Phyre^2

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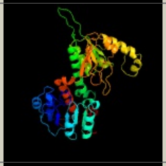
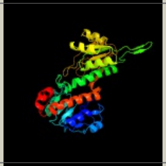
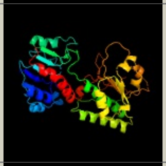
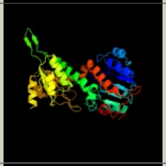
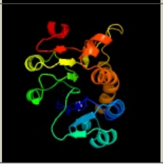
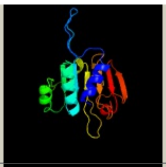
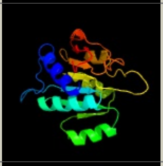
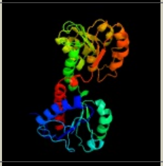
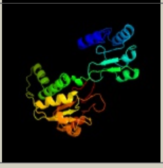
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3p2yA_	Alignment		100.0	74	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
2	c4izhA_	Alignment		100.0	49	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad/nadp transhydrogenase alpha subunit 1; **PDBTitle:** crystal structure of the alpha1 dimer of thermus thermophilus2 transhydrogenase in p6
3	c2bruB_	Alignment		100.0	41	**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
4	c4dioB_	Alignment		100.0	47	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase subunit alpha part 1; **PDBTitle:** the crystal structure of transhydrogenase from sinorhizobium meliloti
5	c1pjcA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (l-alanine dehydrogenase); **PDBTitle:** l-alanine dehydrogenase complexed with nad
6	c2qrlA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase, nad+, l-lysine-forming; **PDBTitle:** crystal structure of oxalylglycine-bound saccharopine dehydrogenase2 (l-lys forming) from saccharomyces cerevisiae
7	c1l7eC_	Alignment		100.0	47	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
8	c2eezG_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase from themus thermophilus
9	c2vhyB_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from mycobacterium2 tuberculosis
10	d1l7da2	Alignment		100.0	38	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
11	d1pjca2	Alignment		100.0	30	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like

12	d1l7da1	Alignment		100.0	55	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
13	d1pjca1	Alignment		100.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
14	c2rirA_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
15	c3d4oA_	Alignment		99.9	18	**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
16	c1wwkA_	Alignment		99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
17	c6f3oC_	Alignment		99.6	18	**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
18	c2eklA_	Alignment		99.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
19	c2gcgB_	Alignment		99.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
20	c2g76A_	Alignment		99.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
21	c6ih2B_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphite dehydrogenase; **PDBTitle:** crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
22	c2cukC_	Alignment	not modelled	99.5	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
23	c4g2nA_	Alignment	not modelled	99.4	16	**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
24	c1gdhA_	Alignment	not modelled	99.4	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
25	c4e5kC_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**phosphite dehydrogenase (thermostable variant); **PDBTitle:** thermostable phosphite dehydrogenase in complex with nad and sulfite
26	c3evtA_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
27	c3n7uD_	Alignment	not modelled	99.4	16	**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

28	c4njmA_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase, putative; **PDBTitle:** crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
29	c3fn4A_	Alignment	not modelled	99.4	15	**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
30	c2dbqA_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
31	c6aphA_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
32	c4zgsE_	Alignment	not modelled	99.3	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative d-lactate dehydrogenase; **PDBTitle:** identification of the pyruvate reductase of chlamydomonas reinhardtii
33	c2nacA_	Alignment	not modelled	99.3	16	**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
34	c3k5pA_	Alignment	not modelled	99.3	19	**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
35	c1ygyA_	Alignment	not modelled	99.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
36	c1ybaC_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
37	c5mh5A_	Alignment	not modelled	99.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-2-hydroxyacid dehydrogenase; **PDBTitle:** d-2-hydroxyacid dehydrogenases (d2-hdh) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
38	c3wwzB_	Alignment	not modelled	99.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-lactate dehydrogenase (fermentative); **PDBTitle:** the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
39	c3gvpB_	Alignment	not modelled	99.3	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
40	c3wwyA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
41	c5j23D_	Alignment	not modelled	99.2	14	**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
42	c3bazA_	Alignment	not modelled	99.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyphenylpyruvate reductase; **PDBTitle:** structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
43	c1xdwA_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad+-dependent (r)-2-hydroxyglutarate **PDBTitle:** nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
44	c2d0iC_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
45	c2j6iC_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal mutant
46	c4cukA_	Alignment	not modelled	99.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** structure of salmonella d-lactate dehydrogenase in complex2 with nadh
47	c1j4aA_	Alignment	not modelled	99.2	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
48	c4zqbB_	Alignment	not modelled	99.2	20	**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
49	c3gg9C_	Alignment	not modelled	99.2	15	**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
50	c5tx7A_	Alignment	not modelled	99.2	20	**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
51	c2pi1C_	Alignment	not modelled	99.2	16	**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
						PDB header:oxidoreductase

52	c1dxyA_	Alignment	not modelled	99.2	18	**Chain:** A: **PDB Molecule:**d-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** structure of d-2-hydroxyisocaproate dehydrogenase
53	c3hg7A_	Alignment	not modelled	99.2	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
54	c3x2fA_	Alignment	not modelled	99.2	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** a thermophilic s-adenosylhomocysteine hydrolase
55	c2yq4C_	Alignment	not modelled	99.1	20	**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
56	c4s1vD_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase-related protein; **PDBTitle:** crystal structure of phosphoglycerate oxidoreductase from vibrio2 cholerae o395
57	c3wnvA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of a glyoxylate reductase from paecilomyes2 thermophila
58	c4dgsA_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystals structure of dehydrogenase from rhizobium meliloti
59	c4xkjA_	Alignment	not modelled	99.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** a novel d-lactate dehydrogenase from sporolactobacillus sp
60	c4lswA_	Alignment	not modelled	99.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-2-hydroxyacid dehydrogensase protein; **PDBTitle:** crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonicigenium vulgare y25
61	c1d4fD_	Alignment	not modelled	99.1	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
62	c2w2kB_	Alignment	not modelled	99.1	22	**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.
63	c5dt9A_	Alignment	not modelled	99.1	22	**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
64	c4prkB_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-phosphoerythronate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase (d-ldh) from2 lactobacillus jensenii
65	c2omeA_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
66	c1v8bA_	Alignment	not modelled	99.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
67	c3n58D_	Alignment	not modelled	99.1	28	**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
68	d1mx3a1	Alignment	not modelled	99.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
69	d1li4a1	Alignment	not modelled	99.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
70	d1ygya1	Alignment	not modelled	99.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
71	d2naca1	Alignment	not modelled	99.1	18	**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	99.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
73	c5v96A_	Alignment	not modelled	99.0	21	**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
74	c3dhyC_	Alignment	not modelled	99.0	28	**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
75	c5hm8C_	Alignment	not modelled	99.0	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.
76	c3oetF_	Alignment	not modelled	99.0	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad

77	c2o4cB_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
78	c3oneA_	Alignment	not modelled	99.0	29	**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
79	c4xcvA_	Alignment	not modelled	99.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadp-dependent 2-hydroxyacid dehydrogenase; **PDBTitle:** probable 2-hydroxyacid dehydrogenase from rhizobium etli cfn 42 in2 complex with nadph
80	d1v8ba1	Alignment	not modelled	99.0	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
81	c1gpjA_	Alignment	not modelled	99.0	25	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
82	c4n18A_	Alignment	not modelled	99.0	15	**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
83	d1j4aa1	Alignment	not modelled	99.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
84	d2dlda1	Alignment	not modelled	98.9	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
85	c4hy3D_	Alignment	not modelled	98.9	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**phosphoglycerate oxidoreductase; **PDBTitle:** crystal structure of a phosphoglycerate oxidoreductase from rhizobium2 etli
86	c3d64A_	Alignment	not modelled	98.9	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
87	d1dxya1	Alignment	not modelled	98.9	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
88	c4weqA_	Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent dehydrogenase; **PDBTitle:** crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc02828 (smghra) from sinorhizobium meliloti in complex3 with nadp and sulfate
89	c4xa8A_	Alignment	not modelled	98.9	21	**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	c3kboB_	Alignment	not modelled	98.9	16	**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
91	d1gpja2	Alignment	not modelled	98.9	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
92	c3gvxA_	Alignment	not modelled	98.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerate dehydrogenase related protein; **PDBTitle:** crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
93	c1qp8A_	Alignment	not modelled	98.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
94	d1qp8a1	Alignment	not modelled	98.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
95	d1sc6a1	Alignment	not modelled	98.8	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
96	c4n7rB_	Alignment	not modelled	98.7	22	**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
97	c6aqjB_	Alignment	not modelled	98.6	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase (nadp(+)); **PDBTitle:** crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
98	c3oj0A_	Alignment	not modelled	98.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
99	d1a4ia1	Alignment	not modelled	98.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
100	c4tskA_	Alignment	not modelled	98.5	20	**PDB header:**oxidoreductase,isomerase **Chain:** A: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
101	d1np3a2	Alignment	not modelled	98.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain

102	d1c1da1	Alignment	not modelled	98.4	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
103	d1b0aa1	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
104	c3c24A_	Alignment	not modelled	98.4	27	**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
105	c5b37A_	Alignment	not modelled	98.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophan dehydrogenase; **PDBTitle:** crystal structure of l-tryptophan dehydrogenase from nostoc2 punctiforme
106	d2pgda2	Alignment	not modelled	98.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
107	c4wb1B_	Alignment	not modelled	98.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cals8; **PDBTitle:** crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
108	d1vpda2	Alignment	not modelled	98.3	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
109	c4a26B_	Alignment	not modelled	98.3	24	**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
110	c3gg2B_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase **PDBTitle:** crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
111	c5t57A_	Alignment	not modelled	98.3	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**semialdehyde dehydrogenase nad-binding protein; **PDBTitle:** crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
112	c2y0dB_	Alignment	not modelled	98.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
113	c1bxgA_	Alignment	not modelled	98.2	27	**PDB header:**amino acid dehydrogenase **Chain:** A: **PDB Molecule:**phenylalanine dehydrogenase; **PDBTitle:** phenylalanine dehydrogenase structure in ternary complex2 with nad+ and beta-phenylpropionate
114	d1leha1	Alignment	not modelled	98.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
115	c5uscB_	Alignment	not modelled	98.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
116	c1vpdA_	Alignment	not modelled	98.2	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
117	c5nhsB_	Alignment	not modelled	98.2	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** the crystal structure of xanthomonas albilineans n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
118	c4kqxB_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase/oxidoreductase inhibitor **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** mutant slackia exigua kari ddv in complex with nad and an inhibitor
119	c4e21B_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase (decarboxylating); **PDBTitle:** the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
120	c4gbjB_	Alignment	not modelled	98.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase nad-binding; **PDBTitle:** crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans