



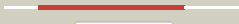


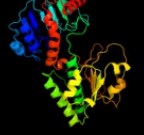






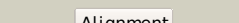

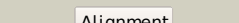


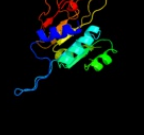
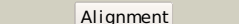



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2bruB_</a>	 Alignment		100.0	99	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha; <b>PDBTitle:</b> complex of the domain i and domain iii of escherichia coli2 transhydrogenase
2	<a href="#">c3p2yA_</a>	 Alignment		100.0	46	<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
3	<a href="#">c1pjcA_</a>	 Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-alanine dehydrogenase); <b>PDBTitle:</b> l-alanine dehydrogenase complexed with nad
4	<a href="#">c2qrlA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase, nad+, l-lysine- <b>PDBTitle:</b> crystal structure of oxalylglycine-bound saccharopine2 dehydrogenase (l-lys forming) from saccharomyces cerevisiae
5	<a href="#">c1l7eC_</a>	 Alignment		100.0	46	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinamide nucleotide transhydrogenase, <b>PDBTitle:</b> crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
6	<a href="#">c2eezG_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
7	<a href="#">c2vhyB_</a>	 Alignment		100.0	29	<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
8	<a href="#">d1pjcA2</a>	 Alignment		100.0	33	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> L-alanine dehydrogenase-like
9	<a href="#">d1l7da2</a>	 Alignment		100.0	38	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Formate/glycerate dehydrogenase catalytic domain-like <b>Family:</b> L-alanine dehydrogenase-like
10	<a href="#">d1l7da1</a>	 Alignment		100.0	55	<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
11	<a href="#">d1pjcA1</a>	 Alignment		100.0	33	<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

12	<a href="#">c3d4oA_</a>	Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
13	<a href="#">c2rirA_</a>	Alignment		99.9	20	<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
14	<a href="#">c1wwkA_</a>	Alignment		99.1	20	<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
15	<a href="#">c2eklA_</a>	Alignment		99.0	17	<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 sulfolobus tokodaii
16	<a href="#">c2g76A_</a>	Alignment		99.0	14	<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
17	<a href="#">c2gcgB_</a>	Alignment		99.0	18	<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
18	<a href="#">c2cukC_</a>	Alignment		98.9	20	<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 thermus thermophilus hb8
19	<a href="#">c1gdhA_</a>	Alignment		98.8	14	<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
20	<a href="#">c3n7uD_</a>	Alignment		98.7	19	<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
21	<a href="#">c3gvpB_</a>	Alignment	not modelled	98.7	28	<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
22	<a href="#">c2dbqA_</a>	Alignment	not modelled	98.7	15	<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 pyrococcus2 horikoshii ot3, complexed with nadp (i41)
23	<a href="#">c1gpjA_</a>	Alignment	not modelled	98.7	25	<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
24	<a href="#">c3evtA_</a>	Alignment	not modelled	98.7	19	<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
25	<a href="#">d1li4a1</a>	Alignment	not modelled	98.6	26	<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
26	<a href="#">c3bazA_</a>	Alignment	not modelled	98.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
27	<a href="#">c2j6iC_</a>	Alignment	not modelled	98.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
28	<a href="#">c2nacA_</a>	Alignment	not modelled	98.6	16	<b>PDB header:</b> oxidoreductase(aldehyde(d),nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> high resolution structures of holo and apo formate dehydrogenase
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c3k5pA</a>	Alignment	not modelled	98.6	22	<b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
30	<a href="#">c1d4fD</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
31	<a href="#">c1v8bA</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
32	<a href="#">c3n58D</a>	Alignment	not modelled	98.6	24	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
33	<a href="#">c3hg7A</a>	Alignment	not modelled	98.5	13	<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
34	<a href="#">c3gg9C</a>	Alignment	not modelled	98.5	14	<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
35	<a href="#">c3d64A</a>	Alignment	not modelled	98.5	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
36	<a href="#">d1gpja2</a>	Alignment	not modelled	98.5	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
37	<a href="#">c1xdwA</a>	Alignment	not modelled	98.5	17	<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
38	<a href="#">c2pi1C</a>	Alignment	not modelled	98.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
39	<a href="#">c1ybaC</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
40	<a href="#">d1v8ba1</a>	Alignment	not modelled	98.4	20	<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="#">d2naca1</a>	Alignment	not modelled	98.4	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
42	<a href="#">c1dxyA</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxisocaproate dehydrogenase
43	<a href="#">c3oneA</a>	Alignment	not modelled	98.4	24	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
44	<a href="#">d1mx3a1</a>	Alignment	not modelled	98.4	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
45	<a href="#">c3dhyC</a>	Alignment	not modelled	98.4	23	<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
46	<a href="#">d1gdha1</a>	Alignment	not modelled	98.4	20	<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
47	<a href="#">d1a4ia1</a>	Alignment	not modelled	98.3	18	<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
48	<a href="#">d1vgya1</a>	Alignment	not modelled	98.3	27	<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
49	<a href="#">c1j4aA</a>	Alignment	not modelled	98.3	19	<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
50	<a href="#">c2omeA</a>	Alignment	not modelled	98.3	16	<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)
51	<a href="#">c1vygA</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
52	<a href="#">d1b0aa1</a>	Alignment	not modelled	98.2	18	<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="#">c3oj0A</a>	Alignment	not modelled	98.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)

