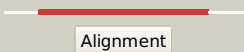

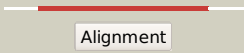



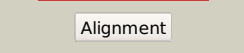



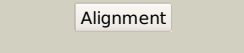

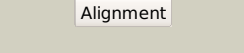



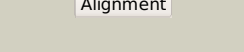

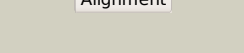

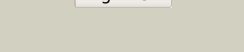



Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2338c_(moeW)_2613117_2614073 |
| Date | Mon Aug 5 13:25:49 BST 2019 |
| Unique Job ID | 3fe910271ce958d5 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c6h77B_ |  Alignment |  | 100.0 | 22 | PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl |
| 2 | d1yovb1 |  Alignment |  | 100.0 | 23 | Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA) |
| 3 | c1zfnA_ |  Alignment |  | 100.0 | 25 | PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif |
| 4 | c3h9gA_ |  Alignment |  | 100.0 | 19 | PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn |
| 5 | d1jw9b_ |  Alignment |  | 100.0 | 23 | Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB |
| 6 | c3gznb_ |  Alignment |  | 100.0 | 23 | PDB header: protein binding/ligase Chain: B: PDB Molecule: nedd8-activating enzyme e1 catalytic subunit; PDBTitle: structure of nedd8-activating enzyme in complex with nedd8 and mln4924 |
| 7 | c5ff5A_ |  Alignment |  | 100.0 | 19 | PDB header: transferase Chain: A: PDB Molecule: paaa; PDBTitle: crystal structure of semet paaa |
| 8 | c4d7aA_ |  Alignment |  | 100.0 | 23 | PDB header: ligase Chain: A: PDB Molecule: trna threonylcarbamoyladenosine dehydratase; PDBTitle: crystal structure of e. coli trna n6-threonylcarbamoyladenosine2 dehydratase, tcda, in complex with amp at 1.801 angstroem3 resolution |
| 9 | c2nvuB_ |  Alignment |  | 100.0 | 22 | PDB header: protein turnover, ligase Chain: B: PDB Molecule: maltose binding protein/nedd8-activating enzyme PDBTitle: structure of appbp1-uba3~nedd8-nedd8-mgatp-ubc12(c111a), a2 trapped ubiquitin-like protein activation complex |
| 10 | c3kydB_ |  Alignment |  | 100.0 | 22 | PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1~sumo1-amp tetrahedral intermediate mimic |
| 11 | c3kycB_ |  Alignment |  | 100.0 | 23 | PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1 complex with a sumo1-amp mimic |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c1y8qD_ | Alignment | | 100.0 | 24 | PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex |
| 13 | c1y8qA_ | Alignment | | 100.0 | 18 | PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex |
| 14 | c3vh1A_ | Alignment | | 100.0 | 18 | PDB header: metal binding protein Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of saccharomyces cerevisiae atg7 (1-595) |
| 15 | c3vh3A_ | Alignment | | 100.0 | 17 | PDB header: metal binding protein/protein transport Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of atg7ctd-atg8 complex |
| 16 | c3cmmA_ | Alignment | | 100.0 | 28 | PDB header: ligase/protein binding Chain: A: PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of the uba1-ubiquitin complex |
| 17 | c6dc6A_ | Alignment | | 100.0 | 20 | PDB header: signaling protein/ligase Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin |
| 18 | c4ii3A_ | Alignment | | 100.0 | 21 | PDB header: ligase Chain: A: PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of s. pombe ubiquitin activating enzyme 1 (uba1) in2 complex with ubiquitin and atp/mg |
| 19 | d1yova1 | Alignment | | 100.0 | 21 | Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA) |
| 20 | c4p22A_ | Alignment | | 100.0 | 22 | PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of n-terminal fragments of e1 |
| 21 | c3wv9D_ | Alignment | not modelled | 100.0 | 18 | PDB header: transferase Chain: D: PDB Molecule: hmd co-occurring protein hcge; PDBTitle: guanylylpyridinol (gp)- and atp-bound hcge from methanothermobacter2 marburgensis |
| 22 | c3gucB_ | Alignment | not modelled | 100.0 | 19 | PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp |
| 23 | c4rl6A_ | Alignment | not modelled | 98.7 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04l03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105 |
| 24 | c1e5IA_ | Alignment | not modelled | 98.7 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea |
| 25 | c2axqA_ | Alignment | not modelled | 98.6 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae |
| 26 | c5l78A_ | Alignment | not modelled | 98.5 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form) |
| 27 | c4bs9A_ | Alignment | not modelled | 98.5 | 18 | PDB header: isomerase Chain: A: PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud |
| | | | | | | PDB header: structural genomics, unknown function |

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|----|--------------------------|-----------|--------------|------|----|---|
| 28 | c3ic5A_ | Alignment | not modelled | 98.3 | 21 | Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi. |
| 29 | d1vi2a1 | Alignment | not modelled | 98.3 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 30 | c4inaA_ | Alignment | not modelled | 98.2 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolfinella2 succinogenes. northeast structural genomics consortium target wsr35 |
| 31 | c3tozA_ | Alignment | not modelled | 98.1 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.2 angstrom crystal structure of shikimate 5-dehydrogenase from2 listeria monocytogenes in complex with nad. |
| 32 | d1pjqa1 | Alignment | not modelled | 98.1 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like |
| 33 | c2z2vA_ | Alignment | not modelled | 98.1 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii |
| 34 | c1vi2B_ | Alignment | not modelled | 98.1 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase 2; PDBTitle: crystal structure of shikimate-5-dehydrogenase with nad |
| 35 | c2nloA_ | Alignment | not modelled | 98.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of the quinate dehydrogenase from corynebacterium2 glutamicum |
| 36 | c4plpB_ | Alignment | not modelled | 98.0 | 17 | PDB header: transferase Chain: B: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase (hss) from2 blastochloris viridis in complex with nad |
| 37 | c1gpjA_ | Alignment | not modelled | 97.9 | 20 | PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri |
| 38 | d1e5qa1 | Alignment | not modelled | 97.9 | 15 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain |
| 39 | d2pgda2 | Alignment | not modelled | 97.9 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 40 | c3pgjB_ | Alignment | not modelled | 97.9 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate dehydrogenase; PDBTitle: 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate |
| 41 | c2eggA_ | Alignment | not modelled | 97.9 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of shikimate 5-dehydrogenase (aroe) from geobacillus2 kaustophilus |
| 42 | d1pzqa1 | Alignment | not modelled | 97.9 | 19 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 43 | c3tumA_ | Alignment | not modelled | 97.9 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase family protein; PDBTitle: 2.15 angstrom resolution crystal structure of a shikimate2 dehydrogenase family protein from pseudomonas putida kt2440 in3 complex with nad+ |
| 44 | c4n7rB_ | Alignment | not modelled | 97.8 | 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 |
| 45 | d1luxja1 | Alignment | not modelled | 97.8 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 46 | d2nu7a1 | Alignment | not modelled | 97.7 | 13 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 47 | c3u62A_ | Alignment | not modelled | 97.7 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from thermotoga maritima |
| 48 | c3o8qB_ | Alignment | not modelled | 97.7 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: shikimate 5-dehydrogenase i alpha; PDBTitle: 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae |
| 49 | d1oi7a1 | Alignment | not modelled | 97.7 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 50 | c2hjrK_ | Alignment | not modelled | 97.7 | 18 | PDB header: oxidoreductase Chain: K: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of cryptosporidium parvum malate2 dehydrogenase |
| 51 | c6iauB_ | Alignment | not modelled | 97.6 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine |
| 52 | c4bgvB_ | Alignment | not modelled | 97.6 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: malate dehydrogenase; PDBTitle: 1.8 a resolution structure of the malate dehydrogenase from2 picrophilus torridus in its apo form |
| 53 | c1npyA_ | Alignment | not modelled | 97.6 | 19 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical shikimate 5-dehydrogenase-like protein hi0607; PDBTitle: structure of shikimate 5-dehydrogenase-like protein |

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|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | hi0607 |
| 54 | c1pjtB | Alignment | not modelled | 97.6 | 19 | PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatase for3 siroheme synthesis |
| 55 | c3donA | Alignment | not modelled | 97.6 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis |
| 56 | c1pggA | Alignment | not modelled | 97.6 | 18 | PDB header: oxidoreductase (chod(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 |
| 57 | d9ldta1 | Alignment | not modelled | 97.6 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 58 | d1gpja2 | Alignment | not modelled | 97.6 | 23 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 59 | d1pgja2 | Alignment | not modelled | 97.6 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 60 | c2ph5A | Alignment | not modelled | 97.5 | 19 | PDB header: transferase Chain: A: PDB Molecule: homospemidine synthase; PDBTitle: crystal structure of the homospemidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54 |
| 61 | c6fqzB | Alignment | not modelled | 97.5 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate |
| 62 | c3fwnB | Alignment | not modelled | 97.5 | 15 | 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 |
| 63 | c2iz1C | Alignment | not modelled | 97.5 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data |
| 64 | c4tskA | Alignment | not modelled | 97.5 | 25 | PDB header: oxidoreductase,isomerase Chain: A: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: ketol-acid reductoisomerase from alicyclobacillus acidocaldarius |
| 65 | d1pjca1 | Alignment | not modelled | 97.5 | 18 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain |
| 66 | d1npya1 | Alignment | not modelled | 97.5 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 67 | c4xijA | Alignment | not modelled | 97.5 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate 5-dehydrogenase; PDBTitle: crystal structure of a shikimate 5-dehydrogenase from mycobacterium2 fortuitum determined by iodide sad phasing |
| 68 | c2fnzA | Alignment | not modelled | 97.5 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid) |
| 69 | c4ypoB | Alignment | not modelled | 97.5 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+ |
| 70 | c1pgjA | Alignment | not modelled | 97.5 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei |
| 71 | c4e21B | Alignment | not modelled | 97.5 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens |
| 72 | c3pvzD | Alignment | not modelled | 97.5 | 14 | PDB header: lyase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri |
| 73 | d1i0za1 | Alignment | not modelled | 97.5 | 12 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 74 | c5swvC | Alignment | not modelled | 97.5 | 12 | PDB header: lyase Chain: C: PDB Molecule: pentafunctional arom polypeptide; PDBTitle: dehydroquinate dehydratase and shikimate dehydrogenase from s. pombe2 arom |
| 75 | c4ywjB | Alignment | not modelled | 97.5 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa |
| 76 | c3pwzA | Alignment | not modelled | 97.5 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase 3; PDBTitle: crystal structure of an ael1 enzyme from pseudomonas putida |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 77 | d1u8xx1 | Alignment | not modelled | 97.5 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 78 | c4kqxB | Alignment | not modelled | 97.5 | 16 | 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 |
| 79 | d1np3a2 | Alignment | not modelled | 97.5 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |
| 80 | c1pzfD | Alignment | not modelled | 97.5 | 25 | PDB header: oxidoreductase Chain: D: PDB Molecule: lactate dehydrogenase; PDBTitle: t.gondii ldh1 ternary complex with apad+ and oxalate |
| 81 | c4xdzB | Alignment | not modelled | 97.5 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans |
| 82 | c5yeqB | Alignment | not modelled | 97.5 | 15 | PDB header: isomerase Chain: B: PDB Molecule: ketol-acid reductoisomerase (nadp(+)); PDBTitle: the structure of sac-kari protein |
| 83 | c3nzoB | Alignment | not modelled | 97.5 | 14 | PDB header: lyase Chain: B: PDB Molecule: udp-n-acetylglucosamine 4,6-dehydratase; PDBTitle: udp-n-acetylglucosamine 4,6-dehydratase from vibrio fischeri. |
| 84 | c1bg6A | Alignment | not modelled | 97.4 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c |
| 85 | c3k6jA | Alignment | not modelled | 97.4 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans |
| 86 | c4omuA | Alignment | not modelled | 97.4 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase; PDBTitle: crystal structure of shikimate dehydrogenase (aroe) from pseudomonas2 putida |
| 87 | d1euca1 | Alignment | not modelled | 97.4 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain |
| 88 | c1ldbA | Alignment | not modelled | 97.4 | 25 | PDB header: oxidoreductase(choh(d)-nad(a)) Chain: A: PDB Molecule: apo-l-lactate dehydrogenase; PDBTitle: structure determination and refinement of bacillus2 stearothermophilus lactate dehydrogenase |
| 89 | c5nfrI | Alignment | not modelled | 97.4 | 13 | PDB header: oxidoreductase Chain: I: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from plasmodium falciparum2 (pfmdh) |
| 90 | c5dzsA | Alignment | not modelled | 97.4 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: shikimate dehydrogenase (nadp(+)); PDBTitle: 1.5 angstrom crystal structure of shikimate dehydrogenase 1 from2 peptoclostridium difficile. |
| 91 | c2p4qA | Alignment | not modelled | 97.4 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae |
| 92 | c4ezbA | Alignment | not modelled | 97.4 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein from2 sinorhizobium meliloti 1021 |
| 93 | c1np3B | Alignment | not modelled | 97.4 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoxyhydroxy acid isomereoreductase from2 pseudomonas aeruginosa |
| 94 | c6iaqA | Alignment | not modelled | 97.4 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis |
| 95 | c1z7eC | Alignment | not modelled | 97.4 | 21 | PDB header: hydrolase Chain: C: PDB Molecule: protein arna; PDBTitle: crystal structure of full length arna |
| 96 | c4mp6A | Alignment | not modelled | 97.4 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative ornithine cyclodeaminase; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbnb bound to citrate2 and nad+ |
| 97 | c1u4sA | Alignment | not modelled | 97.4 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase; PDBTitle: plasmodium falciparum lactate dehydrogenase complexed with 2,6-2 naphthalenedisulphonic acid |
| 98 | c5ugjC | Alignment | not modelled | 97.3 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis |
| 99 | c4xcvA | Alignment | not modelled | 97.3 | 20 | 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 |
| 100 | d1s6ya1 | Alignment | not modelled | 97.3 | 17 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 101 | c1drwA | Alignment | not modelled | 97.3 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 102 | c1m67A_ | Alignment | not modelled | 97.3 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine |
| 103 | d1i10a1 | Alignment | not modelled | 97.3 | 9 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 104 | d1nvtA1 | Alignment | not modelled | 97.3 | 20 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain |
| 105 | c6ihdA_ | Alignment | not modelled | 97.3 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of malate dehydrogenase from metallosphaera sedula |
| 106 | c2dc1A_ | Alignment | not modelled | 97.3 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus |
| 107 | c1mldA_ | Alignment | not modelled | 97.2 | 28 | PDB header: oxidoreductase(nad(a)-chod(d)) Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases |
| 108 | c4plcA_ | Alignment | not modelled | 97.2 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: lactate dehydrogenase; PDBTitle: crystal structure of ancestral apicomplexan lactate dehydrogenase with2 malate. |
| 109 | c3k96B_ | Alignment | not modelled | 97.2 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii |
| 110 | d2ldxa1 | Alignment | not modelled | 97.2 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 111 | d2jfga1 | Alignment | not modelled | 97.2 | 20 | Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain |
| 112 | d1obba1 | Alignment | not modelled | 97.2 | 14 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 113 | c2v65A_ | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-lactate dehydrogenase a chain; PDBTitle: apo ldh from the psychrophile c. gunnari |
| 114 | d5ldha1 | Alignment | not modelled | 97.2 | 10 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like |
| 115 | c3db2C_ | Alignment | not modelled | 97.2 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution |
| 116 | c2qx7A_ | Alignment | not modelled | 97.2 | 12 | PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum |
| 117 | c5y8mA_ | Alignment | not modelled | 97.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba) |
| 118 | c4n18A_ | Alignment | not modelled | 97.1 | 26 | 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 |
| 119 | c3pqeD_ | Alignment | not modelled | 97.1 | 28 | PDB header: oxidoreductase Chain: D: PDB Molecule: l-lactate dehydrogenase; PDBTitle: crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation |
| 120 | d1n1ea2 | Alignment | not modelled | 97.1 | 11 | Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain |