled	79.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
51	c3pefA_	Alignment	not modelled	79.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, nad-binding; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
52	c3krtC_	Alignment	not modelled	78.6	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**crotonyl coa reductase; **PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
53	c3cumA_	Alignment	not modelled	76.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
54	c2rgwD_	Alignment	not modelled	76.7	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
55	d1ekxa2	Alignment	not modelled	74.8	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
56	c3pduF_	Alignment	not modelled	74.3	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
57	c2vhyB_	Alignment	not modelled	72.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
58	c3eywA_	Alignment	not modelled	72.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
59	d1bg6a2	Alignment	not modelled	72.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
60	c1ml4A_	Alignment	not modelled	72.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
61	d1wdka3	Alignment	not modelled	71.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c2g5cD_	Alignment	not modelled	70.2	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
63	c2eghA_	Alignment	not modelled	66.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
64	c2bruB_	Alignment	not modelled	65.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase subunit alpha; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
65	d1otha2	Alignment	not modelled	64.6	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
66	c2vq3B_	Alignment	not modelled	63.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**metalloreductase steap3; **PDBTitle:** crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
67	d3cuma2	Alignment	not modelled	63.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
68	c3grkE_	Alignment	not modelled	62.1	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
69	c2q2qG_	Alignment	not modelled	60.8	17	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
70	c3d4oA_	Alignment	not modelled	60.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution

71	d1n1ea2	Alignment	not modelled	60.2	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c3ktdC_	Alignment	not modelled	60.1	10	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
73	c1pjcA_	Alignment	not modelled	59.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
74	c1m67A_	Alignment	not modelled	59.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
75	c1vpdA_	Alignment	not modelled	59.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
76	c3ezlA_	Alignment	not modelled	58.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
77	c1l7eC_	Alignment	not modelled	58.2	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
78	d1tt7a2	Alignment	not modelled	57.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
79	c3ga7A_	Alignment	not modelled	57.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetyl esterase; **PDBTitle:** 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
80	c3l6dB_	Alignment	not modelled	57.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
81	c3ggpA_	Alignment	not modelled	54.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
82	c1m75B_	Alignment	not modelled	54.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
83	c3p2yA_	Alignment	not modelled	53.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
84	c3oj0A_	Alignment	not modelled	53.6	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
85	c1vlvA_	Alignment	not modelled	53.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
86	d1vpda2	Alignment	not modelled	53.3	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
87	d1trba1	Alignment	not modelled	53.1	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
88	c3uf0A_	Alignment	not modelled	53.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
89	c2qx7A_	Alignment	not modelled	52.6	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
90	d1f0ya2	Alignment	not modelled	52.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
91	c3q98A_	Alignment	not modelled	52.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
92	d1pvva2	Alignment	not modelled	51.3	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
93	d1ja9a_	Alignment	not modelled	50.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	c3k6jA_	Alignment	not modelled	50.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
95	d1pg5a2	Alignment	not modelled	50.1	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase

						Family: Aspartate/ornithine carbamoyltransferase
96	d1tuga1	Alignment	not modelled	49.8	16	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
97	c3mogA_	Alignment	not modelled	49.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
98	c3c1oA_	Alignment	not modelled	49.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
99	c4a10A_	Alignment	not modelled	49.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**octenoyl-coa reductase/carboxylase; **PDBTitle:** apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
100	d1pjca1	Alignment	not modelled	48.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
101	c3d64A_	Alignment	not modelled	48.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
102	d1fl2a1	Alignment	not modelled	48.0	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
103	c3iccA_	Alignment	not modelled	47.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
104	c1jrxA_	Alignment	not modelled	46.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
105	d1x87a_	Alignment	not modelled	46.5	17	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
106	c2w62A_	Alignment	not modelled	46.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycolipid-anchored surface protein 2; **PDBTitle:** saccharomyces cerevisiae gas2p in complex with2 laminaripentaose
107	d1llua2	Alignment	not modelled	46.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
108	c1gthD_	Alignment	not modelled	46.1	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
109	c3oidA_	Alignment	not modelled	46.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-[acyl-carrier-protein] reductase [nadph]; **PDBTitle:** crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
110	c3ed1E_	Alignment	not modelled	45.9	11	**PDB header:**hydrolase receptor **Chain:** E: **PDB Molecule:**gibberellin receptor gid1; **PDBTitle:** crystal structure of rice gid1 complexed with ga3
111	d1duvg2	Alignment	not modelled	45.1	20	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
112	c3k8zD_	Alignment	not modelled	44.9	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nad-specific glutamate dehydrogenase; **PDBTitle:** crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
113	d1hyua1	Alignment	not modelled	44.8	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
114	c3qhaB_	Alignment	not modelled	44.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
115	c2w37A_	Alignment	not modelled	43.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
116	d1vdca1	Alignment	not modelled	43.4	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
117	c3llvA_	Alignment	not modelled	43.3	12	**PDB header:**nad(p) binding protein **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
118	c2p2gD_	Alignment	not modelled	43.3	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
119	d1uwka_	Alignment	not modelled	43.1	22	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
120	c2q1uA_	Alignment	not modelled	43.0	13	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase;

PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp