



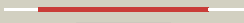

















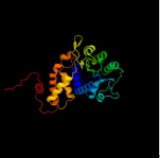
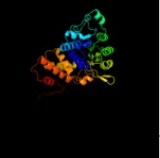
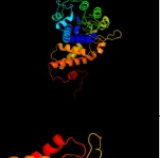

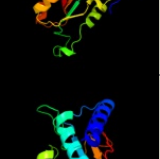
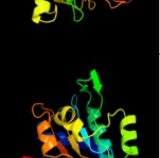
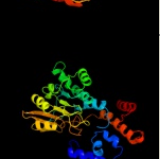
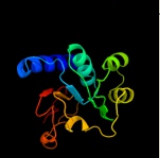
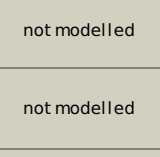


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1o0sB_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: crystal structure of ascaris suum malic enzyme complexed with nadh
2	c1gz3B_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
3	c1qr6A_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: malic enzyme 2; PDBTitle: human mitochondrial nad(p)-dependent malic enzyme
4	c2aw5A_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent malic enzyme; PDBTitle: crystal structure of a human malic enzyme
5	c3nv9A_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: malic enzyme; PDBTitle: crystal structure of entamoeba histolytica malic enzyme
6	c1ww8A_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: malate oxidoreductase; PDBTitle: crystal structure of malic enzyme from pyrococcus2 horikoshii ot3
7	c1vl6C_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: malate oxidoreductase; PDBTitle: crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution
8	c2a9fB_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative malic enzyme ((s)-malate:nad+ PDBTitle: crystal structure of a putative malic enzyme ((s)-2 malate:nad+ oxidoreductase (decarboxylating))
9	d1o0sa2	 Alignment		100.0	45	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
10	d1pj3a2	 Alignment		100.0	46	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
11	d1gq2a2	 Alignment		100.0	48	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain

12	dlo0sa1	Alignment		100.0	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
13	d1pj3a1	Alignment		100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
14	d1gq2a1	Alignment		100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
15	d1vl6a1	Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
16	d1vl6a2	Alignment		100.0	24	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Malic enzyme N-domain
17	d1euza1	Alignment		98.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
18	d1li4a1	Alignment		98.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
19	c3n58D	Alignment		97.7	19	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
20	d1v9la1	Alignment		97.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
21	d1v8ba1	Alignment	not modelled	97.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
22	c3aogA	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
23	c3dhyc	Alignment	not modelled	97.3	21	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
24	d1uxja1	Alignment	not modelled	97.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
25	c3gvpB	Alignment	not modelled	97.2	16	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
26	c2rirA	Alignment	not modelled	97.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
27	c2bmaA	Alignment	not modelled	97.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
28	c3d4oA	Alignment	not modelled	97.1	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a

					(np_243269.1)2 from bacillus halodurans at 2.10 a resolution
29	c1d4fD_	Alignment	not modelled	97.0	15 PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
30	d1t2da1	Alignment	not modelled	97.0	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
31	c3aoeC_	Alignment	not modelled	96.9	15 PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
32	d1pzga1	Alignment	not modelled	96.8	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
33	d1gpja2	Alignment	not modelled	96.7	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
34	d1l7da1	Alignment	not modelled	96.7	19 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
35	c1v9lA_	Alignment	not modelled	96.6	15 PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
36	d1u8xx1	Alignment	not modelled	96.6	20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
37	c1pzfD_	Alignment	not modelled	96.6	19 PDB header: oxidoreductase Chain: D: PDB Molecule: lactate dehydrogenase; PDBTitle: t.gondii ldh1 ternary complex with apad+ and oxalate
38	c3d64A_	Alignment	not modelled	96.6	17 PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
39	d1bvua1	Alignment	not modelled	96.5	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
40	c1gpjA_	Alignment	not modelled	96.5	21 PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
41	d1vi2a1	Alignment	not modelled	96.5	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
42	c1bvuf_	Alignment	not modelled	96.4	19 PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
43	c1obbB_	Alignment	not modelled	96.4	24 PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
44	c1nr1A_	Alignment	not modelled	96.3	16 PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate2 dehydrogenase
45	c1pjca_	Alignment	not modelled	96.2	24 PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
46	d1s6ya1	Alignment	not modelled	96.2	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
47	c3toza_	Alignment	not modelled	96.1	18 PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
48	d1l1da1	Alignment	not modelled	96.0	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
49	c1hrdA_	Alignment	not modelled	96.0	16 PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
50	c2fnza_	Alignment	not modelled	96.0	18 PDB header: oxidoreductase Chain: A: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
51	c3fefB_	Alignment	not modelled	96.0	28 PDB header: hydrolase Chain: B: PDB Molecule: putative glucosidase lpld; PDBTitle: crystal structure of putative glucosidase lpld from2 bacillus subtilis
52	c2eezG_	Alignment	not modelled	96.0	17 PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
53	d1a4ia1	Alignment	not modelled	95.8	22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
54	d1i10a1	Alignment	not modelled	95.8	23 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
					PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine

55	c3p2yA_	Alignment	not modelled	95.7	18	nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
56	c1u8xX_	Alignment	not modelled	95.7	17	PDB header: hydrolase Chain: X: PDB Molecule: maltose-6'-phosphate glucosidase; PDBTitle: crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
57	d9ldta1	Alignment	not modelled	95.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
58	d1obba1	Alignment	not modelled	95.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
59	d1vjta1	Alignment	not modelled	95.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
60	c2ep9A_	Alignment	not modelled	95.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
61	d1b0aa1	Alignment	not modelled	95.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
62	d1ldna1	Alignment	not modelled	95.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
63	c1v8bA_	Alignment	not modelled	95.5	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
64	c3l07B_	Alignment	not modelled	95.4	22	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
65	d1gtma1	Alignment	not modelled	95.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
66	d1ojuu1	Alignment	not modelled	95.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
67	c1a4iB_	Alignment	not modelled	95.4	22	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
68	d1guza1	Alignment	not modelled	95.3	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
69	c1ur5C_	Alignment	not modelled	95.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface
70	c2hjrk_	Alignment	not modelled	95.3	21	PDB header: oxidoreductase Chain: K: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of cryptosporidium parvum malate2 dehydrogenase
71	d1pjca1	Alignment	not modelled	95.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
72	d1ez4a1	Alignment	not modelled	95.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
73	c3oneA_	Alignment	not modelled	95.2	20	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
74	d1b26a1	Alignment	not modelled	95.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
75	c1u4sA_	Alignment	not modelled	95.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
76	c1wwkA_	Alignment	not modelled	95.1	26	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
77	d1a5za1	Alignment	not modelled	95.1	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
78	c2tmgD_	Alignment	not modelled	95.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
79	c2v6bB_	Alignment	not modelled	95.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
80	d1gv0a1	Alignment	not modelled	95.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
81	d1y6ja1	Alignment	not modelled	95.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like

82	c2j6iC_	Alignment	not modelled	95.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
83	c3evtA_	Alignment	not modelled	95.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
84	c4a5oB_	Alignment	not modelled	95.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
85	c1s6yA_	Alignment	not modelled	94.9	17	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: 2.3a crystal structure of phospho-beta-glucosidase
86	c3d0oA_	Alignment	not modelled	94.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase 1; PDBTitle: crystal structure of lactate dehydrogenase from2 staphylococcus aureus
87	c3p2oA_	Alignment	not modelled	94.7	24	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
88	c3p2oB_	Alignment	not modelled	94.5	23	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
89	c4a26B_	Alignment	not modelled	94.5	27	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
90	c2cukC_	Alignment	not modelled	94.5	27	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
91	c1ez4B_	Alignment	not modelled	94.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
92	c3gviB_	Alignment	not modelled	94.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
93	c3nepX_	Alignment	not modelled	94.4	24	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
94	c3k8zD_	Alignment	not modelled	94.4	20	PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
95	d1hwxal	Alignment	not modelled	94.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
96	d1llcal	Alignment	not modelled	94.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
97	dli0zal	Alignment	not modelled	94.3	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
98	d1hyhal	Alignment	not modelled	94.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	c3donA_	Alignment	not modelled	94.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
100	d1bgval	Alignment	not modelled	94.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
101	d1jw9b_	Alignment	not modelled	94.0	16	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
102	c3u62A_	Alignment	not modelled	93.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima
103	c2gcqB_	Alignment	not modelled	93.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
104	c1zfnA_	Alignment	not modelled	93.9	16	PDB header: transferase Chain: A: PDB Molecule: adenyllyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
105	c2hk8B_	Alignment	not modelled	93.9	24	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
106	d5ldhal	Alignment	not modelled	93.8	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
						PDB header: oxidoreductase

107	c2d4aC_	Alignment	not modelled	93.6	19	Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: structure of the malate dehydrogenase from aeropyrum pernix
108	c1up6F_	Alignment	not modelled	93.6	25	PDB header: hydrolase Chain: F: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: structure of the 6-phospho-beta glucosidase from thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal form3 with manganese, nad+ and glucose-6-phosphate
109	c1vjtA_	Alignment	not modelled	93.6	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
110	c1ojuA_	Alignment	not modelled	93.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.
111	c1b0aA_	Alignment	not modelled	93.4	22	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
112	c3h9gA_	Alignment	not modelled	93.4	14	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
113	c3gucB_	Alignment	not modelled	93.3	24	PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
114	c8ldhA_	Alignment	not modelled	93.3	24	PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: m4 apo-lactate dehydrogenase; PDBTitle: refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
115	c1luaA_	Alignment	not modelled	93.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
116	c1ldbA_	Alignment	not modelled	93.2	17	PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: apo-l-lactate dehydrogenase; PDBTitle: structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase
117	d1ldma1	Alignment	not modelled	93.1	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
118	d1luaa1	Alignment	not modelled	93.1	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
119	d1mlda1	Alignment	not modelled	93.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
120	c3vh1A_	Alignment	not modelled	93.0	20	PDB header: metal binding protein Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of saccharomyces cerevisiae atg7 (1-595)