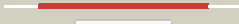



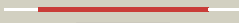

















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2150c_(ftsZ)_2408393_2409532
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	b2e0757adfb2c3e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w59B_	 Alignment		100.0	45	PDB header: cell division Chain: B: PDB Molecule: cell division protein ftsz homolog 1; PDBTitle: ftsz dimer, empty (m. jannaschii)
2	c1w5fA_	 Alignment		100.0	46	PDB header: cell division Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz, t7 mutated, domain swapped (t. maritima)
3	c2r6r1_	 Alignment		100.0	44	PDB header: cell cycle Chain: 1: PDB Molecule: cell division protein ftsz; PDBTitle: aquifex aeolicus ftsz
4	c2vawA_	 Alignment		100.0	52	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: ftsz pseudomonas aeruginosa gdp
5	c1ofuB_	 Alignment		100.0	52	PDB header: bacterial cell division inhibitor Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of sula:ftsZ from pseudomonas aeruginosa
6	c2vxyA_	 Alignment		100.0	66	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: the structure of ftsz from bacillus subtilis at 1.7a2 resolution
7	c4dxdA_	 Alignment		100.0	63	PDB header: cell cycle/inhibitor Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: staphylococcal aureus ftsz in complex with 723
8	c4e6eA_	 Alignment		100.0	80	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of a putative cell division protein ftsz (tfu_1113)2 from thermobifida fusca yx-er1 at 2.22 a resolution (psi community3 target, van wezel g.p.)
9	c2rhoB_	 Alignment		100.0	66	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: synthetic gene encoded bacillus subtilis ftsz ncs dimer with bound gdp2 and gtp-gamma-s
10	c2q1yB_	 Alignment		100.0	100	PDB header: cell cycle, signaling protein Chain: B: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
11	c4b45A_	 Alignment		100.0	23	PDB header: structural protein Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: cetz2 from haloferax volcanii - gtpgs bound protofilament

12	c4b46A_	Alignment		100.0	25	PDB header: structural protein Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: cetz1 from haloferax volcanii - gdp bound monomer
13	c5v68A_	Alignment		100.0	97	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsz; PDBTitle: crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis bounded via the t9 loop
14	c4ei8A_	Alignment		100.0	17	PDB header: replication Chain: A: PDB Molecule: plasmid replication protein repx; PDBTitle: crystal structure of bacillus cereus tubz, apo-form
15	c3v3tA_	Alignment		100.0	15	PDB header: structural protein Chain: A: PDB Molecule: cell division gtpase ftsz, diverged; PDBTitle: crystal structure of clostridium botulinum phage c-st tubz
16	c3zidB_	Alignment		100.0	23	PDB header: gtp-binding protein Chain: B: PDB Molecule: tubulin/fts, gtpase; PDBTitle: cetz from methanosaeta thermophila strain dsm 6194
17	d2vapa1	Alignment		100.0	50	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
18	c3rb8A_	Alignment		100.0	13	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of the phage tubulin phuz(semet)-gdp
19	d1ofua1	Alignment		100.0	57	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
20	c3m8kA_	Alignment		100.0	17	PDB header: structural protein Chain: A: PDB Molecule: fts, tubulin-related protein; PDBTitle: protein structure of type iii plasmid segregation tubz
21	d1rq2a1	Alignment	not modelled	100.0	99	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
22	d1w5fa1	Alignment	not modelled	100.0	53	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
23	c3zbqA_	Alignment	not modelled	100.0	16	PDB header: viral protein Chain: A: PDB Molecule: phikz039; PDBTitle: protofilament of tubz from bacteriophage phikz
24	d1w5fa2	Alignment	not modelled	100.0	35	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
25	d2vapa2	Alignment	not modelled	100.0	39	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
26	d1rq2a2	Alignment	not modelled	100.0	100	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
27	d1ofua2	Alignment	not modelled	100.0	44	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
28	c5flzC_	Alignment	not modelled	99.8	13	PDB header: cell cycle Chain: C: PDB Molecule: tubulin gamma chain; PDBTitle: cryo-em structure of gamma-tusc oligomers in a closed conformation PDB header: transport protein Chain: B: PDB Molecule: tubulin beta chain;

29	c2p4nB	Alignment	not modelled	99.7	15	PDBTitle: human monomeric kinesin (1bg2) and bovine tubulin (1jff) docked into2 the 9-angstrom cryo-em map of nucleotide-free kinesin complexed to3 the microtubule
30	c3edlA	Alignment	not modelled	99.7	15	PDB header: structural protein Chain: A: PDB Molecule: alpha-tubulin; PDBTitle: kinesin13-microtubule ring complex
31	c1z5wA	Alignment	not modelled	99.7	15	PDB header: structural protein Chain: A: PDB Molecule: tubulin gamma-1 chain; PDBTitle: crystal structure of gamma-tubulin bound to gtp
32	c2btqB	Alignment	not modelled	99.7	17	PDB header: structural protein Chain: B: PDB Molecule: tubulin btubb; PDBTitle: structure of btubab heterodimer from prosthecobacter dejongei
33	c2btoA	Alignment	not modelled	99.7	19	PDB header: cytoskeletal protein Chain: A: PDB Molecule: tubulin btuba; PDBTitle: structure of btuba from prosthecobacter dejongei
34	d1tubb1	Alignment	not modelled	99.6	19	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
35	d2btoa1	Alignment	not modelled	99.6	18	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
36	d1tuba1	Alignment	not modelled	99.6	16	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
37	d1i10a1	Alignment	not modelled	97.1	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
38	c2v65A	Alignment	not modelled	96.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase a chain; PDBTitle: apo ldh from the psychrophile c. gunnari
39	d1llda1	Alignment	not modelled	96.5	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
40	c1pzfD	Alignment	not modelled	96.5	23	PDB header: oxidoreductase Chain: D: PDB Molecule: lactate dehydrogenase; PDBTitle: t.gondii ldh1 ternary complex with apad+ and oxalate
41	c4bgvB	Alignment	not modelled	96.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: 1.8 a resolution structure of the malate dehydrogenase from2 picrophilus torridus in its apo form
42	c1ldbA	Alignment	not modelled	96.4	26	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
43	d1pzga1	Alignment	not modelled	96.4	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
44	c1ez4B	Alignment	not modelled	96.3	19	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
45	d9ldta1	Alignment	not modelled	96.2	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
46	d1ldna1	Alignment	not modelled	96.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
47	c3d0oA	Alignment	not modelled	96.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase 1; PDBTitle: crystal structure of lactate dehydrogenase from staphylococcus aureus
48	d1u8xx1	Alignment	not modelled	96.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
49	c1u4sA	Alignment	not modelled	96.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
50	c3pqeD	Alignment	not modelled	96.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
51	c3wsvC	Alignment	not modelled	96.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of minor l-lactate dehydrogenase from enterococcus2 mundtii in the ligands-unbound form
52	c6or9B	Alignment	not modelled	95.9	27	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: structure of l-lactate dehydrogenase from trichoplusia ni
53	d1ldma1	Alignment	not modelled	95.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
54	d2cmda1	Alignment	not modelled	95.7	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
55	c8ldhA	Alignment	not modelled	95.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: m4 apo-lactate dehydrogenase; PDBTitle: refined crystal structure of dogfish m4 apo-lactate dehydrogenase

56	c1a5zA	Alignment	not modelled	95.6	32	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: lactate dehydrogenase from thermotoga maritima (tmdlh)
57	d1y6ja1	Alignment	not modelled	95.6	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
58	d1i0za1	Alignment	not modelled	95.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
59	c3fefB	Alignment	not modelled	95.6	25	PDB header: hydrolase Chain: B: PDB Molecule: putative glucosidase lpld, alpha-galacturonidase; PDBTitle: crystal structure of putative glucosidase lpld from bacillus subtilis
60	c4ln1B	Alignment	not modelled	95.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase 1; PDBTitle: crystal structure of l-lactate dehydrogenase from bacillus cereus atcc2 14579 complexed with calcium, nysgrc target 029452
61	d2ldxa1	Alignment	not modelled	95.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
62	c1obbB	Alignment	not modelled	95.5	31	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase a, agla, from thermotoga maritima in complex with2 maltose and nad+
63	c6ct6B	Alignment	not modelled	95.5	21	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
64	c3dl2A	Alignment	not modelled	95.5	16	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
65	d1ez4a1	Alignment	not modelled	95.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
66	c1lldA	Alignment	not modelled	95.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
67	d1hyha1	Alignment	not modelled	95.3	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
68	d1mlda1	Alignment	not modelled	95.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
69	c3gucB	Alignment	not modelled	95.3	12	PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
70	c1hyhA	Alignment	not modelled	95.3	25	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
71	c3h9gA	Alignment	not modelled	95.1	20	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
72	c3p7mC	Alignment	not modelled	95.1	25	PDB header: oxidoreductase Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
73	d1a5za1	Alignment	not modelled	95.1	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
74	c4q3nA	Alignment	not modelled	95.0	23	PDB header: hydrolase Chain: A: PDB Molecule: mgs-m5; PDBTitle: crystal structure of mgs-m5, a lactate dehydrogenase enzyme from a2 medee basin deep-sea metagenome library
75	c2v6bB	Alignment	not modelled	95.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
76	c1y6jA	Alignment	not modelled	95.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: l-lactate dehydrogenase from clostridium thermocellum cth-1135
77	d1up7a1	Alignment	not modelled	95.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
78	c1hygA	Alignment	not modelled	94.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate/malate dehydrogenase; PDBTitle: crystal structure of mj0490 gene product, the family of2 lactate/malate dehydrogenase
79	c1ojuA	Alignment	not modelled	94.9	22	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.
80	d7mdha1	Alignment	not modelled	94.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
81	c3ic5A	Alignment	not modelled	94.8	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine

						dehydrogenase from ruegeria2 pomeroyi.
82	c2e37B	Alignment	not modelled	94.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: l-lactate dehydrogenase; PDBTitle: structure of tt0471 protein from thermus thermophilus
83	c2dfdD	Alignment	not modelled	94.7	20	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of human malate dehydrogenase type 2
84	d5ldha1	Alignment	not modelled	94.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
85	d1obba1	Alignment	not modelled	94.7	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
86	c2hjrK	Alignment	not modelled	94.6	26	PDB header: oxidoreductase Chain: K: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of cryptosporidium parvum malate2 dehydrogenase
87	c4plcA	Alignment	not modelled	94.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of ancestral apicomplexan lactate dehydrogenase with2 malate.
88	d1jw9b	Alignment	not modelled	94.2	22	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
89	d1p3da1	Alignment	not modelled	94.2	24	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
90	d1ojua1	Alignment	not modelled	94.1	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
91	c1u8xX	Alignment	not modelled	94.0	22	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
92	c2ldxA	Alignment	not modelled	93.9	24	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
93	c1gv1D	Alignment	not modelled	93.8	24	PDB header: oxidoreductase Chain: D: PDB Molecule: malate dehydrogenase; PDBTitle: structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
94	d1gv0a1	Alignment	not modelled	93.7	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
95	c1mldA	Alignment	not modelled	93.6	19	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
96	d1t2da1	Alignment	not modelled	93.6	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
97	d1luxj1	Alignment	not modelled	93.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
98	d1pjqa1	Alignment	not modelled	93.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
99	c3gviB	Alignment	not modelled	93.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
100	d1s6ya1	Alignment	not modelled	93.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
101	c3triB	Alignment	not modelled	93.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
102	c1ur5C	Alignment	not modelled	93.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: malate dehydrogenase; PDBTitle: stabilization of a tetrameric malate dehydrogenase by introduction of2 a disulfide bridge at the dimer/dimer interface
103	c6qssA	Alignment	not modelled	93.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of iginococcus islandicus malate dehydrogenase co-2 crystallized with 10 mm tb-xo4
104	d1guza1	Alignment	not modelled	93.3	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
105	c4uupB	Alignment	not modelled	93.3	24	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: reconstructed ancestral trichomonad malate dehydrogenase in2 complex with nadh, so4, and po4
106	c6ihdA	Alignment	not modelled	93.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from metallosphaera sedula
107	c1smkD	Alignment	not modelled	93.0	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
108	c1sevA_	Alignment	not modelled	93.0	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
109	c1s6yA_	Alignment	not modelled	93.0	27	PDB header: hydrolase Chain: A: PDB Molecule: 6-phospho-beta-glucosidase; PDBTitle: 2.3a crystal structure of phospho-beta-glucosidase
110	d1llca1	Alignment	not modelled	93.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
111	c5nfrl_	Alignment	not modelled	92.9	23	PDB header: oxidoreductase Chain: I: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from plasmodium falciparum2 (pfmdh)
112	c6pblA_	Alignment	not modelled	92.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from legionella pneumophila2 philadelphia 1
113	c2axqA_	Alignment	not modelled	92.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
114	c2fnzA_	Alignment	not modelled	92.7	20	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)
115	c1up6F_	Alignment	not modelled	92.7	24	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
116	c5I78A_	Alignment	not modelled	92.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
117	d1y7ta1	Alignment	not modelled	92.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
118	c4tvoB_	Alignment	not modelled	92.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: structure of malate dehydrogenase from mycobacterium tuberculosis
119	c2nvuB_	Alignment	not modelled	92.4	24	PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex
120	c1y8qD_	Alignment	not modelled	92.3	21	PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex