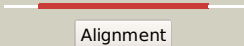

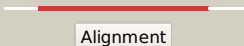

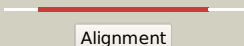







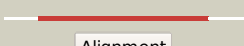



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3141_(fadB4)_3508092_3509063
 Date Thu Aug 8 16:20:32 BST 2019
 Unique Job ID 7d3198513577f10

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c3krtC_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: C: PDB Molecule: crotonyl coa reductase; PDBTitle: crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2) |
| 2 | c4gi2B_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: crotonyl-coa carboxylase/reductase; PDBTitle: crotonyl-coa carboxylase/reductase |
| 3 | c2j8zA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of human p53 inducible oxidoreductase (2 tp53i3.pig3) |
| 4 | c4y0kA_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: ante; PDBTitle: structure of crotonyl-coa carboxylase/reductase ante in complex with2 nadp |
| 5 | c3qwbC_ |  Alignment |  | 100.0 | 26 | PDB header: oxidoreductase Chain: C: PDB Molecule: probable quinone oxidoreductase; PDBTitle: crystal structure of saccharomyces cerevisiae zeta-crystallin-like2 quinone oxidoreductase zta1 complexed with nadph |
| 6 | c4a10A_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: octenoyl-coa reductase/carboxylase; PDBTitle: apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp. |
| 7 | c2vcyA_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: trans-2-enoyl-coa reductase; PDBTitle: crystal structure of 2-enoyl thioester reductase of human fas ii |
| 8 | c3jynA_ |  Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structures of pseudomonas syringae pv. tomato dc30002 quinone oxidoreductase complexed with nadph |
| 9 | c3ukoA_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase class-3; PDBTitle: crystal structure of s-nitrosoglutathione reductase from arabidopsis2 thaliana, complex with nadh |
| 10 | c4z6kD_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase from the antarctic psychrophile moraxella sp.2 tae 123 |
| 11 | c3uogB_ |  Alignment |  | 100.0 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021 |

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|----|------------------------|-----------|---|-------|----|---|
| 12 | c4gkvC | Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase, propanol-preferring; PDBTitle: structure of escherichia coli adh p (ethanol-inducible dehydrogenase)2 with bound nad |
| 13 | c4rvsA | Alignment |  | 100.0 | 29 | PDB header: electron transport Chain: A: PDB Molecule: probable quinone reductase qor (nadh:quinone reductase) PDBTitle: the native structure of mycobacterial quinone oxidoreductase rv154c. |
| 14 | c3gmsA | Alignment |  | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative nadph:quinone reductase; PDBTitle: crystal structure of putative nadph:quinone reductase from bacillus2 thuringiensis |
| 15 | c5zxnA | Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent oxidoreductase; PDBTitle: crystal structure of cura from vibrio vulnificus |
| 16 | c2hcyD | Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: yeast alcohol dehydrogenase I, saccharomyces cerevisiae fermentative2 enzyme |
| 17 | c1ma0B | Alignment |  | 100.0 | 21 | 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 |
| 18 | c2eihA | Alignment |  | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of nad-dependent alcohol dehydrogenase |
| 19 | c1yb5A | Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of human zeta-crystallin with bound nadp |
| 20 | c1f8fA | Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: benzyl alcohol dehydrogenase; PDBTitle: crystal structure of benzyl alcohol dehydrogenase from acinetobacter2 calcoaceticus |
| 21 | c5tnxA | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase zinc-binding domain protein; PDBTitle: crystal structure of alcohol dehydrogenase zinc-binding domain protein2 from burkholderia ambifaria |
| 22 | c2xaaC | Alignment | not modelled | 100.0 | 23 | 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 |
| 23 | c1y9eB | Alignment | not modelled | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein yhfp; PDBTitle: crystal structure of bacillus subtilis protein yhfp with nad bound |
| 24 | c4j6fB | Alignment | not modelled | 100.0 | 28 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase from sinorhizobium2 meliloti 1021, nysgrc-target 012230 |
| 25 | c1wlyA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-haloacrylate reductase; PDBTitle: crystal structure of 2-haloacrylate reductase |
| 26 | c1rjwA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of nad(+)-dependent alcohol dehydrogenase2 from bacillus stearothermophilus strain lld-r |
| 27 | 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 |
| 28 | c4rquA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase crystal structure in complex with nad |
| | | | | | | PDB header: oxidoreductase (ch-oh(d)-nad(a)) |

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|----|------------------------|-----------|--------------|-------|----|---|
| 29 | c1cdoB | Alignment | not modelled | 100.0 | 20 | Chain: B: PDB Molecule: alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc |
| 30 | c5gxeA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: acrylyl-coa reductase acui; PDBTitle: crystal structure of acryloyl-coa reductase acui in complex with nadph |
| 31 | c1r37B | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase from sulfobolus solfataricus2 complexed with nad(h) and 2-ethoxyethanol |
| 32 | c1lluD | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase; PDBTitle: the ternary complex of pseudomonas aeruginosa alcohol2 dehydrogenase with its coenzyme and weak substrate |
| 33 | c1qorA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of escherichia coli quinone oxidoreductase complexed2 with nadph |
| 34 | c6n7IB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of an alcohol dehydrogenase from elizabethkingia2 anophelis nuhp1 |
| 35 | c1n9gF | Alignment | not modelled | 100.0 | 18 | PDB header: hydrolase Chain: F: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: mitochondrial 2-enoyl thioester reductase etr1p/etr2p heterodimer from2 candida tropicalis |
| 36 | c4jxkA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase rop_24000 (target efi-506400) from2 rhodococcus opacus b4 |
| 37 | c5a3jF | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: F: PDB Molecule: putative quinone-oxidoreductase homolog, chloroplastic; PDBTitle: crystal structure of the chloroplastic gamma-ketol reductase from2 arabidopsis thaliana bound to 13-oxo-9(z),11(e),15(z)-3 octadecatrienoic acid. |
| 38 | c6c49A | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of alcohol dehydrogenase from acetobacter2 baumannii |
| 39 | c1o89A | Alignment | not modelled | 100.0 | 20 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yhdh; PDBTitle: crystal structure of e. coli k-12 ydh |
| 40 | c2c0cB | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: zinc binding alcohol dehydrogenase, domain containing 2; PDBTitle: structure of the mgc45594 gene product |
| 41 | c4jbiB | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase (zinc); PDBTitle: 2.35a resolution structure of nadph bound thermostable alcohol2 dehydrogenase from pyrobaculum aerophilum |
| 42 | c1vj0B | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: crystal structure of alcohol dehydrogenase (tm0436) from thermotoga2 maritima at 2.00 a resolution |
| 43 | c5kiaA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: crystal structure of l-threonine 3-dehydrogenase from burkholderia2 thailandensis |
| 44 | c1hf3A | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase e chain; PDBTitle: atomic x-ray structure of liver alcohol dehydrogenase containing2 cadmium and a hydroxide adduct to nadh |
| 45 | c3cosD | Alignment | not modelled | 100.0 | 21 | 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 |
| 46 | c3gazA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase superfamily protein; PDBTitle: crystal structure of an alcohol dehydrogenase superfamily protein from2 novosphingobium aromaticivorans |
| 47 | c4eezB | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase 1; PDBTitle: crystal structure of lactococcus lactis alcohol dehydrogenase variant2 re1 |
| 48 | c2cf5A | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: cinnamyl alcohol dehydrogenase; PDBTitle: crystal structures of the arabidopsis cinnamyl alcohol2 dehydrogenases, atcad5 |
| 49 | c3b70A | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl reductase; PDBTitle: crystal structure of aspergillus terreus trans-acting lovastatin2 polyketide enoyl reductase (lovv) with bound nadp |
| 50 | c4a27A | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: synaptic vesicle membrane protein vat-1 homolog-like; PDBTitle: crystal structure of human synaptic vesicle membrane protein vat-12 homolog-like protein |
| 51 | c1p0fA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: crystal structure of the binary complex: nadp(h)-dependent vertebrate2 alcohol dehydrogenase (adh8) with the cofactor nadp |
| 52 | c1pl6A | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: sorbitol dehydrogenase; PDBTitle: human sdh/nadh/inhibitor complex |
| 53 | c2dfvB | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable l-threonine 3-dehydrogenase; PDBTitle: hyperthermophilic threonine dehydrogenase from pyrococcus horikoshii |

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|----|------------------------|-----------|--------------|-------|----|---|
| 54 | c5ynB | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: zinc dependent alcohol dehydrogenase 2 from streptococcus pneumonia -2 apo form |
| 55 | c2ejvA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-threonine 3-dehydrogenase; PDBTitle: crystal structure of threonine 3-dehydrogenase complexed with nad+ |
| 56 | c5k1sD | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, zinc-binding dehydrogenase family; PDBTitle: crystal structure of aibc |
| 57 | c4cpdA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: alcohol dehydrogenase tadh from thermus sp. atn1 |
| 58 | 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 |
| 59 | c5fi5A | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: tetrahydroalstonine synthase; PDBTitle: heteroyohimbine synthase thas1 from catharanthus roseus - apo form |
| 60 | c1yqxB | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: sinapyl alcohol dehydrogenase; PDBTitle: sinapyl alcohol dehydrogenase at 2.5 angstrom resolution |
| 61 | c4a2cB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: galactitol-1-phosphate 5-dehydrogenase; PDBTitle: crystal structure of galactitol-1-phosphate dehydrogenase from2 escherichia coli |
| 62 | c2j3iB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent oxidoreductase p1; PDBTitle: crystal structure of arabidopsis thaliana double bond2 reductase (at5g16970)-binary complex |
| 63 | c4dviA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative zinc-dependent alcohol dehydrogenase protein; PDBTitle: crystal structure of a putative zinc-dependent alcohol dehydrogenase2 protein from rhizobium etli cfn 42 |
| 64 | c1h2bA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a resolution |
| 65 | c5vktB | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: cinnamyl alcohol dehydrogenases (sbcad4); PDBTitle: cinnamyl alcohol dehydrogenases (sbcad4) from sorghum bicolor (l.)2 moench |
| 66 | c4b7cB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of hypothetical protein pa1648 from2 pseudomonas aeruginosa. |
| 67 | c2dphA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: formaldehyde dismutase; PDBTitle: crystal structure of formaldehyde dismutase |
| 68 | c5dp1A | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: curk; PDBTitle: crystal structure of curk enoyl reductase |
| 69 | c4oaqA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: r-specific carbonyl reductase; PDBTitle: crystal structure of the r-specific carbonyl reductase from candida2 parapsilosis atcc 7330 |
| 70 | c4ilkB | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: starvation sensing protein rspb; PDBTitle: crystal structure of short chain alcohol dehydrogenase (rspb) from e.2 coli cft073 (efi target efi-506413) complexed with cofactor nadh |
| 71 | c1piwA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase 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 |
| 72 | c1uufA | Alignment | not modelled | 100.0 | 17 | 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 |
| 73 | c2ouiB | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica |
| 74 | c2w4qA | Alignment | not modelled | 100.0 | 17 | 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 |
| 75 | c5h81A | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: heteroyohimbine synthase thas2; PDBTitle: heteroyohimbine synthase thas2 from catharanthus roseus - complex with2 nadp+ |
| 76 | c4eyeA | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase; PDBTitle: crystal structure of a probable oxidoreductase from mycobacterium2 abscessus solved by iodide ion sad |
| 77 | c1xa0B | Alignment | not modelled | 100.0 | 21 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nadph dependent oxidoreductases; PDBTitle: crystal structure of mcsg target apc35536 from bacillus2 stearothermophilus |
| | | | | | | PDB header: oxidoreductase |

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|-----|------------------------|-----------|--------------|-------|----|--|
| 78 | c5dp2A | Alignment | not modelled | 100.0 | 18 | Chain: A: PDB Molecule: curf; PDBTitle: curf er cyclopropanase from curacin a biosynthetic pathway |
| 79 | c3ip1C | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol dehydrogenase, zinc-containing; PDBTitle: structure of putative alcohol dehydrogenase (tm_042) from thermotoga2 maritima |
| 80 | c1e3jA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadp(h)-dependent ketose reductase; PDBTitle: ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly |
| 81 | c3tqhA | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinone oxidoreductase; PDBTitle: structure of the quinone oxidoreductase from coxiella burnetii |
| 82 | c4dupB | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: quinone oxidoreductase; PDBTitle: crystal structure of a quinone oxidoreductase from rhizobium etli cfm2 42 |
| 83 | c4ejmA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative zinc-binding dehydrogenase; PDBTitle: crystal structure of a putative zinc-binding dehydrogenase (target2 psi-012003) from sinorhizobium meliloti 1021 bound to nadp |
| 84 | c5vm2A | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of eck1772, an oxidoreductase/dehydrogenase of2 unknown specificity involved in membrane biogenesis from escherichia3 coli |
| 85 | c1kevB | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent alcohol dehydrogenase; PDBTitle: structure of nadp-dependent alcohol dehydrogenase |
| 86 | c1kolA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: formaldehyde dehydrogenase; PDBTitle: crystal structure of formaldehyde dehydrogenase |
| 87 | c3iupB | Alignment | not modelled | 100.0 | 19 | 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 |
| 88 | c4mkrC | Alignment | not modelled | 100.0 | 16 | PDB header: plant protein Chain: C: PDB Molecule: zingiber officinale double bond reductase; PDBTitle: structure of the apo form of a zingiber officinale double bond2 reductase |
| 89 | c2cdaA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucose dehydrogenase; PDBTitle: sulfolobus solfataricus glucose dehydrogenase 1 in complex with nadp |
| 90 | c6dkhC | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: l-idonate 5-dehydrogenase (nad(p)(+)); PDBTitle: the crystal structure of l-idonate 5-dehydrogenase from escherichia2 coli str. k-12 substr. mg1655 |
| 91 | c2vvpA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucose dehydrogenase; PDBTitle: haloferax mediterranei glucose dehydrogenase in complex with nadph and2 zn. |
| 92 | c3gohA | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase 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 |
| 93 | c6eowC | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: C: PDB Molecule: ketone/zingerone synthase 1; PDBTitle: structure of raspberry ketone synthase with hydroxybenzalacetone |
| 94 | c5dovB | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: jamj; PDBTitle: crystal structure of jamj enoyl reductase (apo form) |
| 95 | c2vn8B | Alignment | not modelled | 100.0 | 20 | PDB header: receptor inhibitor Chain: B: PDB Molecule: reticulon-4-interacting protein 1; PDBTitle: crystal structure of human reticulon 4 interacting protein 1 in2 complex with nadph |
| 96 | c1zsvB | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent leukotriene b4 12- PDBTitle: crystal structure of human nadp-dependent leukotriene b4 12-2 hydroxydehydrogenase |
| 97 | c3widC | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: C: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: structure of a glucose dehydrogenase t277f mutant in complex with nadp |
| 98 | c1iz0A | Alignment | not modelled | 100.0 | 29 | 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 |
| 99 | c3m6iA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinitol 4-dehydrogenase; PDBTitle: l-arabinitol 4-dehydrogenase |
| 100 | c4idbA | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: ripening-induced protein; PDBTitle: structure of the fragaria x ananassa enone oxidoreductase in complex2 with nadp+ |
| 101 | c2h6eA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-arabinose 1-dehydrogenase; PDBTitle: crystal structure of the d-arabinose dehydrogenase from sulfolobus2 solfataricus |
| 102 | c3slkB | Alignment | not modelled | 100.0 | 28 | PDB header: oxidoreductase Chain: B: PDB Molecule: polyketide synthase extender module 2; PDBTitle: structure of ketoreductase and enoylreductase didomain from modular2 polyketide synthase |
| 103 | c6fn6A | Alignment | not modelled | 100.0 | 23 | PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase 1, isoform a; |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 103 | dlu0a1 | Alignment | not modelled | 99.9 | 43 | PDBTitle: modifying region (dh-er-kr) of an insect fatty acid synthase (fas) |
| 104 | dluufa1 | Alignment | not modelled | 99.9 | 15 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 105 | dlp0fa1 | Alignment | not modelled | 99.9 | 17 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 106 | dlf8fa1 | Alignment | not modelled | 99.9 | 15 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 107 | dlpl8a1 | Alignment | not modelled | 99.8 | 11 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 108 | dlcdoa1 | Alignment | not modelled | 99.8 | 22 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 109 | dlu3wa1 | Alignment | not modelled | 99.8 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 110 | dlyb5a1 | Alignment | not modelled | 99.8 | 28 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 111 | dld1ta1 | Alignment | not modelled | 99.8 | 24 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 112 | dlu3ta1 | Alignment | not modelled | 99.8 | 23 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 113 | dlpiwa1 | Alignment | not modelled | 99.8 | 21 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 114 | dlgu7a1 | Alignment | not modelled | 99.8 | 15 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 115 | dljvba1 | Alignment | not modelled | 99.8 | 18 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 116 | dlu3ua1 | Alignment | not modelled | 99.8 | 21 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 117 | dlo89a1 | Alignment | not modelled | 99.8 | 16 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 118 | d1llua1 | Alignment | not modelled | 99.8 | 29 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 119 | dlvj0a1 | Alignment | not modelled | 99.8 | 16 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |
| 120 | dlxa0a1 | Alignment | not modelled | 99.8 | 26 | Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain |