























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1jw9b_</a>	 Alignment		100.0	100	<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
2	<a href="#">c1zfnA_</a>	 Alignment		100.0	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylyltransferase thif; <b>PDBTitle:</b> structural analysis of escherichia coli thif
3	<a href="#">c3h9gA_</a>	 Alignment		100.0	25	<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
4	<a href="#">d1yovb1</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)
5	<a href="#">c3gznb_</a>	 Alignment		100.0	25	<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 nedd82 and mln4924
6	<a href="#">c3vh3A_</a>	 Alignment		100.0	26	<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
7	<a href="#">c2nvuB_</a>	 Alignment		100.0	26	<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
8	<a href="#">c3kydB_</a>	 Alignment		100.0	32	<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
9	<a href="#">c3vh1A_</a>	 Alignment		100.0	27	<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)
10	<a href="#">c1y8qD_</a>	 Alignment		100.0	32	<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
11	<a href="#">c1y8qA_</a>	 Alignment		100.0	24	<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

12	<a href="#">c3cmmA_</a>	Alignment		100.0	27	<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
13	<a href="#">c3gucB_</a>	Alignment		100.0	21	<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
14	<a href="#">d1yova1</a>	Alignment		100.0	19	<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)
15	<a href="#">c1e5lA_</a>	Alignment		98.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
16	<a href="#">d1pjqa1</a>	Alignment		98.1	25	<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
17	<a href="#">c2axqA_</a>	Alignment		98.1	21	<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
18	<a href="#">d1vi2a1</a>	Alignment		98.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
19	<a href="#">c2nloA_</a>	Alignment		97.9	33	<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
20	<a href="#">c3ic5A_</a>	Alignment		97.9	23	<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 pomeroyi.
21	<a href="#">c1vi2B_</a>	Alignment	not modelled	97.8	23	<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
22	<a href="#">c1gpjA_</a>	Alignment	not modelled	97.8	26	<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
23	<a href="#">c3tozA_</a>	Alignment	not modelled	97.7	21	<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.
24	<a href="#">d1pzga1</a>	Alignment	not modelled	97.7	18	<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
25	<a href="#">c2z2vA_</a>	Alignment	not modelled	97.7	22	<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
26	<a href="#">c3pgjB_</a>	Alignment	not modelled	97.6	22	<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
27	<a href="#">c2hjrK_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase
28	<a href="#">d1gpja2</a>	Alignment	not modelled	97.6	28	<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

29	<a href="#">c1pjtB_</a>	Alignment	not modelled	97.6	21	<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/ferrochelataase for4 siroheme synthesis
30	<a href="#">c2eggA_</a>	Alignment	not modelled	97.5	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
31	<a href="#">d9lta1</a>	Alignment	not modelled	97.5	17	<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
32	<a href="#">d1np3a2</a>	Alignment	not modelled	97.5	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucanate dehydrogenase-like, N-terminal domain
33	<a href="#">c2g1uA_</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm1088a; <b>PDBTitle:</b> crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
34	<a href="#">c3o8qB_</a>	Alignment	not modelled	97.4	22	<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
35	<a href="#">c3donA_</a>	Alignment	not modelled	97.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
36	<a href="#">c1u4sA_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
37	<a href="#">d1e5qa1</a>	Alignment	not modelled	97.4	24	<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
38	<a href="#">c3u62A_</a>	Alignment	not modelled	97.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from thermotoga maritima
39	<a href="#">d1i0za1</a>	Alignment	not modelled	97.4	21	<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
40	<a href="#">c1pzfD_</a>	Alignment	not modelled	97.4	17	<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
41	<a href="#">c1bg6A_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
42	<a href="#">c2fnzA_</a>	Alignment	not modelled	97.3	18	<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)
43	<a href="#">d1lssa_</a>	Alignment	not modelled	97.3	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
44	<a href="#">d1luxa1</a>	Alignment	not modelled	97.3	16	<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
45	<a href="#">c3d1lB_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadp oxidoreductase bf3122; <b>PDBTitle:</b> crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
46	<a href="#">c3k96B_</a>	Alignment	not modelled	97.3	17	<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 coxiella burnetii
47	<a href="#">d1pjca1</a>	Alignment	not modelled	97.3	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
48	<a href="#">c3dfzB_</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
49	<a href="#">c3pwzA_</a>	Alignment	not modelled	97.2	32	<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
50	<a href="#">c2ew2B_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase, putative; <b>PDBTitle:</b> crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
51	<a href="#">c3eywA_</a>	Alignment	not modelled	97.2	23	<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="#">d1nvta1</a>	Alignment	not modelled	97.2	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
53	<a href="#">c1pggA_</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphoglucanate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue

						and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
54	<a href="#">c1zczA_</a>	Alignment	not modelled	97.2	15	<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
55	<a href="#">d1kyqa1</a>	Alignment	not modelled	97.2	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
56	<a href="#">d2pgda2</a>	Alignment	not modelled	97.2	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
57	<a href="#">c3k6jA_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein f01g10.3, confirmed by transcript evidence; <b>PDBTitle:</b> crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
58	<a href="#">c1np3B_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
59	<a href="#">c1m67A_</a>	Alignment	not modelled	97.1	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
60	<a href="#">c2x58B_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa
61	<a href="#">c1ur5C_</a>	Alignment	not modelled	97.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
62	<a href="#">d1t2da1</a>	Alignment	not modelled	97.1	14	<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
63	<a href="#">d1gtea4</a>	Alignment	not modelled	97.1	8	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
64	<a href="#">d5ldha1</a>	Alignment	not modelled	97.1	19	<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
65	<a href="#">c3cumA_</a>	Alignment	not modelled	97.1	24	<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
66	<a href="#">c1z82A_</a>	Alignment	not modelled	97.1	17	<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
67	<a href="#">d1ldna1</a>	Alignment	not modelled	97.1	18	<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
68	<a href="#">c1pgjA_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
69	<a href="#">d1i10a1</a>	Alignment	not modelled	97.0	21	<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
70	<a href="#">c8ldha_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
71	<a href="#">c1hyhA_</a>	Alignment	not modelled	97.0	25	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
72	<a href="#">c2ph5A_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
73	<a href="#">c1gthD_</a>	Alignment	not modelled	97.0	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
74	<a href="#">c1ldbA_</a>	Alignment	not modelled	97.0	21	<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 bacillus2 stearothermophilus lactate dehydrogenase
75	<a href="#">d2ldxa1</a>	Alignment	not modelled	96.9	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
76	<a href="#">c2p4qA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating 1; <b>PDBTitle:</b> crystal structure analysis of gnd1 in saccharomyces cerevisiae
77	<a href="#">d1hyha1</a>	Alignment	not modelled	96.9	25	<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
78	<a href="#">c1wpqB_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad+],

						<b>PDBTitle:</b> ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
79	<a href="#">c3tl2A_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
80	<a href="#">c3pqeD_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
81	<a href="#">c2hk8B_</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
82	<a href="#">d1n1ea2</a>	Alignment	not modelled	96.9	9	<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
83	<a href="#">c3fwnB_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
84	<a href="#">c1nvtA_</a>	Alignment	not modelled	96.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate 5'-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
85	<a href="#">c3djeA_</a>	Alignment	not modelled	96.9	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase; <b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
86	<a href="#">d2hmva1</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Potassium channel NAD-binding domain
87	<a href="#">d1ldma1</a>	Alignment	not modelled	96.9	18	<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
88	<a href="#">d1bg6a2</a>	Alignment	not modelled	96.8	18	<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
89	<a href="#">c3llvA_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> nad(p) binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyphosphatase-related protein; <b>PDBTitle:</b> the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
90	<a href="#">c3mogA_</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
91	<a href="#">c3dhyc_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
92	<a href="#">c2iz1C_</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
93	<a href="#">c1ojuA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
94	<a href="#">d1obba1</a>	Alignment	not modelled	96.8	16	<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
95	<a href="#">c2dfdD_</a>	Alignment	not modelled	96.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2
96	<a href="#">d2jfga1</a>	Alignment	not modelled	96.8	20	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
97	<a href="#">c2v65A_</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase a chain; <b>PDBTitle:</b> apo ldh from the psychrophile c. gunnari
98	<a href="#">c3fi9B_</a>	Alignment	not modelled	96.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
99	<a href="#">c2ldxA_</a>	Alignment	not modelled	96.8	22	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> apo-lactate dehydrogenase; <b>PDBTitle:</b> characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
100	<a href="#">c1m75B_</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
101	<a href="#">d1llda1</a>	Alignment	not modelled	96.8	19	<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
102	<a href="#">d1pgia2</a>	Alignment	not modelled	96.8	12	<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



103	<a href="#">c2wtbA</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
104	<a href="#">c3gvpB</a>	Alignment	not modelled	96.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteinase 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteinase 3
105	<a href="#">d1v8ba1</a>	Alignment	not modelled	96.8	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
106	<a href="#">c2e37B</a>	Alignment	not modelled	96.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure of tt0471 protein from thermus thermophilus
107	<a href="#">c1mldA</a>	Alignment	not modelled	96.7	25	<b>PDB header:</b> oxidoreductase(nad(a)-choh(d)) <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
108	<a href="#">c2d0iC</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
109	<a href="#">c3d0oA</a>	Alignment	not modelled	96.7	28	<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 from2 staphylococcus aureus
110	<a href="#">c1pj6A</a>	Alignment	not modelled	96.7	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n,n-dimethylglycine oxidase; <b>PDBTitle:</b> crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
111	<a href="#">c1gv1D</a>	Alignment	not modelled	96.7	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
112	<a href="#">c2d4aC</a>	Alignment	not modelled	96.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of the malate dehydrogenase from aeropyrum pernix
113	<a href="#">c1txgA</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
114	<a href="#">d1s6ya1</a>	Alignment	not modelled	96.7	16	<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
115	<a href="#">c1kyqC</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
116	<a href="#">d1u8xx1</a>	Alignment	not modelled	96.7	14	<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
117	<a href="#">c3n7uD</a>	Alignment	not modelled	96.7	18	<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 arabidopsis2 thaliana in complex with nad and azide
118	<a href="#">d1txga2</a>	Alignment	not modelled	96.7	15	<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
119	<a href="#">c3hg7A</a>	Alignment	not modelled	96.7	20	<b>PDB header:</b> oxidoreductase <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
120	<a href="#">c3hwrA</a>	Alignment	not modelled	96.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution