



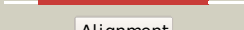

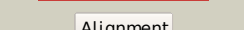

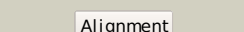







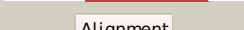

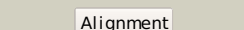

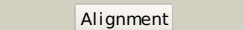



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1u8xX_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> maltose-6'-phosphate glucosidase; <b>PDBTitle:</b> crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
2	<a href="#">c1s6yA_</a>	 Alignment		100.0	53	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> 2.3a crystal structure of phospho-beta-glucosidase
3	<a href="#">c1up6F_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> 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
4	<a href="#">c1vjta_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
5	<a href="#">c1obbB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
6	<a href="#">c3fefB_</a>	 Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glucosidase lp1d; <b>PDBTitle:</b> crystal structure of putative glucosidase lp1d from2 bacillus subtilis
7	<a href="#">d1u8xx2</a>	 Alignment		100.0	18	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AglA-like glucosidase
8	<a href="#">d1s6ya2</a>	 Alignment		100.0	43	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AglA-like glucosidase
9	<a href="#">d1up7a2</a>	 Alignment		100.0	29	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AglA-like glucosidase
10	<a href="#">d1obbA2</a>	 Alignment		100.0	21	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AglA-like glucosidase
11	<a href="#">d1vjta2</a>	 Alignment		100.0	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> AglA-like glucosidase

12	<a href="#">c3p7mC_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
13	<a href="#">c1pzfD_</a>	Alignment		100.0	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
14	<a href="#">c2ldxA_</a>	Alignment		100.0	18	<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
15	<a href="#">c2v65A_</a>	Alignment		100.0	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
16	<a href="#">d1vjta1</a>	Alignment		100.0	26	<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
17	<a href="#">c1ez4B_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
18	<a href="#">c2fnzA_</a>	Alignment		100.0	19	<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)
19	<a href="#">c2hjrK_</a>	Alignment		100.0	20	<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
20	<a href="#">d1s6ya1</a>	Alignment		100.0	68	<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
21	<a href="#">c8ldhA_</a>	Alignment	not modelled	100.0	15	<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
22	<a href="#">c3d0oA_</a>	Alignment	not modelled	100.0	18	<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
23	<a href="#">c3gviB_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
24	<a href="#">c1a5zA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> lactate dehydrogenase from thermotoga maritima (tml dh)
25	<a href="#">c1lldA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase(choh (d)-nad (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
26	<a href="#">d1u8xx1</a>	Alignment	not modelled	100.0	35	<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
27	<a href="#">c3tt2A_</a>	Alignment	not modelled	100.0	18	<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.
28	<a href="#">c1u4sA_</a>	Alignment	not modelled	100.0	18	<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
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

29	<a href="#">dlup7a1</a>	Alignment	not modelled	100.0	38	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
30	<a href="#">clojuA_</a>	Alignment	not modelled	100.0	19	<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.
31	<a href="#">c1llcA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
32	<a href="#">c1hyhA_</a>	Alignment	not modelled	100.0	20	<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
33	<a href="#">c3nepX_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
34	<a href="#">c3pqeD_</a>	Alignment	not modelled	100.0	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
35	<a href="#">c1ur5C_</a>	Alignment	not modelled	100.0	20	<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
36	<a href="#">c1hygA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate/malate dehydrogenase; <b>PDBTitle:</b> crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
37	<a href="#">d1obba1</a>	Alignment	not modelled	100.0	26	<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
38	<a href="#">c7mdhA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> chloroplastic malate dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
39	<a href="#">c2e37B_</a>	Alignment	not modelled	100.0	18	<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
40	<a href="#">c1b8vA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> malate dehydrogenase from aquaspirillum arcticum
41	<a href="#">c2v6bB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
42	<a href="#">c1gv1D_</a>	Alignment	not modelled	100.0	22	<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
43	<a href="#">c2pwzG_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo form of e.coli malate dehydrogenase
44	<a href="#">c2d4aC_</a>	Alignment	not modelled	100.0	16	<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
45	<a href="#">c5mdhB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
46	<a href="#">c1ldbA_</a>	Alignment	not modelled	100.0	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
47	<a href="#">c1y6jA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> l-lactate dehydrogenase from clostridium thermocellum cth-1135
48	<a href="#">c1wziA_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
49	<a href="#">c3dl2A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 3; <b>PDBTitle:</b> hexagonal structure of the ldh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
50	<a href="#">c3fi9B_</a>	Alignment	not modelled	100.0	19	<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
51	<a href="#">c1smkD_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
52	<a href="#">c1sevA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal precursor; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
						<b>PDB header:</b> oxidoreductase

53	<a href="#">c2dfdD</a>	Alignment	not modelled	100.0	15	<b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2
54	<a href="#">c1mldA</a>	Alignment	not modelled	100.0	15	<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
55	<a href="#">c2hlpB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
56	<a href="#">d1i0za1</a>	Alignment	not modelled	99.9	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
57	<a href="#">d1o6za1</a>	Alignment	not modelled	99.9	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
58	<a href="#">d1pzga1</a>	Alignment	not modelled	99.9	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
59	<a href="#">d1i10a1</a>	Alignment	not modelled	99.9	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
60	<a href="#">d1t2da1</a>	Alignment	not modelled	99.9	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
61	<a href="#">d5ldha1</a>	Alignment	not modelled	99.9	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
62	<a href="#">d9ldta1</a>	Alignment	not modelled	99.9	20	<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="#">d1y7ta1</a>	Alignment	not modelled	99.9	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
64	<a href="#">d1a5za1</a>	Alignment	not modelled	99.9	23	<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="#">d1ojua1</a>	Alignment	not modelled	99.9	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
66	<a href="#">d1b8pa1</a>	Alignment	not modelled	99.9	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
67	<a href="#">d1ldna1</a>	Alignment	not modelled	99.9	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
68	<a href="#">d1guza1</a>	Alignment	not modelled	99.9	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
69	<a href="#">d2ldxa1</a>	Alignment	not modelled	99.9	23	<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="#">d1llda1</a>	Alignment	not modelled	99.9	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
71	<a href="#">d1ldma1</a>	Alignment	not modelled	99.9	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
72	<a href="#">d2cmda1</a>	Alignment	not modelled	99.9	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
73	<a href="#">d1hyha1</a>	Alignment	not modelled	99.9	20	<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="#">d5mdha1</a>	Alignment	not modelled	99.9	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
75	<a href="#">d1llca1</a>	Alignment	not modelled	99.9	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
76	<a href="#">d7mdha1</a>	Alignment	not modelled	99.9	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
77	<a href="#">d1gv0a1</a>	Alignment	not modelled	99.9	20	<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="#">d1civa1</a>	Alignment	not modelled	99.8	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
79	<a href="#">d1luxa1</a>	Alignment	not modelled	99.8	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
80	<a href="#">d1y6ja1</a>	Alignment	not modelled	99.8	20	<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

Rank	Accession	Model	Model description	Score	Count	Annotation
81	<a href="#">d1ez4a1</a>	Alignment	not modelled	99.7	30	<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
82	<a href="#">d1hyea1</a>	Alignment	not modelled	99.7	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
83	<a href="#">d1mlda1</a>	Alignment	not modelled	99.6	20	<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
84	<a href="#">d9ldta2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
85	<a href="#">d1i10a2</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
86	<a href="#">d1i0za2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
87	<a href="#">d1oc4a2</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
88	<a href="#">d1ldma2</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
89	<a href="#">d1a5za2</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
90	<a href="#">d1t2da2</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
91	<a href="#">d2ldxa2</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
92	<a href="#">d1pzga2</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
93	<a href="#">d1llda2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
94	<a href="#">d5mdha2</a>	Alignment	not modelled	99.5	16	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
95	<a href="#">d1ldna2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
96	<a href="#">d1civa2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
97	<a href="#">d7mdha2</a>	Alignment	not modelled	99.4	13	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
98	<a href="#">d1uxja2</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
99	<a href="#">d1gv0a2</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
100	<a href="#">d1guza2</a>	Alignment	not modelled	99.4	19	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
101	<a href="#">d1o6za2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
102	<a href="#">d1ez4a2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
103	<a href="#">d1hyha2</a>	Alignment	not modelled	99.4	18	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
104	<a href="#">d1b8pa2</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
105	<a href="#">d1y7ta2</a>	Alignment	not modelled	99.4	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
106	<a href="#">d1hyea2</a>	Alignment	not modelled	99.3	17	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
107	<a href="#">d1ojua2</a>	Alignment	not modelled	99.3	19	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
108	<a href="#">d1y6ja2</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain



109	<a href="#">d1llca2</a>	Alignment	not modelled	99.2	14	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
110	<a href="#">d1mlda2</a>	Alignment	not modelled	99.1	11	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
111	<a href="#">d2cmda2</a>	Alignment	not modelled	99.0	11	<b>Fold:</b> LDH C-terminal domain-like <b>Superfamily:</b> LDH C-terminal domain-like <b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain
112	<a href="#">c3prjB_</a>	Alignment	not modelled	98.8	18	<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.
113	<a href="#">c1m75B_</a>	Alignment	not modelled	98.7	18	<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
114	<a href="#">c1mv8A_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose 6-dehydrogenase; <b>PDBTitle:</b> 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
115	<a href="#">d1dlja2</a>	Alignment	not modelled	98.6	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
116	<a href="#">d1txga2</a>	Alignment	not modelled	98.5	10	<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
117	<a href="#">c3k96B_</a>	Alignment	not modelled	98.5	16	<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
118	<a href="#">c2y0dB_</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
119	<a href="#">c2q3eH_</a>	Alignment	not modelled	98.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
120	<a href="#">c3plnA_</a>	Alignment	not modelled	98.5	20	<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