54	<a href="#">c3oetF_</a>	Alignment	not modelled	98.2	14	<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
55	<a href="#">c2d0iC_</a>	Alignment	not modelled	98.2	14	<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
56	<a href="#">c4a26B_</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
57	<a href="#">d2dl da1</a>	Alignment	not modelled	98.1	27	<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="#">dlj4aa1</a>	Alignment	not modelled	98.1	25	<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="#">c2w2kB_</a>	Alignment	not modelled	98.1	26	<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 rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
60	<a href="#">c2o4cB_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
61	<a href="#">c1a4iB_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
62	<a href="#">c2hk8B_</a>	Alignment	not modelled	98.0	20	<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
63	<a href="#">c3kboB_</a>	Alignment	not modelled	98.0	16	<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) from2 salmonella typhimurium in complex with nadp
64	<a href="#">dlqp8a1</a>	Alignment	not modelled	98.0	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
65	<a href="#">c3l07B_</a>	Alignment	not modelled	98.0	28	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella tularensis.
66	<a href="#">dl dxya1</a>	Alignment	not modelled	98.0	26	<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
67	<a href="#">dlc1da1</a>	Alignment	not modelled	98.0	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
68	<a href="#">c1luaA_</a>	Alignment	not modelled	97.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methylene tetrahydromethanopterin dehydrogenase; <b>PDBTitle:</b> structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
69	<a href="#">c4a5oB_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
70	<a href="#">c3p2oB_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
71	<a href="#">dl np3a2</a>	Alignment	not modelled	97.9	20	<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
72	<a href="#">c3p2oA_</a>	Alignment	not modelled	97.9	20	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
73	<a href="#">d2pgda2</a>	Alignment	not modelled	97.8	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
74	<a href="#">c1e5lA_</a>	Alignment	not modelled	97.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
75	<a href="#">c1qp8A_</a>	Alignment	not modelled	97.8	22	<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
76	<a href="#">c1b0aA_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fold bifunctional protein); <b>PDBTitle:</b> 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
77	<a href="#">c3gvxA_</a>	Alignment	not modelled	97.8	18	<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
78	<a href="#">c3c24A_</a>	Alignment	not modelled	97.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution

79	<a href="#">dlsc6a1</a>	Alignment	not modelled	97.8	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
80	<a href="#">dlvpda2</a>	Alignment	not modelled	97.7	26	<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
81	<a href="#">c3pgjB_</a>	Alignment	not modelled	97.6	21	<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
82	<a href="#">c1vpdA_</a>	Alignment	not modelled	97.6	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronate semialdehyde reductase; <b>PDBTitle:</b> x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
83	<a href="#">c1nytC_</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> shikimate dehydrogenase aroe complexed with nadp+
84	<a href="#">c3toza_</a>	Alignment	not modelled	97.6	20	<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.
85	<a href="#">c3donA_</a>	Alignment	not modelled	97.5	16	<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
86	<a href="#">dlbg6a2</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-phosphogluconate dehydrogenase-like, N-terminal domain
87	<a href="#">c3cumA_</a>	Alignment	not modelled	97.5	18	<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
88	<a href="#">dlleha1</a>	Alignment	not modelled	97.5	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
89	<a href="#">c3gg2B_</a>	Alignment	not modelled	97.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
90	<a href="#">c1bxgA_</a>	Alignment	not modelled	97.5	24	<b>PDB header:</b> amino acid dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine dehydrogenase; <b>PDBTitle:</b> phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
91	<a href="#">d2f1ka2</a>	Alignment	not modelled	97.4	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
92	<a href="#">c2eggA_</a>	Alignment	not modelled	97.4	19	<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
93	<a href="#">c3ktdC_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
94	<a href="#">c1p74B_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
95	<a href="#">c2g5cD_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus
96	<a href="#">c2y0dB_</a>	Alignment	not modelled	97.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
97	<a href="#">c3ojlA_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cap50; <b>PDBTitle:</b> native structure of the udp-n-acetyl-mannosamine dehydrogenase cap502 from staphylococcus aureus
98	<a href="#">c3nglA_</a>	Alignment	not modelled	97.4	19	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
99	<a href="#">c1np3B_</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetoxy acid isomeroreductase from2 pseudomonas aeruginosa
100	<a href="#">c1lehB_</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> leucine dehydrogenase; <b>PDBTitle:</b> leucine dehydrogenase from bacillus sphaericus
101	<a href="#">c2f1kD_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
102	<a href="#">d3cuma2</a>	Alignment	not modelled	97.3	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
103	<a href="#">dlnya1</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> Aminoacid dehydrogenase-like, C-terminal domain



104	<a href="#">c2c2xB_</a>	Alignment	not modelled	97.3	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase- <b>PDBTitle:</b> three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
105	<a href="#">c3o8qB_</a>	Alignment	not modelled	97.3	24	<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
106	<a href="#">c2o3jC_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of caenorhabditis elegans udp-glucose dehydrogenase
107	<a href="#">c1edzA_</a>	Alignment	not modelled	97.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 5,10-methylenetetrahydrofolate dehydrogenase; <b>PDBTitle:</b> structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
108	<a href="#">c3plnA_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
109	<a href="#">c3prjB_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
110	<a href="#">c3d1lB_</a>	Alignment	not modelled	97.2	17	<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
111	<a href="#">c2axqA_</a>	Alignment	not modelled	97.2	15	<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
112	<a href="#">c1nvtA_</a>	Alignment	not modelled	97.1	20	<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+
113	<a href="#">c3l6dB_</a>	Alignment	not modelled	97.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
114	<a href="#">d1xa0a2</a>	Alignment	not modelled	97.1	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
115	<a href="#">d1dlja2</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> 6-phosphogluconate dehydrogenase-like, N-terminal domain
116	<a href="#">c3qsgA_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-binding phosphogluconate dehydrogenase-like protein; <b>PDBTitle:</b> crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
117	<a href="#">c2ev9B_</a>	Alignment	not modelled	97.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> shikimate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
118	<a href="#">c3fwnB_</a>	Alignment	not modelled	97.1	18	<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
119	<a href="#">c3u62A_</a>	Alignment	not modelled	97.1	21	<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
120	<a href="#">c2cdaA_</a>	Alignment	not modelled	97.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> sulfolobus solfataricus glucose dehydrogenase 1 in complex2 with nadp