

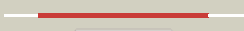





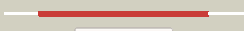















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pwzG_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: G: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of the apo form of e.coli malate dehydrogenase
2	c1mldA_	 Alignment		100.0	59	PDB header: oxidoreductase(nad(a)-choh(d)) Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
3	c2dfdD_	 Alignment		100.0	59	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of human malate dehydrogenase type 2
4	c1sevA_	 Alignment		100.0	54	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase, glyoxysomal precursor; PDBTitle: mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
5	c1smkD_	 Alignment		100.0	54	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase, glyoxysomal; PDBTitle: mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
6	c7mdhA_	 Alignment		100.0	24	PDB header: chloroplastic malate dehydrogenase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: structural basis for light activation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
7	c5mdhB_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and nad at 2.4 angstroms resolution
8	c1b8vA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (malate dehydrogenase); PDBTitle: malate dehydrogenase from aquaspirillum arcticum
9	c1hyhA_	 Alignment		100.0	20	PDB header: oxidoreductase (choh(d)-nad+(a)) Chain: A: PDB Molecule: l-2-hydroxyisocaproate dehydrogenase; PDBTitle: crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
10	c1ez4B_	 Alignment		100.0	24	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
11	c1ojua_	 Alignment		100.0	26	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.

12	c1hygA_	Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate/malate dehydrogenase; PDBTitle: crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
13	c8ldhA_	Alignment		100.0	22	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
14	c1lldA_	Alignment		100.0	27	PDB header: oxidoreductase(choh (d)-nad (a)) Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
15	c3nepX_	Alignment		100.0	27	PDB header: oxidoreductase Chain: X: PDB Molecule: malate dehydrogenase; PDBTitle: 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
16	c3d0oA_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase 1; PDBTitle: crystal structure of lactate dehydrogenase from2 staphylococcus aureus
17	c1a5zA_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tml dh)
18	c1wziA_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
19	c1y6iA_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: l-lactate dehydrogenase from clostridium thermocellum cth-1135
20	c2d4aC_	Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: structure of the malate dehydrogenase from aeropyrum pernix
21	c1pzfD_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: D: PDB Molecule: lactate dehydrogenase; PDBTitle: t.gondii ldh1 ternary complex with apad+ and oxalate
22	c2ldxA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: apo-lactate dehydrogenase; PDBTitle: characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
23	c2e37B_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: structure of tt0471 protein from thermus thermophilus
24	c3dl2A_	Alignment	not modelled	100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 variant 3; PDBTitle: hexagonal structure of the ldh domain of human ubiquitin-2 conjugating enzyme e2-like isoform a
25	c3p7mC_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
26	c1ur5C_	Alignment	not modelled	100.0	27	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
27	c1gv1D_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
28	c3gviB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of lactate/malate dehydrogenase from2

						brucella melitensis in complex with adp
29	c1u4sA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
30	c1ldbA_	Alignment	not modelled	100.0	24	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
31	c3pqeD_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
32	c2v65A_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase a chain; PDBTitle: apo ldh from the psychrophile c. gunnari
33	c2hjrK_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: K: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of cryptosporidium parvum malate2 dehydrogenase
34	c2fnzA_	Alignment	not modelled	100.0	29	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)
35	c2v6bB_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
36	c3fi9B_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
37	c3tl2A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
38	c1lcA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: structure determination of the allosteric l-lactate dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution
39	c2hlpB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of the e267r mutant of a halophilic2 malate dehydrogenase in the apo form
40	c3fefB_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: putative glucosidase lpld; PDBTitle: crystal structure of putative glucosidase lpld from2 bacillus subtilis
41	c1s6yA_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: 2.3a crystal structure of phospho-beta-glucosidase
42	c1up6F_	Alignment	not modelled	100.0	18	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
43	d2cmda2	Alignment	not modelled	100.0	99	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
44	d1mlda2	Alignment	not modelled	100.0	53	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
45	c1u8xX_	Alignment	not modelled	100.0	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
46	d1ez4a2	Alignment	not modelled	100.0	22	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
47	d1pzga2	Alignment	not modelled	100.0	23	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
48	d1civa2	Alignment	not modelled	100.0	22	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
49	d5mdha2	Alignment	not modelled	100.0	18	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
50	d1a5za2	Alignment	not modelled	100.0	25	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
51	d1o6za2	Alignment	not modelled	100.0	25	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
52	d1ldna2	Alignment	not modelled	100.0	21	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
53	d1gv0a2	Alignment	not modelled	100.0	28	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
54	d1oc4a2	Alignment	not modelled	100.0	24	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like

					Family: Lactate & malate dehydrogenases, C-terminal domain
55	d5mdha1	Alignment	not modelled	100.0	27 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
56	d7mdha2	Alignment	not modelled	100.0	22 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
57	d1hyha2	Alignment	not modelled	100.0	19 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
58	d1b8pa1	Alignment	not modelled	100.0	29 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
59	d1o6za1	Alignment	not modelled	100.0	28 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
60	d1llda2	Alignment	not modelled	100.0	21 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
61	d7mdha1	Alignment	not modelled	100.0	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
62	d9ldta2	Alignment	not modelled	100.0	24 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
63	d1i0za2	Alignment	not modelled	100.0	23 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
64	d1y7ta2	Alignment	not modelled	100.0	19 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
65	d1t2da2	Alignment	not modelled	100.0	23 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
66	d2cmda1	Alignment	not modelled	100.0	99 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
67	d1guza2	Alignment	not modelled	100.0	26 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
68	d1uxja2	Alignment	not modelled	100.0	25 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
69	d1y6ja2	Alignment	not modelled	100.0	22 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
70	d1y7ta1	Alignment	not modelled	100.0	30 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
71	c1obbB	Alignment	not modelled	100.0	18 PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
72	d1ldma2	Alignment	not modelled	100.0	20 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
73	d1i10a2	Alignment	not modelled	100.0	24 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
74	d1civa1	Alignment	not modelled	100.0	27 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
75	d2ldxa2	Alignment	not modelled	100.0	24 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
76	d1b8pa2	Alignment	not modelled	100.0	21 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
77	d1i0za1	Alignment	not modelled	100.0	24 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
78	d1ojua2	Alignment	not modelled	100.0	21 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
79	d1ldma1	Alignment	not modelled	100.0	24 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
80	d1llca2	Alignment	not modelled	100.0	22 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
81	d1i10a1	Alignment	not modelled	100.0	27 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
					Fold: LDH C-terminal domain-like

82	d1hyea2	Alignment	not modelled	100.0	21	Superfamily: LDH C-terminal domain-like Family: Lactate & malate dehydrogenases, C-terminal domain
83	d5ldha1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
84	d2ldxa1	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
85	d9ldta1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
86	d1llda1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
87	d1u8xx1	Alignment	not modelled	100.0	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
88	d1ojua1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
89	d1a5za1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
90	d1s6ya1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
91	d1ldna1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
92	d1up7a1	Alignment	not modelled	99.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
93	d1guza1	Alignment	not modelled	99.9	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
94	d1obba1	Alignment	not modelled	99.9	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
95	d1hyha1	Alignment	not modelled	99.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
96	d1t2da1	Alignment	not modelled	99.9	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
97	c1vjta_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
98	d1mlda1	Alignment	not modelled	99.9	63	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
99	d1pzga1	Alignment	not modelled	99.9	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
100	d1llca1	Alignment	not modelled	99.9	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
101	d1hyea1	Alignment	not modelled	99.9	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
102	d1gv0a1	Alignment	not modelled	99.9	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
103	d1y6ja1	Alignment	not modelled	99.9	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
104	d1ez4a1	Alignment	not modelled	99.9	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
105	d1luxja1	Alignment	not modelled	99.8	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
106	d1vjta1	Alignment	not modelled	99.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
107	d1mv8a2	Alignment	not modelled	98.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
108	c2o3jC_	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
109	c3gg2B_	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2

					porphyromonas gingivalis bound to product udp-glucuronate
110	c3plnA_	Alignment	not modelled	98.5	19 PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
111	d1dlja2	Alignment	not modelled	98.5	22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
112	c1mv8A_	Alignment	not modelled	98.4	14 PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
113	c3prjB_	Alignment	not modelled	98.4	14 PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
114	d1txga2	Alignment	not modelled	98.4	25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
115	d1s6ya2	Alignment	not modelled	98.4	19 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
116	c2y0dB_	Alignment	not modelled	98.4	17 PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
117	d1up7a2	Alignment	not modelled	98.3	18 Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
118	c3g79A_	Alignment	not modelled	98.3	17 PDB header: oxidoreductase Chain: A: PDB Molecule: ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; PDBTitle: crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
119	c2q3eH_	Alignment	not modelled	98.3	14 PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
120	d1n1ea2	Alignment	not modelled	98.2	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain