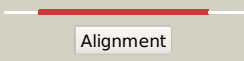

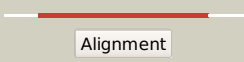

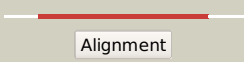
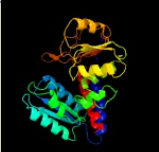
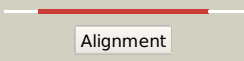

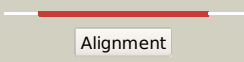

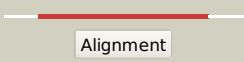
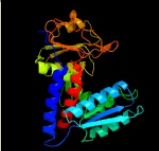
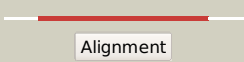

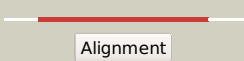

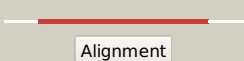

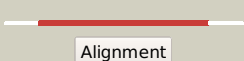

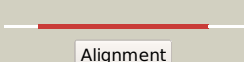
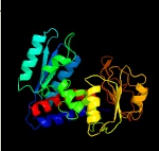


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3356c_(foID)_3769975_3770820
 Date Fri Aug 9 18:20:01 BST 2019
 Unique Job ID 613bcc157a5f8a9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c2xB_			100.0	100	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase from mycobacterium tuberculosis
2	c4b4uB_			100.0	45	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of acinetobacter baumannii n5,2 n10-methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor
3	c4cxA_			100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: c-1-tetrahydrofolate synthase, cytoplasmic, putative; PDBTitle: the crystal structure of trypanosoma brucei n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)3 complexed with nadp cofactor and inhibitor
4	c1b0aA_			100.0	43	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
5	c4a5oB_			100.0	46	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
6	c3i07B_			100.0	42	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
7	c1a4iB_			100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
8	c6apeA_			100.0	39	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional protein fold from helicobacter2 pylori
9	c3p2oA_			100.0	42	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
10	c3p2oB_			100.0	42	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
11	c3nglA_			100.0	36	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum

12	c5zf1A_	Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate dehydrogenase; PDBTitle: molecular structure of a novel 5,10-methylenetetrahydrofolate2 dehydrogenase from the silkworm, bombyx mori
13	c5tc4A_	Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: bifunctional methylenetetrahydrofolate PDBTitle: crystal structure of human mitochondrial methylenetetrahydrofolate2 dehydrogenase-cyclohydrolase (mthfd2) in complex with ly345899 and3 cofactors
14	c4a26B_	Alignment		100.0	47	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
15	c5nhsB_	Alignment		100.0	46	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
16	c1edzA_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate dehydrogenase; PDBTitle: structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
17	d1b0aa1	Alignment		100.0	42	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
18	d1a4ia1	Alignment		100.0	43	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
19	d1edza2	Alignment		100.0	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
20	d1edza1	Alignment		100.0	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
21	d1b0aa2	Alignment	not modelled	100.0	45	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
22	d1a4ia2	Alignment	not modelled	100.0	30	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
23	c3d4oA_	Alignment	not modelled	99.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
24	c1v8bA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
25	c2rirA_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
26	c3oneA_	Alignment	not modelled	99.5	19	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
27	c3x2fA_	Alignment	not modelled	99.1	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
28	c6aphA_	Alignment	not modelled	99.1	24	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
						Fold: NAD(P)-binding Rossmann-fold domains

29	d1li4a1	Alignment	not modelled	99.0	22	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
30	d1v8ba1	Alignment	not modelled	99.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
31	c1d4fD	Alignment	not modelled	98.9	22	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
32	c3gvpB	Alignment	not modelled	98.9	27	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
33	c3d64A	Alignment	not modelled	98.8	23	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
34	c3n58D	Alignment	not modelled	98.8	29	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
35	c5v96A	Alignment	not modelled	98.7	28	PDB header: hydrolase Chain: A: PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
36	c1gpiA	Alignment	not modelled	98.7	26	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
37	d1gpi2	Alignment	not modelled	98.5	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
38	c3dhyC	Alignment	not modelled	98.5	24	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
39	c5hm8C	Alignment	not modelled	98.5	26	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
40	c2dbqA	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
41	c4njmA	Alignment	not modelled	98.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
42	c6f3oC	Alignment	not modelled	98.3	26	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
43	c3oj0A	Alignment	not modelled	98.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
44	c2ekIA	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
45	c3fbtB	Alignment	not modelled	98.2	18	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
46	c6ih2B	Alignment	not modelled	98.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
47	c3tozA	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad.
48	c2j6iC	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
49	c4n7rB	Alignment	not modelled	98.2	26	PDB header: oxidoreductase/protein binding Chain: B: PDB Molecule: glutamyl-trna reductase 1, chloroplastic; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
50	c3pgjB	Alignment	not modelled	98.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
51	c1xdwA	Alignment	not modelled	98.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
52	c2o4cB	Alignment	not modelled	98.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
53	c2nloA	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from

						corynebacterium2 glutamicum
54	c3n7uD_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
55	c1p74B_	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from haemophilus2 influenzae
56	c2hk8B_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
57	d1l7da1	Alignment	not modelled	98.1	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
58	c3tumA_	Alignment	not modelled	98.1	29	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+
59	c2eggA_	Alignment	not modelled	98.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus
60	c3o8qB_	Alignment	not modelled	98.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
61	c3oetF_	Alignment	not modelled	98.0	25	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
62	c2cukC_	Alignment	not modelled	98.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
63	c3donA_	Alignment	not modelled	97.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
64	c4mp6A_	Alignment	not modelled	97.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative ornithine cyclodeaminase; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbnb bound to citrate2 and nad+
65	c2gcgB_	Alignment	not modelled	97.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
66	c1nvtA_	Alignment	not modelled	97.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
67	c5j23D_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-hydroxyacid dehydrogenase; PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium meliloti in complex3 with 2'-phospho-adp-ribose
68	c1gdhA_	Alignment	not modelled	97.9	13	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
69	c1nytC_	Alignment	not modelled	97.9	19	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
70	c4n18A_	Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from klebsiella pneumoniae 342
71	c3p2yA_	Alignment	not modelled	97.8	29	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
72	c2eezG_	Alignment	not modelled	97.8	29	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
73	d1pjca1	Alignment	not modelled	97.8	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
74	c4e5kC_	Alignment	not modelled	97.8	23	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
75	c5dt9A_	Alignment	not modelled	97.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
76	d1ygya1	Alignment	not modelled	97.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
77	c1j4aA_	Alignment	not modelled	97.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus

78	c5tx7A	Alignment	not modelled	97.8	27	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
79	c3bazA	Alignment	not modelled	97.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
80	c1wwkA	Alignment	not modelled	97.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
81	d1gdha1	Alignment	not modelled	97.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
82	d1vi2a1	Alignment	not modelled	97.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
83	c4dioB	Alignment	not modelled	97.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium meliloti
84	d1mx3a1	Alignment	not modelled	97.7	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
85	c2g76A	Alignment	not modelled	97.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
86	c3pwzA	Alignment	not modelled	97.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
87	d2naca1	Alignment	not modelled	97.6	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
88	c3wnvA	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
89	c4xa8A	Alignment	not modelled	97.6	27	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from xanthobacter autotrophicus py2
90	c5mh5A	Alignment	not modelled	97.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase; PDBTitle: d-2-hydroxyacid dehydrogenases (d2-dhd) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
91	c3evtA	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
92	c2omeA	Alignment	not modelled	97.6	25	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
93	d1nvtA1	Alignment	not modelled	97.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
94	d1qp8a1	Alignment	not modelled	97.6	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
95	d1j4aa1	Alignment	not modelled	97.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
96	c2ev9B	Alignment	not modelled	97.6	22	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from thermus2 thermophilus hb8 in complex with nadp(h) and shikimate
97	c3wvzB	Alignment	not modelled	97.6	30	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
98	c3fn4A	Alignment	not modelled	97.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
99	c4zqbB	Alignment	not modelled	97.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent dehydrogenase; PDBTitle: crystal structure of nadp-dependent dehydrogenase from2 rhodobactersphaeroides in complex with nadp and sulfate
100	c4weqA	Alignment	not modelled	97.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent dehydrogenase; PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxyppyruvate2 reductase smc02828 (smghra) from sinorhizobium meliloti in complex3 with nadp and sulfate
101	c4g2nA	Alignment	not modelled	97.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
						PDB header: oxidoreductase

102	c3hg7A_	Alignment	not modelled	97.5	27	Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 family protein from aeromonas salmonicida subsp. salmonicida a449
103	d1dxya1	Alignment	not modelled	97.5	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
104	c3gvxA_	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
105	c3kboB_	Alignment	not modelled	97.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate/hydroxypyruvate reductase a; PDBTitle: 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
106	c4a7pA_	Alignment	not modelled	97.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized udgd, udp-glucose dehydrogenase from sphingomonas2 elodea
107	c2pi1C_	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
108	c4lswA_	Alignment	not modelled	97.5	18	PDB header: hydrolase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase protein; PDBTitle: crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
109	c2bruB_	Alignment	not modelled	97.4	26	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
110	c1pjcA_	Alignment	not modelled	97.4	26	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
111	d1nyta1	Alignment	not modelled	97.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
112	c3k5pA_	Alignment	not modelled	97.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
113	c3wwyA_	Alignment	not modelled	97.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
114	c4omuA_	Alignment	not modelled	97.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida
115	c2nacA_	Alignment	not modelled	97.4	14	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
116	c4zgsE_	Alignment	not modelled	97.4	21	PDB header: oxidoreductase Chain: E: PDB Molecule: putative d-lactate dehydrogenase; PDBTitle: identification of the pyruvate reductase of chlamydomonas reinhardtii
117	c4cukA_	Alignment	not modelled	97.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
118	c4s1vD_	Alignment	not modelled	97.3	12	PDB header: oxidoreductase Chain: D: PDB Molecule: d-3-phosphoglycerate dehydrogenase-related protein; PDBTitle: crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
119	c2yq4C_	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: C: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase; PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
120	c1luaA_	Alignment	not modelled	97.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp