



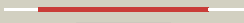



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bmaA_	 Alignment		100.0	52	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase (nadp+); PDBTitle: the crystal structure of plasmodium falciparum glutamate2 dehydrogenase, a putative target for novel antimalarial3 drugs
2	c1hrdA_	 Alignment		100.0	53	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: glutamate dehydrogenase
3	c3aoeC_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: C: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of hetero-hexameric glutamate dehydrogenase from2 thermus thermophilus (leu bound form)
4	c3aogA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase (gdhb) from thermus2 thermophilus (glu bound form)
5	c1v9lA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase; PDBTitle: l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
6	c1bvuf_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: F: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: glutamate dehydrogenase from thermococcus litoralis
7	c2tmgD_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: protein (glutamate dehydrogenase); PDBTitle: thermotoga maritima glutamate dehydrogenase mutant s128r,2 t158e, n117r, s160e
8	c1nr1A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamate dehydrogenase 1; PDBTitle: crystal structure of the r463a mutant of human glutamate2 dehydrogenase
9	c3k8zD_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of gudb1 a decryptified secondary glutamate2 dehydrogenase from b. subtilis
10	c2yfqA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-specific glutamate dehydrogenase; PDBTitle: crystal structure of glutamate dehydrogenase from2 peptoniphilus asaccharolyticus
11	c1bxgA_	 Alignment		100.0	24	PDB header: amino acid dehydrogenase Chain: A: PDB Molecule: phenylalanine dehydrogenase; PDBTitle: phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate

12	c1lehB_	Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: leucine dehydrogenase; PDBTitle: leucine dehydrogenase from bacillus sphaericus
13	dlbgva1	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
14	dlhwxal	Alignment		100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
15	dlgtma1	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
16	dlbvua1	Alignment		100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
17	dlb26a1	Alignment		100.0	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
18	dlbgva2	Alignment		100.0	60	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
19	dleuza1	Alignment		100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
20	dlv9la1	Alignment		100.0	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
21	dlhwxaz	Alignment	not modelled	100.0	27	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
22	dl1lfa2	Alignment	not modelled	100.0	28	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
23	dlv9la2	Alignment	not modelled	100.0	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
24	dleuza2	Alignment	not modelled	100.0	33	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
25	dlgtma2	Alignment	not modelled	100.0	32	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
26	dlbvua2	Alignment	not modelled	100.0	30	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
27	dlb26a2	Alignment	not modelled	100.0	31	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
28	dlleha1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
29	dlclda2	Alignment	not modelled	100.0	23	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain

					Family: Aminoacid dehydrogenases
30	d1leha2	Alignment	not modelled	100.0	21 Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Aminoacid dehydrogenases
31	d1c1da1	Alignment	not modelled	100.0	26 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
32	d1li4a1	Alignment	not modelled	98.4	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
33	c3dhyC	Alignment	not modelled	98.3	14 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 and 3 inhibitors
34	c3oneA	Alignment	not modelled	98.3	18 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
35	c2eklA	Alignment	not modelled	98.3	11 PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
36	c3d4oA	Alignment	not modelled	98.3	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
37	c3gvpB	Alignment	not modelled	98.3	21 PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
38	c2rirA	Alignment	not modelled	98.2	18 PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
39	c1v8ba	Alignment	not modelled	98.2	20 PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
40	c1d4fD	Alignment	not modelled	98.2	18 PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
41	c3n58D	Alignment	not modelled	98.2	20 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
42	d1v8ba1	Alignment	not modelled	98.1	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
43	c3n7uD	Alignment	not modelled	98.1	11 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
44	c2cukC	Alignment	not modelled	98.1	16 PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
45	c1wwkA	Alignment	not modelled	98.1	11 PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
46	c2j6iC	Alignment	not modelled	98.1	13 PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
47	c3d64A	Alignment	not modelled	98.1	19 PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
48	d1nyta1	Alignment	not modelled	98.1	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
49	c2nacA	Alignment	not modelled	98.1	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
50	c2o4cB	Alignment	not modelled	98.0	17 PDB header: oxidoreductase Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
51	c3oetF	Alignment	not modelled	98.0	14 PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
52	c3k5pA	Alignment	not modelled	98.0	14 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
53	c2g76A	Alignment	not modelled	97.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
54	c2gcgB	Alignment	not modelled	97.9	13 PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2

					reductase/hydroxypyruvate reductase
55	c1xdwA	Alignment	not modelled	97.9	17 PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
56	c1o0sB	Alignment	not modelled	97.9	15 PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: crystal structure of ascaris suum malic enzyme complexed with nadh
57	c1ybaC	Alignment	not modelled	97.9	12 PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
58	c1gdhA	Alignment	not modelled	97.8	12 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
59	c1ygyA	Alignment	not modelled	97.8	23 PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
60	d2dl da1	Alignment	not modelled	97.8	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
61	c1j4aA	Alignment	not modelled	97.8	17 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
62	d1qp8a1	Alignment	not modelled	97.8	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
63	d1gdha1	Alignment	not modelled	97.8	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
64	c2w2kB	Alignment	not modelled	97.8	11 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.
65	c3bazA	Alignment	not modelled	97.8	17 PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
66	c1dxyA	Alignment	not modelled	97.7	17 PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxisocaproate dehydrogenase
67	c1gz3B	Alignment	not modelled	97.7	15 PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme; PDBTitle: molecular mechanism for the regulation of human mitochondrial2 nad(p)+-dependent malic enzyme by atp and fumarate
68	c3pgjB	Alignment	not modelled	97.7	16 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
69	d1j4aa1	Alignment	not modelled	97.7	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
70	d2naca1	Alignment	not modelled	97.7	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
71	c3h9eA	Alignment	not modelled	97.7	19 PDB header: oxidoreductase Chain: A: PDB Molecule: PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
72	d1mx3a1	Alignment	not modelled	97.7	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
73	c2eggA	Alignment	not modelled	97.7	17 PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
74	d2nu7a1	Alignment	not modelled	97.7	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
75	c2aw5A	Alignment	not modelled	97.7	17 PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent malic enzyme; PDBTitle: crystal structure of a human malic enzyme
76	c2hk8B	Alignment	not modelled	97.6	13 PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
77	c3gg9C	Alignment	not modelled	97.6	12 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
78	c2dbqA	Alignment	not modelled	97.6	11 PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
79	d1e5qa1	Alignment	not modelled	97.6	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

80	c3gvxA	Alignment	not modelled	97.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
81	c3ingA	Alignment	not modelled	97.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
82	c2omeA	Alignment	not modelled	97.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
83	d1ygya1	Alignment	not modelled	97.6	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
84	c3c8mA	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
85	d1dxya1	Alignment	not modelled	97.6	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
86	c3evtA	Alignment	not modelled	97.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
87	c1e5IA	Alignment	not modelled	97.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
88	c2dc1A	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
89	c2pi1C	Alignment	not modelled	97.6	19	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
90	c2eezG	Alignment	not modelled	97.5	24	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
91	c2d0iC	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
92	c4a26B	Alignment	not modelled	97.5	27	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
93	c1gpiA	Alignment	not modelled	97.5	17	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
94	d1dssg1	Alignment	not modelled	97.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	d1b0aa1	Alignment	not modelled	97.5	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
96	d1sc6a1	Alignment	not modelled	97.5	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
97	d1l7da1	Alignment	not modelled	97.5	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
98	c3kboB	Alignment	not modelled	97.5	15	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
99	c1nytC	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: C: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: shikimate dehydrogenase aroe complexed with nadp+
100	d1gpiA2	Alignment	not modelled	97.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
101	c3donA	Alignment	not modelled	97.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
102	c2axqA	Alignment	not modelled	97.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
103	d1euca1	Alignment	not modelled	97.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
104	c3I07B	Alignment	not modelled	97.4	20	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
						PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate

105	c1ihxD_	Alignment	not modelled	97.4	17	dehydrogenase; PDBTitle: crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
106	d2jfga1	Alignment	not modelled	97.4	13	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
107	c1qp8A_	Alignment	not modelled	97.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
108	d1pjca1	Alignment	not modelled	97.3	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
109	c3d1lB_	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
110	c1pjca_	Alignment	not modelled	97.3	25	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
111	c1a4iB_	Alignment	not modelled	97.2	20	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
112	c1qr6A_	Alignment	not modelled	97.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: malic enzyme 2; PDBTitle: human mitochondrial nad(p)-dependent malic enzyme
113	c2a9fB_	Alignment	not modelled	97.2	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative malic enzyme ((s)-malate:nad+ PDBTitle: crystal structure of a putative malic enzyme ((s)-2 malate:nad+ oxidoreductase (decarboxylating))
114	d1np3a2	Alignment	not modelled	97.2	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
115	c3p2oB_	Alignment	not modelled	97.2	22	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
116	d1a4ia1	Alignment	not modelled	97.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
117	c3dapB_	Alignment	not modelled	97.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
118	d1vl6a1	Alignment	not modelled	97.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
119	c1l7eC_	Alignment	not modelled	97.2	24	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
120	d1lomoa_	Alignment	not modelled	97.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like