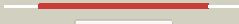



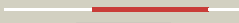














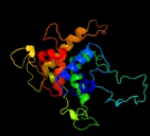

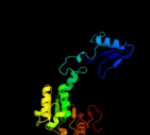





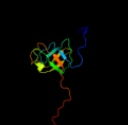






# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0AVT1
Date	Tue Apr 3 14:58:27 BST 2012
Unique Job ID	13c0206945bc8832

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3cmmA_</a>	 Alignment		100.0	43	<b>PDB header:</b> ligase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1; <b>PDBTitle:</b> crystal structure of the uba1-ubiquitin complex
2	<a href="#">c1y8qD_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> ubiquitin-like 2 activating enzyme e1b; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
3	<a href="#">c3kydB_</a>	 Alignment		100.0	30	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2; <b>PDBTitle:</b> human sumo e1~sumo1-amp tetrahedral intermediate mimic
4	<a href="#">c3gzvB_</a>	 Alignment		100.0	33	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> nedd8-activating enzyme e1 catalytic subunit; <b>PDBTitle:</b> structure of nedd8-activating enzyme in complex with nedd8 and mln4924
5	<a href="#">c2nvuB_</a>	 Alignment		100.0	31	<b>PDB header:</b> protein turnover, ligase <b>Chain:</b> B: <b>PDB Molecule:</b> maltose binding protein/nedd8-activating enzyme <b>PDBTitle:</b> structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
6	<a href="#">d1yova1</a>	 Alignment		100.0	25	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
7	<a href="#">d1yovb1</a>	 Alignment		100.0	33	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
8	<a href="#">c1y8qA_</a>	 Alignment		100.0	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like 1 activating enzyme e1a; <b>PDBTitle:</b> sumo e1 activating enzyme sae1-sae2-mg-atp complex
9	<a href="#">c1z71C_</a>	 Alignment		100.0	40	<b>PDB header:</b> ligase <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 1; <b>PDBTitle:</b> crystal structure of fragment of mouse ubiquitin-activating2 enzyme
10	<a href="#">c2px9A_</a>	 Alignment		100.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> sumo-activating enzyme subunit 2; <b>PDBTitle:</b> the intrinsic affinity between e2 and the cys domain of e12 in ubiquitin-like modifications
11	<a href="#">c3h9gA_</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase/antibiotic <b>Chain:</b> A: <b>PDB Molecule:</b> mccb protein; <b>PDBTitle:</b> crystal structure of e. coli mccb + mcca-n7isoasn

12	<a href="#">d1jw9b_</a>	Alignment		100.0	25	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Molybdenum cofactor biosynthesis protein MoeB
13	<a href="#">c1zfnA_</a>	Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenyllyltransferase thif; <b>PDBTitle:</b> structural analysis of escherichia coli thif
14	<a href="#">c3vh3A_</a>	Alignment		100.0	20	<b>PDB header:</b> metal binding protein/protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7; <b>PDBTitle:</b> crystal structure of atg7ctd-atg8 complex
15	<a href="#">c3vh1A_</a>	Alignment		100.0	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-like modifier-activating enzyme atg7; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae atg7 (1-595)
16	<a href="#">c3gucB_</a>	Alignment		100.0	17	<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
17	<a href="#">c2v31A_</a>	Alignment		99.9	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1 x; <b>PDBTitle:</b> structure of first catalytic cysteine half-domain of mouse2 ubiquitin-activating enzyme
18	<a href="#">c3ongA_</a>	Alignment		97.7	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-activating enzyme e1-like; <b>PDBTitle:</b> crystal structure of uba2ufd-ubc9: insights into e1-e2 interactions in2 sumo pathways
19	<a href="#">d1piqa1</a>	Alignment		97.4	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
20	<a href="#">c2axqA_</a>	Alignment		97.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
21	<a href="#">c3ic5A_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeryoi.
22	<a href="#">c1e51A_</a>	Alignment	not modelled	96.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
23	<a href="#">c2z2vA_</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
24	<a href="#">d1vkna1</a>	Alignment	not modelled	96.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glycerol dehydrogenase-like, N-terminal domain
25	<a href="#">c1gpiA_</a>	Alignment		96.4	19	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
26	<a href="#">c3dfzB_</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
27	<a href="#">d2naca1</a>	Alignment	not modelled	96.1	23	<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 <b>PDB header:</b> oxidoreductase

28	<a href="#">c3hg7A</a>	Alignment	not modelled	96.0	16	<b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
29	<a href="#">c3gvxA</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase related protein; <b>PDBTitle:</b> crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
30	<a href="#">c1xdwA</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+-dependent (r)-2-hydroxyglutarate <b>PDBTitle:</b> nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
31	<a href="#">c1dxyA</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxyisocaproate dehydrogenase
32	<a href="#">d1y8xb1</a>	Alignment	not modelled	95.8	13	<b>Fold:</b> Activating enzymes of the ubiquitin-like proteins <b>Superfamily:</b> Activating enzymes of the ubiquitin-like proteins <b>Family:</b> Ubiquitin activating enzymes (UBA)
33	<a href="#">d2hjsa1</a>	Alignment	not modelled	95.7	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	<a href="#">c1pjtB</a>	Alignment	not modelled	95.7	15	<b>PDB header:</b> transferase/oxidoreductase/lyase <b>Chain:</b> B: <b>PDB Molecule:</b> siroheme synthase; <b>PDBTitle:</b> the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelataze for4 siroheme synthesis
35	<a href="#">d1l7da1</a>	Alignment	not modelled	95.6	18	<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
36	<a href="#">d1lpfa2</a>	Alignment	not modelled	95.6	28	<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
37	<a href="#">c2gcbB</a>	Alignment	not modelled	95.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
38	<a href="#">c3pgjB</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
39	<a href="#">d1gtea4</a>	Alignment	not modelled	95.5	17	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
40	<a href="#">d1gdha1</a>	Alignment	not modelled	95.5	16	<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
41	<a href="#">c2nloA</a>	Alignment	not modelled	95.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
42	<a href="#">d2gz1a1</a>	Alignment	not modelled	95.4	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	<a href="#">c1vi2B</a>	Alignment	not modelled	95.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase 2; <b>PDBTitle:</b> crystal structure of shikimate-5-dehydrogenase with nad
44	<a href="#">d1vi2a1</a>	Alignment	not modelled	95.4	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
45	<a href="#">c1qp8A</a>	Alignment	not modelled	95.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
46	<a href="#">c1vknC</a>	Alignment	not modelled	95.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tm1782) from thermotoga maritima at 1.80 a resolution
47	<a href="#">c2yv3B</a>	Alignment	not modelled	95.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
48	<a href="#">d3lada2</a>	Alignment	not modelled	95.2	29	<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
49	<a href="#">d2dl da1</a>	Alignment	not modelled	95.2	19	<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
50	<a href="#">d1f0ya2</a>	Alignment	not modelled	95.2	11	<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
51	<a href="#">d1ebda2</a>	Alignment	not modelled	95.1	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
52	<a href="#">d1e5qa1</a>	Alignment	not modelled	95.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
53	<a href="#">c2g76A_</a>	Alignment	not modelled	95.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
54	<a href="#">c2qz9B_</a>	Alignment	not modelled	94.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
55	<a href="#">c2cukC_</a>	Alignment	not modelled	94.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermophilus hb8
56	<a href="#">d2q49a1</a>	Alignment	not modelled	94.9	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceroldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	<a href="#">d1qp8a1</a>	Alignment	not modelled	94.8	18	<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
58	<a href="#">d1dxya1</a>	Alignment	not modelled	94.8	17	<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
59	<a href="#">d1wdka3</a>	Alignment	not modelled	94.8	14	<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
60	<a href="#">c3eywA_</a>	Alignment	not modelled	94.8	16	<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
61	<a href="#">d1h6va2</a>	Alignment	not modelled	94.7	21	<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
62	<a href="#">d1j4aa1</a>	Alignment	not modelled	94.7	22	<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
63	<a href="#">c2ep5B_</a>	Alignment	not modelled	94.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 350aa long hypothetical aspartate-semialdehyde <b>PDBTitle:</b> structural study of project id st1242 from sulfolobus tokodaii strain7
64	<a href="#">d1ygya1</a>	Alignment	not modelled	94.6	17	<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
65	<a href="#">c1z82A_</a>	Alignment	not modelled	94.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
66	<a href="#">c1j4aA_</a>	Alignment	not modelled	94.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
67	<a href="#">c2ofpB_</a>	Alignment	not modelled	94.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketopantoate reductase; <b>PDBTitle:</b> crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
68	<a href="#">c1pzfD_</a>	Alignment	not modelled	94.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> t.gondii ldh1 ternary complex with apad+ and oxalate
69	<a href="#">c3pwzA_</a>	Alignment	not modelled	94.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase 3; <b>PDBTitle:</b> crystal structure of an ael1 enzyme from pseudomonas putida
70	<a href="#">c3oetF_</a>	Alignment	not modelled	94.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> d-erythronate-4-phosphate dehydrogenase complexed with nad
71	<a href="#">d1mx3a1</a>	Alignment	not modelled	94.4	10	<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
72	<a href="#">c1wwkA_</a>	Alignment	not modelled	94.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
73	<a href="#">d1pzga1</a>	Alignment	not modelled	94.4	22	<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
74	<a href="#">d1gesa2</a>	Alignment	not modelled	94.3	17	<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
75	<a href="#">d1gpja2</a>	Alignment	not modelled	94.3	26	<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
76	<a href="#">c1gdhA_</a>	Alignment	not modelled	94.3	16	<b>PDB header:</b> oxidoreductase(choh (d)-nad(p)+ (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
77	<a href="#">c3evtA_</a>	Alignment	not modelled	94.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum

78	<a href="#">c3kboB</a>	Alignment	not modelled	94.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate/hydroxypyruvate reductase a; <b>PDBTitle:</b> 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from <i>Salmonella typhimurium</i> in complex with nadp
79	<a href="#">d1kyqa1</a>	Alignment	not modelled	94.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Siroheme synthase N-terminal domain-like
80	<a href="#">d1onfa2</a>	Alignment	not modelled	94.2	27	<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="#">c2qx7A</a>	Alignment	not modelled	94.1	21	<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 <i>Ocimum basilicum</i>
82	<a href="#">c3n7uD</a>	Alignment	not modelled	94.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant <i>Arabidopsis thaliana</i> in complex with nad and azide
83	<a href="#">d1i24a</a>	Alignment	not modelled	94.1	13	<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="#">c2ek1A</a>	Alignment	not modelled	94.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> structure of st1218 protein from <i>Sulfolobus tokodaii</i>
85	<a href="#">d1pjca1</a>	Alignment	not modelled	94.1	23	<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
86	<a href="#">c2dbqA</a>	Alignment	not modelled	94.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of glyoxylate reductase (ph0597) from <i>Pyrococcus horikoshii</i> ot3, complexed with nadp (i41)
87	<a href="#">c2omeA</a>	Alignment	not modelled	94.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
88	<a href="#">d1v59a2</a>	Alignment	not modelled	93.9	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
89	<a href="#">c1ldbA</a>	Alignment	not modelled	93.9	18	<b>PDB header:</b> oxidoreductase (choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination and refinement of <i>Bacillus stearothermophilus</i> lactate dehydrogenase
90	<a href="#">c3k96B</a>	Alignment	not modelled	93.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from <i>Coxiella burnetii</i>
91	<a href="#">c2hjrK</a>	Alignment	not modelled	93.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of <i>Cryptosporidium parvum</i> malate2 dehydrogenase
92	<a href="#">c3bazA</a>	Alignment	not modelled	93.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from <i>Coleus blumei</i> in2 complex with nadp+
93	<a href="#">c2j6iC</a>	Alignment	not modelled	93.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> <i>Candida boidinii</i> formate dehydrogenase (fdh) c-terminal2 mutant
94	<a href="#">d2nu7a1</a>	Alignment	not modelled	93.7	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
95	<a href="#">d1luxj1</a>	Alignment	not modelled	93.6	28	<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="#">c4dioB</a>	Alignment	not modelled	93.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from <i>Sinorhizobium meliloti</i>
97	<a href="#">c3d0oA</a>	Alignment	not modelled	93.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from <i>Staphylococcus aureus</i>
98	<a href="#">c2w2kB</a>	Alignment	not modelled	93.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo forms of <i>Rhodotorula graminis</i> 2 d-mandelate dehydrogenase at 1.8a.
99	<a href="#">d1nhpa1</a>	Alignment	not modelled	93.5	15	<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="#">c2d0iC</a>	Alignment	not modelled	93.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from <i>Pyrococcus horikoshii</i> ot3
101	<a href="#">d1nvt1</a>	Alignment	not modelled	93.4	25	<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
102	<a href="#">c1zcyjA</a>	Alignment	not modelled	93.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase
103	<a href="#">d1mv8a2</a>	Alignment	not modelled	93.4	19	<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
104	<a href="#">c2fnzA_</a>	Alignment	not modelled	93.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
105	<a href="#">d2f1ka2</a>	Alignment	not modelled	93.4	22	<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
106	<a href="#">c2ozpA_</a>	Alignment	not modelled	93.4	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tha1904) from thermus thermophilus
107	<a href="#">d1m6ia2</a>	Alignment	not modelled	93.4	16	<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
108	<a href="#">d1xhca2</a>	Alignment	not modelled	93.4	24	<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
109	<a href="#">c1ys4A_</a>	Alignment	not modelled	93.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
110	<a href="#">c3o8qB_</a>	Alignment	not modelled	93.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase i alpha; <b>PDBTitle:</b> 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroE) from vibrio cholerae
111	<a href="#">d1hyea1</a>	Alignment	not modelled	93.3	12	<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
112	<a href="#">c1zejA_</a>	Alignment	not modelled	93.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
113	<a href="#">c3tozA_</a>	Alignment	not modelled	93.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
114	<a href="#">c3gg9C_</a>	Alignment	not modelled	93.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase oxidoreductase protein; <b>PDBTitle:</b> crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
115	<a href="#">d3grsa2</a>	Alignment	not modelled	93.2	23	<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
116	<a href="#">d1d7ya2</a>	Alignment	not modelled	93.2	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
117	<a href="#">d1gera2</a>	Alignment	not modelled	93.1	23	<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
118	<a href="#">c1vl6C_</a>	Alignment	not modelled	93.1	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
119	<a href="#">c1drwA_</a>	Alignment	not modelled	93.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
120	<a href="#">c2hjsA_</a>	Alignment	not modelled	93.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> usg-1 protein homolog; <b>PDBTitle:</b> the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa