
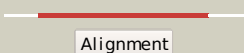

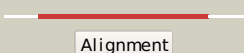
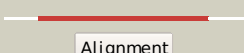





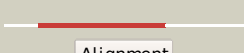
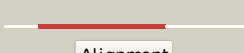














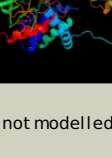

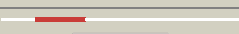
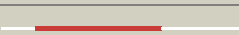
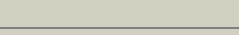
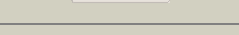
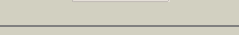
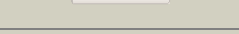
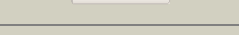
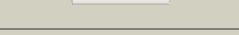
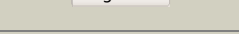
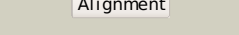

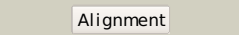
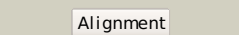
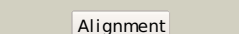









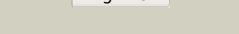


| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|---|
| 1 | c3cp8C_ |  Alignment |  | 100.0 | 48 | PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum |
| 2 | c2zziC_ |  Alignment |  | 100.0 | 52 | PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal |
| 3 | c3g05B_ |  Alignment |  | 100.0 | 100 | PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mmmg |
| 4 | c3cesB_ |  Alignment |  | 100.0 | 100 | PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of e.coli mmmg (gida), a highly- conserved trna2 modifying enzyme |
| 5 | c3g5rA_ |  Alignment |  | 100.0 | 28 | PDB header: transferase Chain: A: PDB Molecule: methylenetetrahydrofolate--trna-(uracil-5-)- PDBTitle: crystal structure of thermus thermophilus trmfo in complex with 2 tetrahydrofolate |
| 6 | d2cula1 |  Alignment |  | 100.0 | 25 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GidA-like |
| 7 | c2i0zA_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-utilizing dehydrogenases; PDBTitle: crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases |
| 8 | c1jrxA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina |
| 9 | c3p4rM_ |  Alignment |  | 99.9 | 20 | PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate |
| 10 | c1kf6A_ |  Alignment |  | 99.9 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno |
| 11 | c2fjaC_ |  Alignment |  | 99.9 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with2 substrate |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | d2gqfa1 | Alignment |  | 99.9 | 23 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like |
| 13 | c1d4cB_ | Alignment |  | 99.9 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1 |
| 14 | c1yq4A_ | Alignment |  | 99.9 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone |
| 15 | c1qo8A_ | Alignment |  | 99.9 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase |
| 16 | c2gqfA_ | Alignment |  | 99.9 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd |
| 17 | c3nlcA_ | Alignment |  | 99.9 | 17 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vp0956; PDBTitle: crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147 |
| 18 | c2aczA_ | Alignment |  | 99.9 | 16 | PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site |
| 19 | c3v76A_ | Alignment |  | 99.9 | 16 | PDB header: flavoprotein Chain: A: PDB Molecule: flavoprotein; PDBTitle: the crystal structure of a flavoprotein from sinorhizobium meliloti |
| 20 | c2bs3A_ | Alignment |  | 99.9 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes |
| 21 | c3gyxA_ | Alignment | not modelled | 99.9 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas |
| 22 | c1chuA_ | Alignment | not modelled | 99.9 | 20 | PDB header: flavoenzyme Chain: A: PDB Molecule: protein (l-aspartate oxidase); PDBTitle: structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family |
| 23 | c2e5vA_ | Alignment | not modelled | 99.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii |
| 24 | d1qo8a2 | Alignment | not modelled | 99.8 | 24 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 25 | d1y0pa2 | Alignment | not modelled | 99.8 | 24 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 26 | d1d4ca2 | Alignment | not modelled | 99.8 | 26 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 27 | c1x31A_ | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96 |
| 28 | c1hyuA_ | Alignment | not modelled | 99.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf |
| | | | | | | Fold: FAD/NAD(P)-binding domain |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | d1chua2 | Alignment | not modelled | 99.8 | 28 | Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 30 | d2i0za1 | Alignment | not modelled | 99.7 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like |
| 31 | d2bs2a2 | Alignment | not modelled | 99.7 | 24 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 32 | c3ab1B_ | Alignment | not modelled | 99.7 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase |
| 33 | c3r9uA_ | Alignment | not modelled | 99.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni. |
| 34 | c3fbsB_ | Alignment | not modelled | 99.7 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens |
| 35 | c2v6oA_ | Alignment | not modelled | 99.7 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtrg) |
| 36 | d1jnra2 | Alignment | not modelled | 99.7 | 20 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 37 | c2zbwA_ | Alignment | not modelled | 99.7 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8 |
| 38 | c3f8rD_ | Alignment | not modelled | 99.6 | 17 | PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trx-3); PDBTitle: crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules |
| 39 | c2w0hA_ | Alignment | not modelled | 99.6 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph |
| 40 | d1lpfa1 | Alignment | not modelled | 99.6 | 18 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 41 | c1ndaD_ | Alignment | not modelled | 99.6 | 23 | PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state |
| 42 | c2gmhA_ | Alignment | not modelled | 99.6 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone |
| 43 | c3o0hA_ | Alignment | not modelled | 99.6 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae |
| 44 | c1fi2A_ | Alignment | not modelled | 99.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli |
| 45 | d1kf6a2 | Alignment | not modelled | 99.6 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 46 | c2q0lA_ | Alignment | not modelled | 99.6 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+ |
| 47 | c1ojtA_ | Alignment | not modelled | 99.6 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase |
| 48 | d3grsa1 | Alignment | not modelled | 99.6 | 20 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 49 | c2c3dB_ | Alignment | not modelled | 99.6 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxopropyl-com reductase; PDBTitle: 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site |
| 50 | c1tytA_ | Alignment | not modelled | 99.6 | 10 | PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase, oxidized form; PDBTitle: crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution |
| 51 | c2a87A_ | Alignment | not modelled | 99.6 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase |
| 52 | c1f6mF_ | Alignment | not modelled | 99.6 | 13 | PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+ |
| 53 | c1zmcG_ | Alignment | not modelled | 99.6 | 13 | PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+ |
| 54 | c3lzxB_ | Alignment | not modelled | 99.6 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii) |

| | | | | | | |
|----|-------------------------|---|--------------|------|----|---|
| 55 | c3da1A |  Alignment | not modelled | 99.6 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167. |
| 56 | c3jskN |  Alignment | not modelled | 99.6 | 23 | PDB header: biosynthetic protein Chain: N: PDB Molecule: cypbp37 protein; PDBTitle: thiazole synthase from neurospora crassa |
| 57 | c2eq8E |  Alignment | not modelled | 99.6 | 35 | PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp |
| 58 | c1vdcA |  Alignment | not modelled | 99.5 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase |
| 59 | d3lada1 |  Alignment | not modelled | 99.5 | 18 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 60 | c3dgzA |  Alignment | not modelled | 99.5 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation |
| 61 | d1rp0a1 |  Alignment | not modelled | 99.5 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like |
| 62 | c1y56A |  Alignment | not modelled | 99.5 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii |
| 63 | d1w4xa1 |  Alignment | not modelled | 99.5 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 64 | c2rghA |  Alignment | not modelled | 99.5 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 65 | c1dxcC |  Alignment | not modelled | 99.5 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum |
| 66 | c3ic9D |  Alignment | not modelled | 99.5 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h. |
| 67 | d1lvia1 |  Alignment | not modelled | 99.5 | 20 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 68 | c2q7vA |  Alignment | not modelled | 99.5 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase |
| 69 | c3ka7A |  Alignment | not modelled | 99.5 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208 |
| 70 | c1v59B |  Alignment | not modelled | 99.5 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+ |
| 71 | c2hqmB |  Alignment | not modelled | 99.5 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae |
| 72 | d1ryia1 |  Alignment | not modelled | 99.5 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 73 | d1neka2 |  Alignment | not modelled | 99.5 | 23 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 74 | c1ltxR |  Alignment | not modelled | 99.5 | 20 | PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid |
| 75 | d1dxa1 |  Alignment | not modelled | 99.5 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 76 | c3d8xB |  Alignment | not modelled | 99.5 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1 |
| 77 | c2rgoA |  Alignment | not modelled | 99.5 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 78 | c3ctyA |  Alignment | not modelled | 99.5 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase |
| 79 | d1h6va1 |  Alignment | not modelled | 99.5 | 18 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | domains |
| 80 | d1feca1 | Alignment | not modelled | 99.5 | 16 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 81 | c1lpfB | Alignment | not modelled | 99.5 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties |
| 82 | c1s3bB | Alignment | not modelled | 99.5 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase [flavin-containing] b; PDBTitle: crystal structure of maob in complex with n-methyl-n-2 propargyl-1(r)-aminoindan |
| 83 | d1pj5a2 | Alignment | not modelled | 99.5 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 84 | c3atrA | Alignment | not modelled | 99.5 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand |
| 85 | c3dmeB | Alignment | not modelled | 99.5 | 17 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141 |
| 86 | c1pj6A | Alignment | not modelled | 99.5 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: n,n-dimethylglycine oxidase; PDBTitle: crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid |
| 87 | c2a8xA | Alignment | not modelled | 99.5 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis |
| 88 | d2gf3a1 | Alignment | not modelled | 99.5 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 89 | c2r4jA | Alignment | not modelled | 99.5 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap |
| 90 | c2ardA | Alignment | not modelled | 99.5 | 17 | PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase prna; PDBTitle: the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination |
| 91 | c3k30B | Alignment | not modelled | 99.5 | 24 | PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex |
| 92 | c3djeA | Alignment | not modelled | 99.5 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine: oxygen oxidoreductase; PDBTitle: crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa |
| 93 | c1w4xA | Alignment | not modelled | 99.4 | 19 | PDB header: oxygenase Chain: A: PDB Molecule: phenylacetone monooxygenase; PDBTitle: phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase |
| 94 | d1vg0a1 | Alignment | not modelled | 99.4 | 20 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 95 | c3e1tA | Alignment | not modelled | 99.4 | 23 | PDB header: flavoprotein Chain: A: PDB Molecule: halogenase; PDBTitle: structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases |
| 96 | d1d5ta1 | Alignment | not modelled | 99.4 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 97 | d2gmha1 | Alignment | not modelled | 99.4 | 13 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 98 | c2cfyB | Alignment | not modelled | 99.4 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1 |
| 99 | d1ojta1 | Alignment | not modelled | 99.4 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 100 | c1bwcA | Alignment | not modelled | 99.4 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate |
| 101 | c2pyxA | Alignment | not modelled | 99.4 | 15 | PDB header: biosynthetic protein Chain: A: PDB Molecule: tryptophan halogenase; PDBTitle: crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution |
| 102 | c1fcdB | Alignment | not modelled | 99.4 | 17 | PDB header: electron transport(flavocytochrome) Chain: B: PDB Molecule: flavocytochrome c sulfide dehydrogenase (flavin- PDBTitle: the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution |
| 103 | c3gwdA | Alignment | not modelled | 99.4 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase |
| 104 | d1v59a1 | Alignment | not modelled | 99.4 | 22 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 104 | d1v39a1 | Alignment | not modelled | 99.4 | 42 | Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 105 | c3i3lA_ | Alignment | not modelled | 99.4 | 16 | PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase |
| 106 | d2bcgg1 | Alignment | not modelled | 99.4 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 107 | c2e4gB_ | Alignment | not modelled | 99.4 | 20 | PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp |
| 108 | c1lviA_ | Alignment | not modelled | 99.4 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the refined structure of pseudomonas putida lipamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution |
| 109 | c1geuA_ | Alignment | not modelled | 99.4 | 20 | PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site |
| 110 | c1gthD_ | Alignment | not modelled | 99.4 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpg) from pig, ternary2 complex with nadph and 5-iodouracil |
| 111 | c3l8kB_ | Alignment | not modelled | 99.4 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus |
| 112 | d1aoga1 | Alignment | not modelled | 99.4 | 13 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 113 | c1zx9A_ | Alignment | not modelled | 99.4 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera |
| 114 | c2qaeA_ | Alignment | not modelled | 99.4 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipamide2 dehydrogenase |
| 115 | d1trba1 | Alignment | not modelled | 99.4 | 22 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains |
| 116 | c2olnA_ | Alignment | not modelled | 99.4 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: nikd protein; PDBTitle: nikd, an unusual amino acid oxidase essential for2 nikkomycin biosynthesis: closed form at 1.15 a resolution |
| 117 | c2eq7B_ | Alignment | not modelled | 99.4 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo |
| 118 | c1zkqA_ | Alignment | not modelled | 99.4 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2 |
| 119 | c1ebdB_ | Alignment | not modelled | 99.4 | 13 | PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase |
| 120 | c3ps9A_ | Alignment | not modelled | 99.4 | 18 | PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmc from e. coli |