Phyre^2

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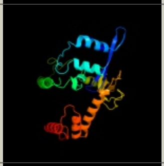
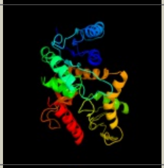
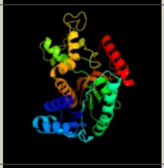
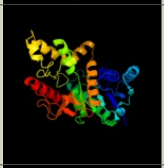
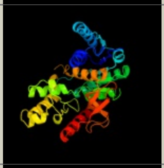
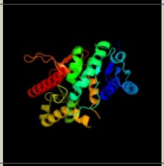
Description	P06720
Date	Thu Jan 5 10:59:23 GMT 2012
Unique Job ID	bd99cfa77d51a854

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u8xX_	Alignment		100.0	23	**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
2	c1s6yA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
3	c1vjtA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
4	c3fefB_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glucosidase lpld; **PDBTitle:** crystal structure of putative glucosidase lpld from2 bacillus subtilis
5	c1up6F_	Alignment		100.0	20	**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
6	c1obbB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
7	d1u8xx2	Alignment		100.0	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
8	d1s6ya2	Alignment		100.0	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
9	d1up7a2	Alignment		100.0	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
10	d1obba2	Alignment		100.0	20	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
11	c1pzfD_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** t.gondii ldh1 ternary complex with apad+ and oxalate

12	c3p7mC_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
13	d1vjta2	Alignment		100.0	20	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**AglA-like glucosidase
14	c2ldxA_	Alignment		100.0	15	**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
15	c2v65A_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase a chain; **PDBTitle:** apo ldh from the psychrophile c. gunnari
16	c1ez4B_	Alignment		100.0	16	**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
17	c3d0oA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
18	c2hjrK_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
19	c2fnzA_	Alignment		100.0	16	**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)
20	c3gviB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
21	c8ldhA_	Alignment	not modelled	100.0	14	**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
22	c1lldA_	Alignment	not modelled	100.0	16	**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
23	c1a5zA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
24	c1u4sA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
25	c3tl2A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
26	d1vjta1	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
27	c3pqeD_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
28	c3nepX_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber
						Fold:NAD(P)-binding Rossmann-fold domains

29	d1u8xx1	Alignment	not modelled	100.0	27	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
30	c1llcA_	Alignment	not modelled	100.0	18	**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
31	c1hyhA_	Alignment	not modelled	100.0	16	**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
32	c1ojuA_	Alignment	not modelled	100.0	18	**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.
33	c1ur5C_	Alignment	not modelled	100.0	16	**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
34	c2e37B_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** structure of tt0471 protein from thermus thermophilus
35	d1s6ya1	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
36	c1hygA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate/malate dehydrogenase; **PDBTitle:** crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
37	c2d4aC_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix
38	c2v6bB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
39	d1up7a1	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
40	c1ldbA_	Alignment	not modelled	100.0	18	**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
41	c1gv1D_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
42	c7mdhA_	Alignment	not modelled	100.0	13	**PDB header:**chloroplastic malate dehydrogenase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
43	c2pwzG_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase
44	c1b8vA_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** malate dehydrogenase from aquaspirillum arcticum
45	c5mdhB_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
46	d1obba1	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
47	c3dl2A_	Alignment	not modelled	100.0	13	**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
48	c3fi9B_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
49	c1wziA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
50	c1y6jA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** l-lactate dehydrogenase from clostridium thermocellum cth-1135
51	c2dfdD_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
52	c1smkD_	Alignment	not modelled	100.0	17	**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
53	c1sevA_	Alignment	not modelled	100.0	17	**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
54	c2hlpB_	Alignment	not modelled	100.0	15	**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
55	c1mldA_	Alignment	not modelled	100.0	16	**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
56	d1pzga1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
57	d1i0za1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
58	d1i10a1	Alignment	not modelled	100.0	16	**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	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
60	d1t2da1	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
61	d5ldha1	Alignment	not modelled	99.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
62	d9ldta1	Alignment	not modelled	99.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
63	d1ldna1	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
64	d1llda1	Alignment	not modelled	99.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
65	d1ojua1	Alignment	not modelled	99.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
66	d2ldxa1	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
67	d1a5za1	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
68	d1guza1	Alignment	not modelled	99.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
69	d1b8pa1	Alignment	not modelled	99.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
70	d1ldma1	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
71	d1y7ta1	Alignment	not modelled	99.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	d1llca1	Alignment	not modelled	99.9	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
73	d1hyha1	Alignment	not modelled	99.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
74	d5mdha1	Alignment	not modelled	99.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
75	d2cmda1	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
76	d7mdha1	Alignment	not modelled	99.9	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
77	d1gv0a1	Alignment	not modelled	99.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
78	d1civa1	Alignment	not modelled	99.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
79	d1uxja1	Alignment	not modelled	99.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
80	d1y6ja1	Alignment	not modelled	99.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like

81	d1ez4a1	Alignment	not modelled	99.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
82	d1hyea1	Alignment	not modelled	99.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
83	d1mlda1	Alignment	not modelled	99.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
84	d1pzga2	Alignment	not modelled	99.6	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
85	d1a5za2	Alignment	not modelled	99.6	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
86	d5mdha2	Alignment	not modelled	99.6	11	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
87	d9ldta2	Alignment	not modelled	99.5	16	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
88	d1o6za2	Alignment	not modelled	99.5	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
89	d1ldna2	Alignment	not modelled	99.5	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
90	d1ez4a2	Alignment	not modelled	99.5	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
91	d1gv0a2	Alignment	not modelled	99.5	17	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
92	d1oc4a2	Alignment	not modelled	99.5	8	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
93	d1i10a2	Alignment	not modelled	99.5	17	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
94	d1llda2	Alignment	not modelled	99.5	11	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
95	d1i0za2	Alignment	not modelled	99.5	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
96	d1ldma2	Alignment	not modelled	99.5	11	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
97	d1t2da2	Alignment	not modelled	99.5	10	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
98	d1uxja2	Alignment	not modelled	99.5	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
99	d1guza2	Alignment	not modelled	99.5	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
100	d1b8pa2	Alignment	not modelled	99.5	9	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
101	d7mdha2	Alignment	not modelled	99.5	12	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
102	d2ldxa2	Alignment	not modelled	99.5	12	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
103	d1civa2	Alignment	not modelled	99.5	13	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
104	d1y7ta2	Alignment	not modelled	99.4	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
105	d1hyha2	Alignment	not modelled	99.4	12	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
106	d1hyea2	Alignment	not modelled	99.4	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
107	d1y6ja2	Alignment	not modelled	99.4	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
108	d1mlda2	Alignment	not modelled	99.4	14	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain

109	d1ojua2	Alignment	not modelled	99.3	15	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
110	d1llca2	Alignment	not modelled	99.3	19	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
111	d2cmda2	Alignment	not modelled	99.1	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
112	c1m75B_	Alignment	not modelled	98.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
113	c3plnA_	Alignment	not modelled	98.7	18	**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
114	c1mv8A_	Alignment	not modelled	98.6	19	**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
115	d1dlja2	Alignment	not modelled	98.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
116	c3prjB_	Alignment	not modelled	98.6	15	**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.
117	c3gg2B_	Alignment	not modelled	98.5	18	**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
118	c2ep9A_	Alignment	not modelled	98.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
119	c2y0dB_	Alignment	not modelled	98.5	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
120	d1mv8a2	Alignment	not modelled	98.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain