Phyre2

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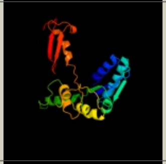
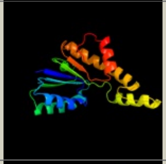
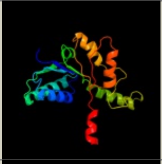
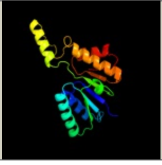
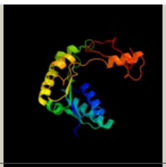
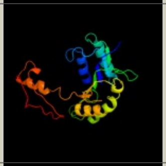
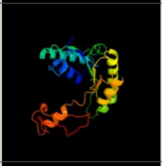
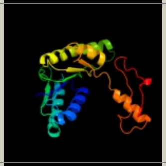
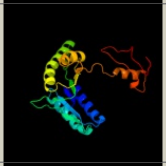
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u8xX_	Alignment		100.0	72	**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	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phospho-beta-glucosidase; **PDBTitle:** 2.3a crystal structure of phospho-beta-glucosidase
3	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
4	c1up6F_	Alignment		100.0	31	**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
5	c1vjtA_	Alignment		100.0	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
6	c1obbB_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-glucosidase; **PDBTitle:** alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
7	d1u8xx1	Alignment		100.0	75	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
8	d1s6ya1	Alignment		100.0	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
9	d1up7a1	Alignment		100.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
10	d1vjta1	Alignment		100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
11	d1obba1	Alignment		100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like

12	c1pzfD_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** t.gondii ldh1 ternary complex with apad+ and oxalate
13	c3p7mC_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
14	c2ldxA_	Alignment		100.0	13	**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	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
16	c2hjrK_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of cryptosporidium parvum malate2 dehydrogenase
17	c1ez4B_	Alignment		100.0	17	**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
18	c8ldhA_	Alignment		100.0	15	**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
19	c1lldA_	Alignment		100.0	18	**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
20	c3gviB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
21	c2fnzA_	Alignment	not modelled	100.0	17	**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)
22	c1a5zA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** lactate dehydrogenase from thermotoga maritima (tmldh)
23	c1ojuA_	Alignment	not modelled	100.0	12	**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.
24	c2v65A_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase a chain; **PDBTitle:** apo ldh from the psychrophile c. gunnari
25	c3tl2A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
26	c1u4sA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
27	c1hyhA_	Alignment	not modelled	100.0	14	**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
28	c3nepX_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** 1.55a resolution structure of malate dehydrogenase from

						salinibacter2 ruber
29	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
30	c2v6bB_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
31	c3pqeD_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
32	c1ur5C_	Alignment	not modelled	100.0	14	**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
33	c1hygA_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate/malate dehydrogenase; **PDBTitle:** crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
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	c2pwzG_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of the apo form of e.coli malate dehydrogenase
36	c2d4aC_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of the malate dehydrogenase from aeropyrum pernix
37	c1b8vA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (malate dehydrogenase); **PDBTitle:** malate dehydrogenase from aquaspirillum arcticum
38	c1gv1D_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
39	c1sevA_	Alignment	not modelled	100.0	21	**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
40	c1smkD_	Alignment	not modelled	100.0	21	**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
41	c1wziA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
42	c7mdhA_	Alignment	not modelled	100.0	16	**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	c2dfdD_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of human malate dehydrogenase type 2
44	d1i0za1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
45	c1ldbA_	Alignment	not modelled	100.0	15	**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
46	c1mldA_	Alignment	not modelled	100.0	20	**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
47	c5mdhB_	Alignment	not modelled	100.0	14	**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
48	c3fi9B_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
49	c3dl2A_	Alignment	not modelled	100.0	15	**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
50	d1o6za1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
51	d1i10a1	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
52	d5ldha1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like

53	c1y6jA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** l-lactate dehydrogenase from clostridium thermocellum cth-1135
54	d1pzga1	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
55	d2ldxa1	Alignment	not modelled	100.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
56	d1b8pa1	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
57	d9ldta1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
58	d1ojua1	Alignment	not modelled	100.0	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
59	d1t2da1	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
60	c2hlpB_	Alignment	not modelled	100.0	12	**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
61	d1ldma1	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
62	d1a5za1	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
63	d5mdha1	Alignment	not modelled	100.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
64	d1y7ta1	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
65	d1guza1	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
66	d1llda1	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
67	d1ldna1	Alignment	not modelled	100.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
68	d7mdha1	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
69	d2cmda1	Alignment	not modelled	100.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
70	d1hyha1	Alignment	not modelled	100.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
71	d1civa1	Alignment	not modelled	100.0	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	d1gv0a1	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
73	d1llca1	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
74	d1uxja1	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	d1y6ja1	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
76	d1ez4a1	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
77	d1hyea1	Alignment	not modelled	99.9	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
78	d1mlda1	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
79	c1mv8A_	Alignment	not modelled	99.2	17	**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
80	c1m75B_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase;

80	c1m75B_	Alignment	not modelled	99.2	16	**PDBTitle:** crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
81	d1dlja2	Alignment	not modelled	99.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
82	d1mv8a2	Alignment	not modelled	99.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
83	c2y0dB_	Alignment	not modelled	99.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
84	c3gg2B_	Alignment	not modelled	99.1	13	**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
85	c3plnA_	Alignment	not modelled	99.1	24	**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
86	c3prjB_	Alignment	not modelled	99.1	12	**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.
87	c2o3jC_	Alignment	not modelled	99.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
88	c2q3eH_	Alignment	not modelled	99.0	13	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
89	c2ep9A_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
90	c3mogA_	Alignment	not modelled	99.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxybutyryl-coa dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
91	d1txga2	Alignment	not modelled	99.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
92	c1zcjA_	Alignment	not modelled	98.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
93	d1f0ya2	Alignment	not modelled	98.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
94	c3k6jA_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
95	d1jaya_	Alignment	not modelled	98.9	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c2wtbA_	Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2); **PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2
97	c3k96B_	Alignment	not modelled	98.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
98	c1m67A_	Alignment	not modelled	98.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
99	c2x58B_	Alignment	not modelled	98.8	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
100	c1txgA_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
101	c1bg6A_	Alignment	not modelled	98.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; **PDBTitle:** crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
102	d1n1ea2	Alignment	not modelled	98.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
103	c1dliA_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
104	c1zejA_	Alignment	not modelled	98.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of the 3-hydroxyacyl-coa

						dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
105	c1yj8C_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
106	c3c7cB_	Alignment	not modelled	98.7	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
107	c3g79A_	Alignment	not modelled	98.7	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
108	c2d3tB_	Alignment	not modelled	98.7	14	**PDB header:**lyase, oxidoreductase/transferase **Chain:** B: **PDB Molecule:**fatty oxidation complex alpha subunit; **PDBTitle:** fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
109	d1wdka3	Alignment	not modelled	98.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	d1bg6a2	Alignment	not modelled	98.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
111	c1wpqB_	Alignment	not modelled	98.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad+], **PDBTitle:** ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
112	c3l6dB_	Alignment	not modelled	98.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
113	c3qhaB_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
114	c2qytA_	Alignment	not modelled	98.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
115	c3dttA_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp oxidoreductase; **PDBTitle:** crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
116	c2ew2B_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
117	c3d1lB_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
118	c3egoB_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
119	c1vpdA_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
120	c3ckyA_	Alignment	not modelled	98.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-hydroxymethyl glutarate dehydrogenase; **PDBTitle:** structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation