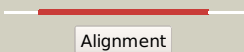
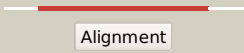
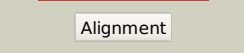
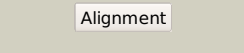
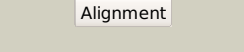
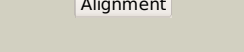
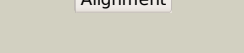
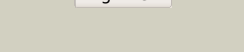


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                                                       |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c1ojuA_</a> |  Alignment   |    | 100.0      | 36     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> 2.8 a resolution structure of malate dehydrogenase from2 archaeoglobus fulgidus in complex with etheno-nad.                                                                                           |
| 2  | <a href="#">c8ldhA_</a> |  Alignment   |    | 100.0      | 25     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase;<br><b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate dehydrogenase                                                                                                                             |
| 3  | <a href="#">c1ez4B_</a> |  Alignment   |    | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution                                                                                  |
| 4  | <a href="#">c1hyhA_</a> |  Alignment   |   | 100.0      | 29     | <b>PDB header:</b> oxidoreductase (choh(d)-nad+(a))<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase;<br><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 |
| 5  | <a href="#">c1lldA_</a> |  Alignment |  | 100.0      | 31     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase                                                                                                                     |
| 6  | <a href="#">c1b8vA_</a> |  Alignment |  | 100.0      | 19     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase);<br><b>PDBTitle:</b> malate dehydrogenase from aquaspirillum arcticum                                                                                                                                            |
| 7  | <a href="#">c4ln1B_</a> |  Alignment |  | 100.0      | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase 1;<br><b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus cereus atcc2 14579 complexed with calcium, nysgrc target 029452                                                                       |
| 8  | <a href="#">c3d0oA_</a> |  Alignment |  | 100.0      | 28     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1;<br><b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus                                                                                                                           |
| 9  | <a href="#">c1a5zA_</a> |  Alignment |  | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> lactate dehydrogenase from thermotoga maritima (tml dh)                                                                                                                                            |
| 10 | <a href="#">c4m1qB_</a> |  Alignment |  | 100.0      | 31     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus2 selenitireducens mls10, nysgrc target 029814.                                                                                          |
| 11 | <a href="#">c1pzfD_</a> |  Alignment |  | 100.0      | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> lactate dehydrogenase;<br><b>PDBTitle:</b> t.gondii ldh1 ternary complex with apad+ and oxalate                                                                                                                                                 |

|    |                         |           |              |       |    |                                                                                                                                                                                                                                                                                              |
|----|-------------------------|-----------|--------------|-------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c7mdhA_</a> | Alignment |              | 100.0 | 17 | <b>PDB header:</b> chloroplatic malate dehydrogenase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase);<br><b>PDBTitle:</b> structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form    |
| 13 | <a href="#">c3nepX_</a> | Alignment |              | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> X: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> 1.55a resolution structure of malate dehydrogenase from salinibacter2 ruber                                                                                             |
| 14 | <a href="#">c1hygA_</a> | Alignment |              | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate/malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase                                                                         |
| 15 | <a href="#">c3p7mC_</a> | Alignment |              | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4                                                                      |
| 16 | <a href="#">c1u4sA_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid                                                                         |
| 17 | <a href="#">c2d4aC_</a> | Alignment |              | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> structure of the malate dehydrogenase from aeropyrum pernix                                                                                                             |
| 18 | <a href="#">c2ldxA_</a> | Alignment |              | 100.0 | 27 | <b>PDB header:</b> oxidoreductase(choh(d)-nad(a))<br><b>Chain:</b> A: <b>PDB Molecule:</b> apo-lactate dehydrogenase;<br><b>PDBTitle:</b> characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4            |
| 19 | <a href="#">c2e37B_</a> | Alignment |              | 100.0 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> structure of tt0471 protein from thermus thermophilus                                                                                                                |
| 20 | <a href="#">c5mdhB_</a> | Alignment |              | 100.0 | 20 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution                               |
| 21 | <a href="#">c2v65A_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase a chain;<br><b>PDBTitle:</b> apo ldh from the psychrophile c. gunnari                                                                                                                     |
| 22 | <a href="#">c2fnzA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lactate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid) |
| 23 | <a href="#">c2hjrK_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase                                                                                                       |
| 24 | <a href="#">c1ur5C_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface                                                 |
| 25 | <a href="#">c3gviB_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp                                                                         |
| 26 | <a href="#">c1gv1D_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases                                                  |
| 27 | <a href="#">c3pqeD_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation                                                                             |
| 28 | <a href="#">c3tl2A_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.                                                                         |
|    |                         |           |              |       |    | <b>PDB header:</b> oxidoreductase(choh(d)-nad(a))                                                                                                                                                                                                                                            |

|    |                         |           |              |       |    |                                                                                                                                                                                                                                                                                                     |
|----|-------------------------|-----------|--------------|-------|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 29 | <a href="#">c1ldbA</a>  | Alignment | not modelled | 100.0 | 31 | <b>Chain:</b> A: <b>PDB Molecule:</b> apo-l-lactate dehydrogenase;<br><b>PDBTitle:</b> structure determination and refinement of bacillus2<br>stearothermophilus lactate dehydrogenase                                                                                                              |
| 30 | <a href="#">c1wziA</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> structural basis for alteration of cofactor specificity of2<br>malate dehydrogenase from thermus flavus                                                                        |
| 31 | <a href="#">c1y6iA</a>  | Alignment | not modelled | 100.0 | 37 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> l-lactate dehydrogenase from clostridium thermocellum<br>cth-1135                                                                                                           |
| 32 | <a href="#">c2v6bB</a>  | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of lactate dehydrogenase from<br>deinococcus2 radiodurans (apo form)                                                                                      |
| 33 | <a href="#">c1l1cA</a>  | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase(choh(d)-nad(a))<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase;<br><b>PDBTitle:</b> structure determination of the allosteric l-lactate<br>dehydrogenase from2 lactobacillus casei at 3.0 angstroms resolution                                  |
| 34 | <a href="#">c3dl2A</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-conjugating enzyme e2 variant 3;<br><b>PDBTitle:</b> hexagonal structure of the ldh domain of human<br>ubiquitin-2 conjugating enzyme e2-like isoform a                                 |
| 35 | <a href="#">c3fi9B</a>  | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of malate dehydrogenase from<br>porphyromonas2 gingivalis                                                                                                    |
| 36 | <a href="#">c4h7pA</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of a putative cytosolic malate<br>dehydrogenase from2 leishmania major friedlin                                                                              |
| 37 | <a href="#">c1smkD</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal;<br><b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2<br>dehydrogenase have different activities and stabilities3 but similar<br>crystal structures              |
| 38 | <a href="#">c1sevA</a>  | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal<br>precursor;<br><b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2<br>dehydrogenase have different activities and stabilities3 but similar<br>crystal structures |
| 39 | <a href="#">c1mldA</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase(nad(a)-choh(d))<br><b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> refined structure of mitochondrial malate<br>dehydrogenase2 from porcine heart and the consensus structure<br>for3 dicarboxylic acid oxidoreductases           |
| 40 | <a href="#">c2dfdD</a>  | Alignment | not modelled | 100.0 | 22 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2                                                                                                                         |
| 41 | <a href="#">c2pwzG</a>  | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the apo form of e.coli malate<br>dehydrogenase                                                                                                            |
| 42 | <a href="#">c2hlpB</a>  | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the e267r mutant of a halophilic2<br>malate dehydrogenase in the apo form                                                                                 |
| 43 | <a href="#">c3fefB</a>  | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative glucosidase lpld, alpha-<br>galacturonidase;<br><b>PDBTitle:</b> crystal structure of putative glucosidase lpld from bacillus<br>subtilis                                                                            |
| 44 | <a href="#">c1s6yA</a>  | Alignment | not modelled | 100.0 | 19 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase;<br><b>PDBTitle:</b> 2.3a crystal structure of phospho-beta-glucosidase                                                                                                                            |
| 45 | <a href="#">c1up6F</a>  | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> F: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase;<br><b>PDBTitle:</b> structure of the 6-phospho-beta glucosidase from<br>thermotoga2 maritima at 2.55 angstrom resolution in the tetragonal<br>form3 with manganese, nad+ and glucose-6-phosphate  |
| 46 | <a href="#">c1u8xX</a>  | Alignment | not modelled | 100.0 | 10 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> X: <b>PDB Molecule:</b> maltose-6'-phosphate glucosidase;<br><b>PDBTitle:</b> crystal structure of glva from bacillus subtilis, a metal-<br>requiring,2 nad-dependent 6-phospho-alpha-glucosidase                                                     |
| 47 | <a href="#">d1a5za2</a> | Alignment | not modelled | 100.0 | 30 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 48 | <a href="#">d1ez4a2</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 49 | <a href="#">d9ldta2</a> | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 50 | <a href="#">d1ldna2</a> | Alignment | not modelled | 100.0 | 31 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 51 | <a href="#">d1oc4a2</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 52 | <a href="#">d1i0za2</a> | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |
| 53 | <a href="#">d1llda2</a> | Alignment | not modelled | 100.0 | 30 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                                                                                                                      |

|    |                          |           |              |       |    |                                                                                                                                                                                                    |
|----|--------------------------|-----------|--------------|-------|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54 | <a href="#">d1i10a2</a>  | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 55 | <a href="#">d1ldma2</a>  | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 56 | <a href="#">d1pzga2</a>  | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 57 | <a href="#">d1t2da2</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 58 | <a href="#">d1o6za2</a>  | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 59 | <a href="#">d2ldxa2</a>  | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 60 | <a href="#">c1obbB</a>   | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase;<br><b>PDBTitle:</b> alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+ |
| 61 | <a href="#">d1gv0a2</a>  | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 62 | <a href="#">d1hyha2</a>  | Alignment | not modelled | 100.0 | 34 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 63 | <a href="#">d1llca2</a>  | Alignment | not modelled | 100.0 | 31 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 64 | <a href="#">d1guza2</a>  | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 65 | <a href="#">d1y6ja2</a>  | Alignment | not modelled | 100.0 | 37 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 66 | <a href="#">d1luxja2</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 67 | <a href="#">d1civa2</a>  | Alignment | not modelled | 100.0 | 14 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 68 | <a href="#">d5mdha2</a>  | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 69 | <a href="#">d1y7ta2</a>  | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 70 | <a href="#">d7mdha2</a>  | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 71 | <a href="#">d1b8pa2</a>  | Alignment | not modelled | 100.0 | 15 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 72 | <a href="#">d1ojua2</a>  | Alignment | not modelled | 100.0 | 33 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 73 | <a href="#">d1hyea2</a>  | Alignment | not modelled | 100.0 | 31 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 74 | <a href="#">d1mlda2</a>  | Alignment | not modelled | 100.0 | 19 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 75 | <a href="#">d2cmda2</a>  | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> LDH C-terminal domain-like<br><b>Superfamily:</b> LDH C-terminal domain-like<br><b>Family:</b> Lactate & malate dehydrogenases, C-terminal domain                                     |
| 76 | <a href="#">d1i0za1</a>  | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> LDH N-terminal domain-like                                         |
| 77 | <a href="#">d1b8pa1</a>  | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> LDH N-terminal domain-like                                         |
| 78 | <a href="#">d1o6za1</a>  | Alignment | not modelled | 100.0 | 33 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> LDH N-terminal domain-like                                         |
| 79 | <a href="#">d5mdha1</a>  | Alignment | not modelled | 100.0 | 21 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> LDH N-terminal domain-like                                         |
| 80 | <a href="#">d1ldma1</a>  | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> NAD(P)-binding Rossmann-fold domains<br><b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains<br><b>Family:</b> LDH N-terminal domain-like                                         |
| 81 | <a href="#">c1vjta</a>   | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase;<br><b>PDBTitle:</b> crystal structure of alpha-glucosidase (tm0752) from                                  |

|     |         |           |              |       |    |                                                                                                                                    |
|-----|---------|-----------|--------------|-------|----|------------------------------------------------------------------------------------------------------------------------------------|
|     |         |           |              |       |    | thermotoga2 maritima at 2.50 a resolution                                                                                          |
| 82  | d7mdha1 | Alignment | not modelled | 100.0 | 20 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 83  | d1i10a1 | Alignment | not modelled | 100.0 | 28 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 84  | d1llda1 | Alignment | not modelled | 100.0 | 33 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 85  | d1y7ta1 | Alignment | not modelled | 100.0 | 25 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 86  | d1civa1 | Alignment | not modelled | 100.0 | 21 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 87  | d1u8xx1 | Alignment | not modelled | 100.0 | 11 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 88  | d5ldha1 | Alignment | not modelled | 100.0 | 29 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 89  | d1ojuu1 | Alignment | not modelled | 100.0 | 38 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 90  | d9ldta1 | Alignment | not modelled | 100.0 | 30 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 91  | d2ldxa1 | Alignment | not modelled | 100.0 | 29 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 92  | d1obba1 | Alignment | not modelled | 100.0 | 17 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 93  | d1guza1 | Alignment | not modelled | 100.0 | 35 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 94  | d1ldna1 | Alignment | not modelled | 100.0 | 29 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 95  | d1a5za1 | Alignment | not modelled | 100.0 | 28 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 96  | d1s6ya1 | Alignment | not modelled | 100.0 | 21 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 97  | d1t2da1 | Alignment | not modelled | 100.0 | 30 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 98  | d1up7a1 | Alignment | not modelled | 100.0 | 21 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 99  | d1hyha1 | Alignment | not modelled | 100.0 | 26 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 100 | d1llca1 | Alignment | not modelled | 100.0 | 29 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 101 | d1pzga1 | Alignment | not modelled | 100.0 | 32 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 102 | d2cmda1 | Alignment | not modelled | 100.0 | 31 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 103 | d1gv0a1 | Alignment | not modelled | 100.0 | 34 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 104 | d1ez4a1 | Alignment | not modelled | 99.9  | 33 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 105 | d1y6ja1 | Alignment | not modelled | 99.9  | 35 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 106 | d1uxja1 | Alignment | not modelled | 99.9  | 34 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 107 | d1hyea1 | Alignment | not modelled | 99.9  | 37 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 108 | d1mlda1 | Alignment | not modelled | 99.9  | 29 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains<br>Family:LDH N-terminal domain-like |
| 109 | d1vjta1 | Alignment | not modelled | 99.8  | 18 | Fold:NAD(P)-binding Rossmann-fold domains<br>Superfamily:NAD(P)-binding Rossmann-fold domains                                      |

|     |                         |           |              |      |                                                                                                                                                                                                                                                                                                                                                                             |
|-----|-------------------------|-----------|--------------|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|     |                         |           |              |      | <b>Family:</b> LDH N-terminal domain-like                                                                                                                                                                                                                                                                                                                                   |
| 110 | <a href="#">c1zcjA_</a> | Alignment | not modelled | 99.3 | 19<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme;<br><b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase                                                                                                                                                                                  |
| 111 | <a href="#">c2x58B_</a> | Alignment | not modelled | 99.3 | 19<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme;<br><b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa                                                                                                                                                                                       |
| 112 | <a href="#">c3k6jA_</a> | Alignment | not modelled | 99.3 | 22<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein f01g10.3, confirmed by transcript evidence;<br><b>PDBTitle:</b> crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans                                                                                                                            |
| 113 | <a href="#">c3mogA_</a> | Alignment | not modelled | 99.3 | 22<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxybutyryl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655                                                                                                                         |
| 114 | <a href="#">c2wtbA_</a> | Alignment | not modelled | 99.3 | 16<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2);<br><b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2                                                                                                                                                                        |
| 115 | <a href="#">c2d3tB_</a> | Alignment | not modelled | 99.2 | 13<br><b>PDB header:</b> lyase, oxidoreductase/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit;<br><b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v                                                                                                                                |
| 116 | <a href="#">c4b3hA_</a> | Alignment | not modelled | 99.2 | 16<br><b>PDB header:</b> oxidoreductase/transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid beta-oxidation complex alpha-chain fadB;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex                                                                                                                     |
| 117 | <a href="#">c4e12A_</a> | Alignment | not modelled | 99.2 | 22<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> diketoreductase;<br><b>PDBTitle:</b> substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase                                                                                                                                                                         |
| 118 | <a href="#">c3rqsB_</a> | Alignment | not modelled | 99.2 | 18<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> hydroxyacyl-coenzyme a dehydrogenase, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership |
| 119 | <a href="#">c1m75B_</a> | Alignment | not modelled | 99.2 | 17<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase;<br><b>PDBTitle:</b> crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa                                                                                                                  |
| 120 | <a href="#">c2o3jC_</a> | Alignment | not modelled | 99.1 | 18<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase;<br><b>PDBTitle:</b> structure of caenorhabditis elegans udp-glucose dehydrogenase                                                                                                                                                                             |