

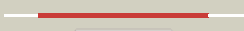





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d0iC_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase; PDBTitle: crystal structure ph0520 protein from pyrococcus horikoshii ot3
2	c1ygyA_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
3	c2dbqA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
4	c2gcbB_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
5	c1ybaC_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
6	c1gdhA_	 Alignment		100.0	30	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
7	c3n7uD_	 Alignment		100.0	24	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
8	c2cukC_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
9	c3k5pA_	 Alignment		100.0	26	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
10	c3bazA_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
11	c2g76A_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase

12	c2omeA_	Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
13	c2eklA_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
14	c1wwkA_	Alignment		100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of the phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
15	c3gg9C_	Alignment		100.0	29	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
16	c2nacA_	Alignment		100.0	22	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
17	c1j4aA_	Alignment		100.0	24	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
18	c2w2kB_	Alignment		100.0	28	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.
19	c2j6iC_	Alignment		100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
20	c3evtA_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
21	c1xdwA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
22	c1dxyA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxysicaproate dehydrogenase; PDBTitle: structure of d-2-hydroxysicaproate dehydrogenase
23	c2pi1C_	Alignment	not modelled	100.0	29	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
24	c3hg7A_	Alignment	not modelled	100.0	28	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
25	c1qp8A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
26	c3kboB_	Alignment	not modelled	100.0	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
27	c3gvxA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
						PDB header: oxidoreductase

28	c2o4cB_	Alignment	not modelled	100.0	26	Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
29	c3oetF_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
30	d1ygya1	Alignment	not modelled	100.0	38	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
31	d1gdha1	Alignment	not modelled	100.0	36	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
32	d1mx3a1	Alignment	not modelled	100.0	33	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
33	d1j4aa1	Alignment	not modelled	100.0	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
34	d2dlad1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
35	d2naca1	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
36	d1dxya1	Alignment	not modelled	100.0	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
37	d1sc6a1	Alignment	not modelled	100.0	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
38	d1qp8a1	Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
39	c1l7eC_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
40	c2eezG_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: G: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of alanine dehydrogenase from themus thermophilus
41	c1pjca_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
42	c2bruB_	Alignment	not modelled	100.0	15	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
43	c3gvpB_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
44	c1d4fD_	Alignment	not modelled	100.0	15	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
45	c2vhyB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: alanine dehydrogenase; PDBTitle: crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
46	d1v8ba1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
47	c3dhyC_	Alignment	not modelled	100.0	13	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
48	c3n58D_	Alignment	not modelled	100.0	15	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
49	c3oneA_	Alignment	not modelled	100.0	10	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
50	c3p2yA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alanine dehydrogenase/pyridine nucleotide transhydrogenase; PDBTitle: crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
51	c1v8bA_	Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
52	d1ygya2	Alignment	not modelled	99.9	28	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
53	d1sc6a2	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like

						Family: Formate/glycerate dehydrogenases, substrate-binding domain
54	d1i4a1	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
55	d1gdha2	Alignment	not modelled	99.9	22	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
56	c3d4oA	Alignment	not modelled	99.9	13	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
57	c3d64A	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteine; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
58	d1np3a2	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
59	d1leha1	Alignment	not modelled	99.9	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
60	c2rirA	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
61	d1pjca1	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
62	d2naca2	Alignment	not modelled	99.8	13	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
63	d1dxya2	Alignment	not modelled	99.8	15	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
64	d2dl da2	Alignment	not modelled	99.8	20	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
65	d1j4aa2	Alignment	not modelled	99.8	16	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
66	d1mx3a2	Alignment	not modelled	99.7	22	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
67	d1cl da1	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
68	c1lehB	Alignment	not modelled	99.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: leucine dehydrogenase; PDBTitle: leucine dehydrogenase from bacillus sphaericus
69	d1l7da1	Alignment	not modelled	99.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
70	c3oj0A	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
71	d3cuma2	Alignment	not modelled	99.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
72	c1np3B	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
73	d2g5ca2	Alignment	not modelled	99.3	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
74	d1vpda2	Alignment	not modelled	99.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
75	d2f1ka2	Alignment	not modelled	99.2	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
76	d2cvza2	Alignment	not modelled	99.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
77	d1v9la1	Alignment	not modelled	99.2	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
						PDB header: oxidoreductase

78	c3cumA	Alignment	not modelled	99.1	12	Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
79	d2pgda2	Alignment	not modelled	99.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
80	c3c24A	Alignment	not modelled	99.1	20	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
81	c3b1fA	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
82	c1yb4A	Alignment	not modelled	99.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
83	c1bxgA	Alignment	not modelled	98.9	15	PDB header: amino acid dehydrogenase Chain: A: PDB Molecule: phenylalanine dehydrogenase; PDBTitle: phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
84	d1b0aa1	Alignment	not modelled	98.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
85	c2p4qA	Alignment	not modelled	98.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
86	c1vpdA	Alignment	not modelled	98.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
87	c2f1kD	Alignment	not modelled	98.9	17	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
88	c3ktdC	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
89	c1pggA	Alignment	not modelled	98.9	14	PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
90	d1a4ia1	Alignment	not modelled	98.9	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
91	c2iz1C	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
92	c3dzba	Alignment	not modelled	98.9	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
93	d1wdka3	Alignment	not modelled	98.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
94	d1f0ya2	Alignment	not modelled	98.8	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
95	c3fwnB	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
96	c3ckyA	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
97	c4a26B	Alignment	not modelled	98.8	21	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
98	c2pv7B	Alignment	not modelled	98.8	18	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
99	c3l6dB	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
100	c2cvzD	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
						PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase,

101	c3pefA_	Alignment	not modelled	98.7	11	nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
102	c3pduF_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase family protein; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
103	c2uyyD_	Alignment	not modelled	98.7	10	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
104	c3prjB_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
105	c1pgiA_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
106	c2q3eH_	Alignment	not modelled	98.6	14	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
107	c3plnA_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
108	d1pgja2	Alignment	not modelled	98.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
109	d1i36a2	Alignment	not modelled	98.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c2g5cD_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
111	c2y0dB_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
112	c4a5oB_	Alignment	not modelled	98.6	25	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
113	c1b0aA_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
114	c1a4iB_	Alignment	not modelled	98.6	19	PDB header: oxidoreductase Chain: B: PDB Molecule: methylenetetrahydrofolate dehydrogenase / PDBTitle: human tetrahydrofolate dehydrogenase / cyclohydrolase
115	c1dliA_	Alignment	not modelled	98.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
116	c3dojA_	Alignment	not modelled	98.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
117	d1pgja2	Alignment	not modelled	98.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
118	c3l07B_	Alignment	not modelled	98.5	19	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methylenetetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
119	c3p2oB_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase, hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: crystal structure of fold bifunctional protein from campylobacter2 jejuni
120	c3g0oA_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium