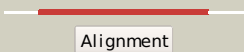

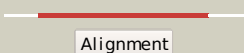

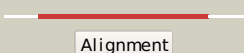

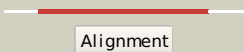

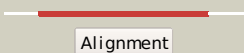

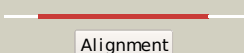

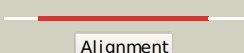

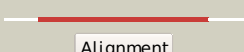

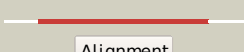

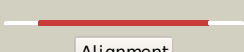

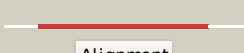












| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3krtC_ |  Alignment |  | 100.0 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2) |
| 2 | c2dphA_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: formaldehyde dismutase; PDBTitle: crystal structure of formaldehyde dismutase |
| 3 | c1pl6A_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: human sdh/nadh/inhibitor complex |
| 4 | c1kolA_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: formaldehyde dehydrogenase; PDBTitle: crystal structure of formaldehyde dehydrogenase |
| 5 | c4a10A_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: octenoyl-coa reductase/carboxylase; PDBTitle: apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp. |
| 6 | c2ejvA_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: crystal structure of threonine 3-dehydrogenase complexed with nad+ |
| 7 | c1hf3A_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase e chain; PDBTitle: atomic x-ray structure of liver alcohol dehydrogenase2 containing cadmium and a hydroxide adduct to nadh |
| 8 | c3ip1C_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: structure of putative alcohol dehydrogenase (tm_042) from thermotoga2 maritima |
| 9 | c2dfvB_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable l-threonine 3-dehydrogenase; PDBTitle: hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii |
| 10 | c1r37B_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol |
| 11 | c1ma0B_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione-dependent formaldehyde dehydrogenase; PDBTitle: ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid |

| | | | | | | |
|----|-------------------------|-----------|---|-------|----|--|
| 12 | c1h2bA_ | Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the alcohol dehydrogenase from the hyperthermophilic archaeon aeropyrum pernix at 1.65 Å resolution |
| 13 | c1p0fA_ | Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: crystal structure of the binary complex: nadp(h)-dependent vertebrate alcohol dehydrogenase (adh8) with the cofactor nadp |
| 14 | c2ouiB_ | Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: d275p mutant of alcohol dehydrogenase from protozoa entamoeba histolytica |
| 15 | c1f8fA_ | Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: benzyl alcohol dehydrogenase; PDBTitle: crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus |
| 16 | c1kevB_ | Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: structure of nadp-dependent alcohol dehydrogenase |
| 17 | c3cosD_ | Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 4; PDBTitle: crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn |
| 18 | c1cdoB_ | Alignment |  | 100.0 | 24 | PDB header: oxidoreductase (ch-oh(d)-nad(a)) Chain: B: PDB Molecule: alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with 2 nicotinamide adenine dinucleotide (nad), and zinc |
| 19 | c2eihA_ | Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of nad-dependent alcohol dehydrogenase |
| 20 | c1e3jA_ | Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp(h)-dependent ketose reductase; PDBTitle: ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly |
| 21 | c1vj0B_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: crystal structure of alcohol dehydrogenase (tm0436) from thermotoga2 maritima at 2.00 Å resolution |
| 22 | c3uogB_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021 |
| 23 | c2hcyD_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: yeast alcohol dehydrogenase i, saccharomyces cerevisiae fermentative2 enzyme |
| 24 | c2xaaC_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: C: PDB Molecule: secondary alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase adh-'a' from rhodococcus ruber dsm2 44541 at ph 8.5 in complex with nad and butane-1,4-diol |
| 25 | c1rjwA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of nad(+) dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain 11d-r |
| 26 | c2cdaA_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucose dehydrogenase; PDBTitle: sulfobolus solfataricus glucose dehydrogenase 1 in complex2 with nadp |
| 27 | c3m6iA_ | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinitol 4-dehydrogenase; PDBTitle: l-arabinitol 4-dehydrogenase |
| 28 | c2cf5A_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: cinnamyl alcohol dehydrogenase; PDBTitle: crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5 |
| | | | | | | PDB header: oxidoreductase |

| | | | | | | |
|----|--------------------------|-----------|--------------|-------|----|---|
| 29 | c1piwA_ | Alignment | not modelled | 100.0 | 16 | Chain: A: PDB Molecule: hypothetical zinc-type alcohol dehydrogenase- PDBTitle: apo and holo structures of an nadp(h)-dependent cinnamyl2 alcohol dehydrogenase from saccharomyces cerevisiae |
| 30 | c1lluD_ | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase; PDBTitle: the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate |
| 31 | c1yqxB_ | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: sinapyl alcohol dehydrogenase; PDBTitle: sinapyl alcohol dehydrogenase at 2.5 angstrom resolution |
| 32 | c3b70A_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl reductase; PDBTitle: crystal structure of aspergillus terreus trans-acting lovastatin2 polyketide enoyl reductase (lovC) with bound nadp |
| 33 | c2j8zA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of human p53 inducible oxidoreductase (2 tp53i3.pig3) |
| 34 | c1uufA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: zinc-type alcohol dehydrogenase-like protein PDBTitle: crystal structure of a zinc-type alcohol dehydrogenase-like2 protein yahk |
| 35 | c2c0cB_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: zinc binding alcohol dehydrogenase, domain PDBTitle: structure of the mgc45594 gene product |
| 36 | c1qorA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of escherichia coli quinone2 oxidoreductase complexed with nadph |
| 37 | c1o89A_ | Alignment | not modelled | 100.0 | 14 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yhdh; PDBTitle: crystal structure of e. coli k-12 yhdh |
| 38 | c2vwpA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucose dehydrogenase; PDBTitle: haloferax mediterranei glucose dehydrogenase in complex2 with nadph and zn. |
| 39 | c1wlY_A_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-haloacrylate reductase; PDBTitle: crystal structure of 2-haloacrylate reductase |
| 40 | c3fbgA_ | Alignment | not modelled | 100.0 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative arginate lyase; PDBTitle: crystal structure of a putative arginate lyase from staphylococcus2 haemolyticus |
| 41 | c1n9gF_ | Alignment | not modelled | 100.0 | 16 | PDB header: hydrolase Chain: F: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: mitochondrial 2-enoyl thioester reductase etr1p/etr2p2 heterodimer from candida tropicalis |
| 42 | c3gazA_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase superfamily protein; PDBTitle: crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans |
| 43 | c3pi7A_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidoreductase; PDBTitle: crystal structure of a putative nadph:quinone reductase (ml13093) from2 mesorhizobium loti at 1.71 a resolution |
| 44 | c3jynA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structures of pseudomonas syringae pv. tomato dc30002 quinone oxidoreductase complexed with nadph |
| 45 | c3iupB_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadph:quinone oxidoreductase; PDBTitle: crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution |
| 46 | c3gmsA_ | Alignment | not modelled | 100.0 | 16 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nadph:quinone reductase; PDBTitle: crystal structure of putative nadph:quinone reductase from2 bacillus thuringiensis |
| 47 | c2j3iB_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent oxidoreductase p1; PDBTitle: crystal structure of arabidopsis thaliana double bond2 reductase (at5g16970)-binary complex |
| 48 | c2h6eA_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-arabinose 1-dehydrogenase; PDBTitle: crystal structure of the d-arabinose dehydrogenase from sulfolobus2 solfataricus |
| 49 | c2vcyA_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of 2-enoyl thioester reductase of human2 fas ii |
| 50 | c2w4qA_ | Alignment | not modelled | 100.0 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin reductase 2; PDBTitle: crystal structure of human zinc-binding alcohol2 dehydrogenase 1 (zadh1) in ternary complex with nadp and3 18beta-glycyrrhetic acid |
| 51 | c1yb5A_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of human zeta-crystallin with bound nadp |
| 52 | c1xa0B_ | Alignment | not modelled | 100.0 | 14 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nadph dependent oxidoreductases; PDBTitle: crystal structure of mcs9 target apc35536 from bacillus2 stearothermophilus |
| 53 | c1x0aB_ | Alignment | not modelled | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein yhf9; |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 53 | c1y9eb | Alignment | not modelled | 100.0 | 18 | PDBTitle: crystal structure of bacillus subtilis protein yhfp with2 nad bound PDB header: oxidoreductase |
| 54 | c3gohA | Alignment | not modelled | 100.0 | 18 | Chain: A: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: crystal structure of alcohol dehydrogenase superfamily protein2 (np_718042.1) from shewanella oneidensis at 1.55 a resolution |
| 55 | c1zsvB | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent leukotriene b4 12- PDBTitle: crystal structure of human nadp-dependent leukotriene b4 12-2 hydroxydehydrogenase |
| 56 | c3tqhA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: structure of the quinone oxidoreductase from coxiella burnetii |
| 57 | c2vn8B | Alignment | not modelled | 100.0 | 17 | PDB header: receptor inhibitor Chain: B: PDB Molecule: reticulon-4-interacting protein 1; PDBTitle: crystal structure of human reticulon 4 interacting protein2 1 in complex with nadph |
| 58 | c1iz0A | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structures of the quinone oxidoreductase from2 thermus thermophilus hb8 and its complex with nadph |
| 59 | d1p18a1 | Alignment | not modelled | 100.0 | 26 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 60 | d1p0fa1 | Alignment | not modelled | 100.0 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 61 | d1uufa1 | Alignment | not modelled | 100.0 | 26 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 62 | d1kola1 | Alignment | not modelled | 99.9 | 26 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 63 | d1piwa1 | Alignment | not modelled | 99.9 | 19 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 64 | d1cdoa1 | Alignment | not modelled | 99.9 | 26 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 65 | d1jqba1 | Alignment | not modelled | 99.9 | 25 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 66 | d1u3ta1 | Alignment | not modelled | 99.9 | 25 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 67 | d2fzwa1 | Alignment | not modelled | 99.9 | 22 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 68 | d2jhfa1 | Alignment | not modelled | 99.9 | 22 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 69 | d1u3wa1 | Alignment | not modelled | 99.9 | 25 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 70 | d1d1ta1 | Alignment | not modelled | 99.9 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 71 | d1jvba1 | Alignment | not modelled | 99.9 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 72 | d1ykfa1 | Alignment | not modelled | 99.9 | 22 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 73 | d1e3ia1 | Alignment | not modelled | 99.9 | 23 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 74 | d1u3ua1 | Alignment | not modelled | 99.9 | 25 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 75 | d1f8fa1 | Alignment | not modelled | 99.9 | 20 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 76 | d1llu1 | Alignment | not modelled | 99.9 | 30 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 77 | d1rjwa1 | Alignment | not modelled | 99.9 | 27 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 78 | d1vj0a1 | Alignment | not modelled | 99.9 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 79 | d1gu7a1 | Alignment | not modelled | 99.9 | 21 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 80 | d1h2ba1 | Alignment | not modelled | 99.9 | 29 | Fold: GroES-like Superfamily: GroES-like |

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|-----|-------------------------|-----------|--------------|------|---|
| | | | | | Family: Alcohol dehydrogenase-like, N-terminal domain |
| 81 | d1xa0a1 | Alignment | not modelled | 99.9 | 17 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 82 | d1e3ja1 | Alignment | not modelled | 99.8 | 29 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 83 | d1o89a1 | Alignment | not modelled | 99.8 | 18 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 84 | d1yb5a1 | Alignment | not modelled | 99.8 | 24 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 85 | d1qora1 | Alignment | not modelled | 99.7 | 18 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 86 | c2vz8B_ | Alignment | not modelled | 99.7 | 14 PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: crystal structure of mammalian fatty acid synthase |
| 87 | d1t7a1 | Alignment | not modelled | 99.7 | 23 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 88 | d1iz0a1 | Alignment | not modelled | 99.6 | 27 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 89 | d1v3va1 | Alignment | not modelled | 99.6 | 14 Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 90 | d1vj0a2 | Alignment | not modelled | 99.3 | 22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 91 | d1f8fa2 | Alignment | not modelled | 99.3 | 23 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 92 | d1ykfa2 | Alignment | not modelled | 99.3 | 22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 93 | d1pl8a2 | Alignment | not modelled | 99.2 | 25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 94 | d1jqba2 | Alignment | not modelled | 99.2 | 20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 95 | d1pqwa_ | Alignment | not modelled | 99.2 | 12 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 96 | d1jvba2 | Alignment | not modelled | 99.2 | 16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 97 | d1h2ba2 | Alignment | not modelled | 99.2 | 22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 98 | d1kola2 | Alignment | not modelled | 99.1 | 19 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 99 | d1rjwa2 | Alignment | not modelled | 99.1 | 25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 100 | d1p0fa2 | Alignment | not modelled | 99.1 | 16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 101 | d1cdoa2 | Alignment | not modelled | 99.1 | 20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 102 | d1llua2 | Alignment | not modelled | 99.1 | 25 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 103 | d1e3ja2 | Alignment | not modelled | 99.1 | 22 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 104 | d1piwa2 | Alignment | not modelled | 99.0 | 16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 105 | d2jhfa2 | Alignment | not modelled | 99.0 | 18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 106 | d1e3ja2 | Alignment | not modelled | 99.0 | 20 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 107 | d1vj1a2 | Alignment | not modelled | 99.0 | 16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| | | | | | Fold: NAD(P)-binding Rossmann-fold domains |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 108 | d1v3va2 | Alignment | not modelled | 99.0 | 13 | Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 109 | d1qora2 | Alignment | not modelled | 99.0 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 110 | d1yb5a2 | Alignment | not modelled | 99.0 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 111 | d2fzwa2 | Alignment | not modelled | 99.0 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 112 | d1d1ta2 | Alignment | not modelled | 98.9 | 13 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 113 | d1uufa2 | Alignment | not modelled | 98.9 | 22 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 114 | d1u3wa2 | Alignment | not modelled | 98.8 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 115 | d1gu7a2 | Alignment | not modelled | 98.7 | 12 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 116 | d1o89a2 | Alignment | not modelled | 98.7 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 117 | d1tt7a2 | Alignment | not modelled | 98.7 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 118 | d1xa0a2 | Alignment | not modelled | 98.7 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 119 | d1iz0a2 | Alignment | not modelled | 98.6 | 21 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain |
| 120 | d1vj1a1 | Alignment | not modelled | 98.5 | 20 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |