



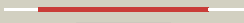






















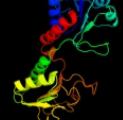


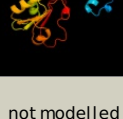


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1b0aA_	 Alignment		100.0	100	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
2	c4a5oB_	 Alignment		100.0	67	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
3	c2c2xB_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase- PDBTitle: three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
4	c3I07B_	 Alignment		100.0	53	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
5	c1a4iB_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
6	c3p2oB_	 Alignment		100.0	53	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
7	c3p2oA_	 Alignment		100.0	53	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
8	c3nglA_	 Alignment		100.0	35	PDB header: oxidoreductase, hydrolase Chain: A: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
9	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
10	c1edzA_	 Alignment		100.0	28	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
11	d1b0aa1	 Alignment		100.0	100	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain

12	d1a4ia1	Alignment		100.0	47	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
13	d1edza1	Alignment		100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
14	d1edza2	Alignment		100.0	22	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
15	d1b0aa2	Alignment		100.0	100	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
16	d1a4ia2	Alignment		100.0	40	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Tetrahydrofolate dehydrogenase/cyclohydrolase
17	c3d4oA	Alignment		100.0	19	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
18	c2rirA	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
19	c1v8bA	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
20	c3oneA	Alignment		99.6	20	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
21	d1li4a1	Alignment	not modelled	99.3	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
22	c3gvpB	Alignment	not modelled	99.3	23	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
23	d1v8ba1	Alignment	not modelled	99.3	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
24	c1d4fD	Alignment	not modelled	99.3	22	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
25	c3d64A	Alignment	not modelled	99.2	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
26	c3n58D	Alignment	not modelled	99.2	26	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
27	c3dhyc	Alignment	not modelled	99.1	20	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
28	c2eklA	Alignment	not modelled	98.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii

29	c3pgjB_	Alignment	not modelled	98.9	20	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
30	c2j6iC_	Alignment	not modelled	98.9	20	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
31	c3o8qB_	Alignment	not modelled	98.8	20	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
32	c1gpjA_	Alignment	not modelled	98.8	27	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
33	c2nloA_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum
34	c2hk8B_	Alignment	not modelled	98.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
35	c3n7uD_	Alignment	not modelled	98.8	18	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
36	c2cukC_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
37	c3fbtB_	Alignment	not modelled	98.8	19	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase PDBTitle: crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
38	c2dbqA_	Alignment	not modelled	98.7	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)
39	c2eggA_	Alignment	not modelled	98.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
40	c1gdhA_	Alignment	not modelled	98.7	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
41	c3tozA_	Alignment	not modelled	98.7	18	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.
42	c3donA_	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
43	d1l7da1	Alignment	not modelled	98.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
44	c1p74B_	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
45	d1gpja2	Alignment	not modelled	98.7	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
46	c3bazA_	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
47	c2pi1C_	Alignment	not modelled	98.6	22	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
48	c1pjca_	Alignment	not modelled	98.6	31	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
49	c3evtA_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
50	c3k5pA_	Alignment	not modelled	98.6	20	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
51	d1pjca1	Alignment	not modelled	98.6	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
52	c1wwkA_	Alignment	not modelled	98.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
53	c1nytC_	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+

54	c2o4cB	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
55	d1ygya1	Alignment	not modelled	98.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
56	c2eezG	Alignment	not modelled	98.6	34	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from thermophilus
57	c3oj0A	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
58	c1xdwA	Alignment	not modelled	98.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
59	c1qp8A	Alignment	not modelled	98.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
60	c3oetF	Alignment	not modelled	98.5	26	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
61	c2ev9B	Alignment	not modelled	98.5	23	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
62	d1mx3a1	Alignment	not modelled	98.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
63	c1dxyA	Alignment	not modelled	98.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxysicaproate dehydrogenase; PDBTitle: structure of d-2-hydroxysicaproate dehydrogenase
64	c3pwzA	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida
65	d1j4aa1	Alignment	not modelled	98.5	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
66	c2g76A	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
67	c1nvtA	Alignment	not modelled	98.5	25	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5'-dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe or2 mj1084) in complex with nadp+
68	c3p2yA	Alignment	not modelled	98.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
69	d1dxya1	Alignment	not modelled	98.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
70	d1vi2a1	Alignment	not modelled	98.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
71	d1qp8a1	Alignment	not modelled	98.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
72	d1gdha1	Alignment	not modelled	98.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
73	c2gcgB	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
74	c1l7eC	Alignment	not modelled	98.5	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
75	c2bruB	Alignment	not modelled	98.4	17	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
76	d2dlda1	Alignment	not modelled	98.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
77	d1npta1	Alignment	not modelled	98.4	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
78	d1npta1	Alignment	not modelled	98.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
79	d2naca1	Alignment	not modelled	98.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

						Family: Formate/glycerate dehydrogenases, NAD-domain
80	c1j4aA_	Alignment	not modelled	98.4	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
81	c3hg7A_	Alignment	not modelled	98.4	18	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 aeromonas salmonicida subsp. salmonicida a449
82	c3gvxA_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
83	c2nacA_	Alignment	not modelled	98.4	17	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
84	c3gg9C_	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
85	c1ybaC_	Alignment	not modelled	98.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
86	c1vgvA_	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
87	c2omeA_	Alignment	not modelled	98.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
88	c3kboB_	Alignment	not modelled	98.3	22	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
89	c1vi2B_	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad
90	c1npyA_	Alignment	not modelled	98.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like PDBTitle: structure of shikimate 5-dehydrogenase-like protein hi0607
91	c2w2kB_	Alignment	not modelled	98.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: d-mandelate dehydrogenase; PDBTitle: crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
92	d1sc6a1	Alignment	not modelled	98.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
93	c2vhyB_	Alignment	not modelled	98.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
94	c2d0iC_	Alignment	not modelled	98.1	25	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
95	d1p77a1	Alignment	not modelled	98.1	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
96	c3u62A_	Alignment	not modelled	98.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima
97	c2ef0A_	Alignment	not modelled	98.0	17	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
98	c2p2gD_	Alignment	not modelled	98.0	17	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
99	c1luaA_	Alignment	not modelled	98.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: methylene tetrahydromethanopterin dehydrogenase; PDBTitle: structure of methylene-tetrahydromethanopterin dehydrogenase from2 methylobacterium extorquens am1 complexed with nadp
100	d1np3a2	Alignment	not modelled	98.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
101	d1npya1	Alignment	not modelled	97.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
102	c3c24A_	Alignment	not modelled	97.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
103	c1vlvA_	Alignment	not modelled	97.9	16	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase

					(tm1097) from2 thermotoga maritima at 2.25 a resolution
104	c2f00A_	Alignment	not modelled	97.8	14 PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
105	d1luaa1	Alignment	not modelled	97.8	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
106	c1fvoB_	Alignment	not modelled	97.7	16 PDB header: transferase Chain: B: PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
107	c1np3B_	Alignment	not modelled	97.7	21 PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
108	c2q3eH_	Alignment	not modelled	97.7	17 PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
109	c3gd5D_	Alignment	not modelled	97.7	14 PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
110	c2y0dB_	Alignment	not modelled	97.6	23 PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
111	c3sdsA_	Alignment	not modelled	97.6	13 PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
112	c3cumA_	Alignment	not modelled	97.5	26 PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
113	c1ortD_	Alignment	not modelled	97.5	13 PDB header: transferase Chain: D: PDB Molecule: ornithine transcarbamoylase; PDBTitle: ornithine transcarbamoylase from pseudomonas aeruginosa
114	c2otcA_	Alignment	not modelled	97.5	17 PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
115	c1a1sA_	Alignment	not modelled	97.5	14 PDB header: transcarbamylase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
116	c2pv7B_	Alignment	not modelled	97.5	19 PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
117	c3gg2B_	Alignment	not modelled	97.5	19 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
118	c3dfzB_	Alignment	not modelled	97.5	15 PDB header: oxidoreductase Chain: B: PDB Molecule: precorrin-2 dehydrogenase; PDBTitle: sirc, precorrin-2 dehydrogenase
119	c3g79A_	Alignment	not modelled	97.4	31 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
120	c3ojlA_	Alignment	not modelled	97.4	21 PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus