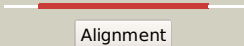

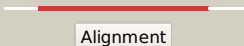

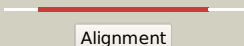







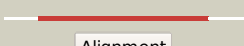




















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2332_(mez)_2605118_2606764
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	be896bc5cb4692d3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5ou5C_</a>	 Alignment		100.0	40	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> malic enzyme; <b>PDBTitle:</b> crystal structure of maize chloroplastic photosynthetic nadp(+)-2 dependent malic enzyme
2	<a href="#">c3wjaA_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent malic enzyme; <b>PDBTitle:</b> the crystal structure of human cytosolic nadp(+)-dependent malic2 enzyme in apo form
3	<a href="#">c1gz3B_</a>	 Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent malic enzyme, mitochondrial; <b>PDBTitle:</b> molecular mechanism for the regulation of human mitochondrial nad(p)+2 dependent malic enzyme by atp and fumarate
4	<a href="#">c1o0sB_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent malic enzyme; <b>PDBTitle:</b> crystal structure of ascaris suum malic enzyme complexed with nadh
5	<a href="#">c1qr6A_</a>	 Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malic enzyme 2; <b>PDBTitle:</b> human mitochondrial nad(p)-dependent malic enzyme
6	<a href="#">c2aw5A_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-dependent malic enzyme; <b>PDBTitle:</b> crystal structure of a human malic enzyme
7	<a href="#">c6c7nD_</a>	 Alignment		100.0	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malic enzyme; <b>PDBTitle:</b> monoclinic form of malic enzyme from sorghum at 2 angstroms resolution
8	<a href="#">c3nv9A_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malic enzyme; <b>PDBTitle:</b> crystal structure of entamoeba histolytica malic enzyme
9	<a href="#">c5ceeA_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent malic enzyme; <b>PDBTitle:</b> malic enzyme from candidatus phytoplasma aywb in complex with nad and2 mg2+
10	<a href="#">c1ww8A_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate oxidoreductase; <b>PDBTitle:</b> crystal structure of malic enzyme from pyrococcus2 horikoshii ot3
11	<a href="#">c1vl6C_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-dependent malic enzyme (tm0542) from2 thermotoga maritima at 2.61 a resolution

12	<a href="#">c2a9fB</a>	Alignment		100.0	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative malic enzyme ((s)-malate:nad+ oxidoreductase <b>PDBTitle:</b> crystal structure of a putative malic enzyme ((s)-malate:nad+2 oxidoreductase (decarboxylating))
13	<a href="#">d1gq2a2</a>	Alignment		100.0	43	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
14	<a href="#">d1pj3a2</a>	Alignment		100.0	39	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
15	<a href="#">d1o0sa2</a>	Alignment		100.0	47	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
16	<a href="#">d1o0sa1</a>	Alignment		100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
17	<a href="#">d1gq2a1</a>	Alignment		100.0	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
18	<a href="#">d1pj3a1</a>	Alignment		100.0	32	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
19	<a href="#">d1v6a1</a>	Alignment		100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
20	<a href="#">d1v6a2</a>	Alignment		100.0	26	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Malic enzyme N-domain
21	<a href="#">d1euza1</a>	Alignment	not modelled	98.4	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
22	<a href="#">d1li4a1</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
23	<a href="#">c6f3oC</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
24	<a href="#">c3n58D</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
25	<a href="#">c3x2fA</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> a thermophilic s-adenosylhomocysteine hydrolase
26	<a href="#">c5v96A</a>	Alignment	not modelled	97.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-l-homocysteine hydrolase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
27	<a href="#">d1v8ba1</a>	Alignment	not modelled	97.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
28	<a href="#">d1v9la1</a>	Alignment	not modelled	97.5	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
						<b>PDB header:</b> hydrolase

29	<a href="#">c1d4fD_</a>	Alignment	not modelled	97.5	13	<b>Chain:</b> D: <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
30	<a href="#">c3d4oA_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
31	<a href="#">c3d64A_</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
32	<a href="#">c2rirA_</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
33	<a href="#">d1uxja1</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
34	<a href="#">c3r3jC_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> kinetic and structural characterization of plasmodium falciparum2 glutamate dehydrogenase 2
35	<a href="#">c2bmaA_</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase (nadp+); <b>PDBTitle:</b> the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
36	<a href="#">c4n7rB_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> glutamyl-trna reductase 1, chloroplastic; <b>PDBTitle:</b> crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
37	<a href="#">c3dhyC_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
38	<a href="#">d1gpja2</a>	Alignment	not modelled	97.1	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
39	<a href="#">c6aphA_</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
40	<a href="#">c3gvpB_</a>	Alignment	not modelled	97.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteinase 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteinase 3
41	<a href="#">d9ldta1</a>	Alignment	not modelled	97.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
42	<a href="#">d1ldna1</a>	Alignment	not modelled	97.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
43	<a href="#">c3fefB_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glucosidase lpld, alpha-galacturonidase; <b>PDBTitle:</b> crystal structure of putative glucosidase lpld from bacillus subtilis
44	<a href="#">c1gpiA_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
45	<a href="#">d1u8xx1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
46	<a href="#">d1llda1</a>	Alignment	not modelled	96.9	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
47	<a href="#">d1t2da1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
48	<a href="#">d1pzga1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
49	<a href="#">c4xgiA_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase from burkholderia2 thailandensis
50	<a href="#">c1pzfD_</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> t.gondii ldh1 ternary complex with apad+ and oxalate
51	<a href="#">d1vi2a1</a>	Alignment	not modelled	96.8	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
52	<a href="#">d1l7da1</a>	Alignment	not modelled	96.8	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
53	<a href="#">c3sboA_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp-specific glutamate dehydrogenase; <b>PDBTitle:</b> structure of e.coli gdh from native source
54	<a href="#">c3d0oA_</a>	Alignment	not modelled	96.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from staphylococcus aureus <b>PDB header:</b> hydrolase

55	<a href="#">c1obbB</a>	Alignment	not modelled	96.6	22	<b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase a, agla, from thermotoga maritima in complex with2 maltose and nad+
56	<a href="#">d1i10a1</a>	Alignment	not modelled	96.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
57	<a href="#">d1bvua1</a>	Alignment	not modelled	96.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
58	<a href="#">c3aogA</a>	Alignment	not modelled	96.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
59	<a href="#">c5hm8C</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
60	<a href="#">c2ep9A</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-gulonate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
61	<a href="#">d1hyha1</a>	Alignment	not modelled	96.5	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
62	<a href="#">c2fnzA</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
63	<a href="#">c3tumA</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase family protein; <b>PDBTitle:</b> 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
64	<a href="#">c2eezG</a>	Alignment	not modelled	96.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
65	<a href="#">c4om8B</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 5-formyl-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
66	<a href="#">d1ez4a1</a>	Alignment	not modelled	96.3	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
67	<a href="#">c1v9IA</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
68	<a href="#">c5nfrl</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from plasmodium falciparum2 (pfmdh)
69	<a href="#">c1v8bA</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
70	<a href="#">c2v6bB</a>	Alignment	not modelled	96.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
71	<a href="#">d1s6ya1</a>	Alignment	not modelled	96.2	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
72	<a href="#">c8ldhA</a>	Alignment	not modelled	96.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate dehydrogenase
73	<a href="#">c4q3nA</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgs-m5; <b>PDBTitle:</b> crystal structure of mgs-m5, a lactate dehydrogenase enzyme from a2 medee basin deep-sea metagenome library
74	<a href="#">d1vjta1</a>	Alignment	not modelled	96.1	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
75	<a href="#">c1pjcA</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-alanine dehydrogenase); <b>PDBTitle:</b> l-alanine dehydrogenase complexed with nad
76	<a href="#">c1u8xX</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> maltose-6'-phosphate glucosidase; <b>PDBTitle:</b> crystal structure of glva from bacillus subtilis, a metal-requiring,2 nad-dependent 6-phospho-alpha-glucosidase
77	<a href="#">c3p2yA</a>	Alignment	not modelled	96.1	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine dehydrogenase/pyridine nucleotide transhydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
78	<a href="#">d1a4ia1</a>	Alignment	not modelled	96.1	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
79	<a href="#">d1gtma1</a>	Alignment	not modelled	96.1	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
80	<a href="#">d1a5za1</a>	Alignment	not modelled	96.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

						<b>Family:</b> LDH N-terminal domain-like
81	<a href="#">c1nr1A</a>	Alignment	not modelled	96.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of the r463a mutant of human glutamate dehydrogenase
82	<a href="#">c6ct6B</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from eimeria maxima with2 nadh and oxamate
83	<a href="#">d1i0za1</a>	Alignment	not modelled	96.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
84	<a href="#">c4e12A</a>	Alignment	not modelled	96.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diketoreductase; <b>PDBTitle:</b> substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
85	<a href="#">c1ur5C</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> stabilization of a tetrameric malate dehydrogenase by introduction of2 a disulfide bridge at the dimer/dimer interface
86	<a href="#">d5ldha1</a>	Alignment	not modelled	96.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
87	<a href="#">d1obba1</a>	Alignment	not modelled	95.9	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
88	<a href="#">d1llca1</a>	Alignment	not modelled	95.9	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
89	<a href="#">c5xviA</a>	Alignment	not modelled	95.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspergillus niger apo- glutamate dehydrogenase
90	<a href="#">c3aoeC</a>	Alignment	not modelled	95.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
91	<a href="#">c4d3fB</a>	Alignment	not modelled	95.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> bcsired from bacillus cereus in complex with nadph
92	<a href="#">d1b0aa1</a>	Alignment	not modelled	95.8	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
93	<a href="#">c2hjrK</a>	Alignment	not modelled	95.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase
94	<a href="#">d1ldma1</a>	Alignment	not modelled	95.8	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
95	<a href="#">d1pjca1</a>	Alignment	not modelled	95.7	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
96	<a href="#">c3i07B</a>	Alignment	not modelled	95.7	23	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
97	<a href="#">c3tozA</a>	Alignment	not modelled	95.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
98	<a href="#">c1hrdA</a>	Alignment	not modelled	95.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> glutamate dehydrogenase
99	<a href="#">c1a4iB</a>	Alignment	not modelled	95.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
100	<a href="#">c3oneA</a>	Alignment	not modelled	95.6	14	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
101	<a href="#">d1ojua1</a>	Alignment	not modelled	95.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
102	<a href="#">d1b26a1</a>	Alignment	not modelled	95.5	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
103	<a href="#">c4dioB</a>	Alignment	not modelled	95.5	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit alpha part 1; <b>PDBTitle:</b> the crystal structure of transhydrogenase from sinorhizobium melloti
104	<a href="#">c1ez4B</a>	Alignment	not modelled	95.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
105	<a href="#">c1up6F</a>	Alignment	not modelled	95.5	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> 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 <b>PDB header:</b> oxidoreductase



106	<a href="#">c1u4sA_</a>	Alignment	not modelled	95.5	16	<b>Chain:</b> A; <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid
107	<a href="#">c6ihdA_</a>	Alignment	not modelled	95.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of malate dehydrogenase from metallosphaera sedula
108	<a href="#">c4plcA_</a>	Alignment	not modelled	95.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of ancestral apicomplexan lactate dehydrogenase with2 malate.
109	<a href="#">c2nloA_</a>	Alignment	not modelled	95.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> shikimate dehydrogenase; <b>PDBTitle:</b> crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
110	<a href="#">d1y6ja1</a>	Alignment	not modelled	95.4	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">c1lldA_</a>	Alignment	not modelled	95.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
112	<a href="#">c1wwkA_</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
113	<a href="#">c3pqcD_</a>	Alignment	not modelled	95.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation
114	<a href="#">c4a5oB_</a>	Alignment	not modelled	95.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
115	<a href="#">c2ldxA_</a>	Alignment	not modelled	95.3	20	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A; <b>PDB Molecule:</b> apo-lactate dehydrogenase; <b>PDBTitle:</b> characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
116	<a href="#">d2cmda1</a>	Alignment	not modelled	95.2	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
117	<a href="#">c4bgvB_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> 1.8 a resolution structure of the malate dehydrogenase from2 picophilus torridus in its apo form
118	<a href="#">c4m1qB_</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-lactate dehydrogenase from bacillus2 selenitireducens mls10, nysgrc target 029814.
119	<a href="#">c2tmgD_</a>	Alignment	not modelled	95.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> protein (glutamate dehydrogenase); <b>PDBTitle:</b> thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
120	<a href="#">c6hrdD_</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of m. tuberculosis fadb2 (rv0468)