

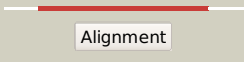

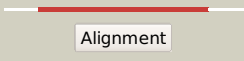

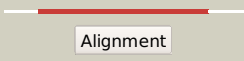

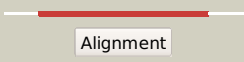
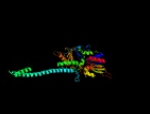
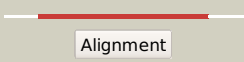
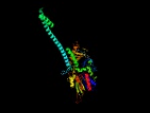
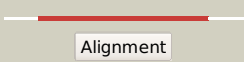

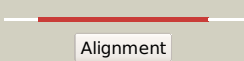

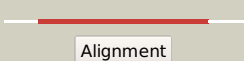

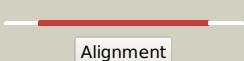

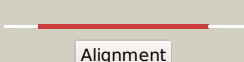



Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD0897c_(-)_1000811_1002418 |
| Date | Fri Jul 26 01:50:49 BST 2019 |
| Unique Job ID | d3513e8583f2279d |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4repA_ |  Alignment |  | 100.0 | 13 | PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase |
| 2 | c5mogB_ |  Alignment |  | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon |
| 3 | c1s3bB_ |  Alignment |  | 100.0 | 15 | 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 |
| 4 | c4i58A_ |  Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a |
| 5 | c2v1dA_ |  Alignment |  | 100.0 | 15 | PDB header: oxidoreductase/repressor Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: structural basis of lsd1-corest selectivity in histone h32 recognition |
| 6 | c2xagA_ |  Alignment |  | 100.0 | 15 | PDB header: transcription Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1-corest in complex with para-bromo-2 (-)-trans-2-phenylcyclopropyl-1-amine |
| 7 | c4iv9B_ |  Alignment |  | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: tryptophan 2-monooxygenase; PDBTitle: structure of the flavoprotein tryptophan-2-monooxygenase |
| 8 | c3rhaA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: putrescine oxidase; PDBTitle: the crystal structure of oxidoreductase from arthrobacter aureus |
| 9 | c3ka7A_ |  Alignment |  | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208 |
| 10 | c2ivdA_ |  Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen |
| 11 | c3bnuA_ |  Alignment |  | 100.0 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase fms1; PDBTitle: crystal structure of polyamine oxidase fms1 from2 saccharomyces cerevisiae in complex with bis-(3s,3's)-3 methylated spermine |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 12 | c2yg4B_ | Alignment | | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: putrescine oxidase; PDBTitle: structure-based redesign of cofactor binding in putrescine2 oxidase: wild type bound to putrescine |
| 13 | c5ttkB_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida |
| 14 | c1f8sA_ | Alignment | | 100.0 | 11 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase; PDBTitle: crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate. |
| 15 | c2hkoA_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1; PDBTitle: crystal structure of lsd1 |
| 16 | c5mbxA_ | Alignment | | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal n(1)-acetyl-spermine/spermidine oxidase; PDBTitle: crystal structure of reduced murine n1-acetylpolyamine oxidase in2 complex with n1-acetylspermine |
| 17 | c5g3sB_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: l-tryptophan oxidase viaa; PDBTitle: the structure of the l-tryptophan oxidase viaa from chromobacterium2 violaceum - samarium derivative |
| 18 | c4dgaA_ | Alignment | | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis |
| 19 | c2vviD_ | Alignment | | 100.0 | 14 | PDB header: oxidoreductase Chain: D: PDB Molecule: monoamine oxidase n; PDBTitle: the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger. |
| 20 | c4gutA_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific histone demethylase 1b; PDBTitle: crystal structure of lsd2-npac |
| 21 | c3x0vA_ | Alignment | not modelled | 100.0 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-lysine oxidase; PDBTitle: structure of l-lysine oxidase |
| 22 | c6cr0A_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-6-hydroxynicotine oxidase; PDBTitle: 1.55 a resolution structure of (s)-6-hydroxynicotine oxidase from2 shinella hzn7 |
| 23 | c2jb1B_ | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in complex2 with l-alanine |
| 24 | c1sezA_ | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase, mitochondrial; PDBTitle: crystal structure of protoporphyrinogen ix oxidase |
| 25 | c3nksA_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of human protoporphyrinogen ix oxidase |
| 26 | c3we0A_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase/monooxygenase; PDBTitle: l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813 |
| 27 | c1ltxR_ | Alignment | not modelled | 100.0 | 12 | PDB header: transferase/protein binding Chain: R: PDB Molecule: rab escort protein 1; PDBTitle: structure of rab escort protein-1 in complex with rab geranylgeranyl2 transferase and isoprenoid |
| 28 | c3uteB_ | Alignment | not modelled | 100.0 | 12 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | c3i6dA_ | Alignment | not modelled | 100.0 | 16 | Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af |
| 30 | c3k7tB_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: 6-hydroxy-l-nicotine oxidase; PDBTitle: crystal structure of apo-form 6-hydroxy-l-nicotine oxidase, crystal2 form p3121 |
| 31 | c1h83A_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyamine oxidase; PDBTitle: structure of polyamine oxidase in complex with2 1,8-diaminooctane |
| 32 | c3lovA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of putative protoporphyrinogen oxidase2 (yp_001813199.1) from exiguobacterium sp. 255-15 at 2.06 a resolution |
| 33 | c4dshB_ | Alignment | not modelled | 100.0 | 13 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of reduced udp-galactopyranose mutase |
| 34 | d1o5wa1 | Alignment | not modelled | 100.0 | 24 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 35 | c2b9yA_ | Alignment | not modelled | 100.0 | 12 | PDB header: isomerase Chain: A: PDB Molecule: putative aminooxidase; PDBTitle: crystal structure of cla-producing fatty acid isomerase2 from p. acnes |
| 36 | c1gndA_ | Alignment | not modelled | 100.0 | 13 | PDB header: gtpase activation Chain: A: PDB Molecule: guanine nucleotide dissociation inhibitor; PDBTitle: guanine nucleotide dissociation inhibitor, alpha-isoform |
| 37 | d2v5za1 | Alignment | not modelled | 100.0 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 38 | c3cpiH_ | Alignment | not modelled | 100.0 | 12 | PDB header: protein transport Chain: H: PDB Molecule: rab gdp-dissociation inhibitor; PDBTitle: crystal structure of yeast rab-gdi |
| 39 | c6c87A_ | Alignment | not modelled | 100.0 | 14 | PDB header: protein transport Chain: A: PDB Molecule: rab gdp dissociation inhibitor alpha; PDBTitle: crystal structure of rab gdp dissociation inhibitor alpha from2 naegleria fowleri |
| 40 | c1v0jB_ | Alignment | not modelled | 100.0 | 19 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis |
| 41 | d1d5ta1 | Alignment | not modelled | 100.0 | 12 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 42 | c1i8tB_ | Alignment | not modelled | 100.0 | 11 | PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli |
| 43 | c3p1wA_ | Alignment | not modelled | 99.9 | 13 | PDB header: protein transport Chain: A: PDB Molecule: rabgdi protein; PDBTitle: crystal structure of rab gdi from plasmodium falciparum, pfl2060c |
| 44 | c6fjhB_ | Alignment | not modelled | 99.9 | 16 | PDB header: flavoprotein Chain: B: PDB Molecule: lkce; PDBTitle: crystal structure of the seleniated lkce from streptomyces rochei |
| 45 | c1naaB_ | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase flavoprotein fragment in complex with2 cellobionolactam |
| 46 | d1vg0a1 | Alignment | not modelled | 99.9 | 16 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 47 | c2bi8A_ | Alignment | not modelled | 99.9 | 11 | PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad |
| 48 | c3hdqI_ | Alignment | not modelled | 99.9 | 13 | PDB header: isomerase Chain: I: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-galactopyranose mutase (oxidized2 form) in complex with substrate |
| 49 | d2bccg1 | Alignment | not modelled | 99.9 | 12 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: GDI-like N domain |
| 50 | c4mo2A_ | Alignment | not modelled | 99.9 | 8 | PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of udp-n-acetylgalactopyranose mutase from2 campylobacter jejuni |
| 51 | c6a2uD_ | Alignment | not modelled | 99.9 | 13 | PDB header: signaling protein/oxidoreductase Chain: D: PDB Molecule: glucose dehydrogenase; PDBTitle: crystal structure of gamma-alpha subunit complex from burkholderia2 cepacia fad glucose dehydrogenase |
| 52 | c3nrrA_ | Alignment | not modelled | 99.9 | 15 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pf1083; PDBTitle: crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223 |
| 53 | d2dw4a2 | Alignment | not modelled | 99.9 | 14 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 54 | c4qi7A_ | Alignment | not modelled | 99.9 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from neurospora crassa, nccdH |
| 55 | c3t37A_ | Alignment | not modelled | 99.9 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: crystal structure of pyridoxine 4-oxidase from mesorhizum |

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|----|-------------------------|-----------|--------------|------|---|
| | | | | | loti |
| 56 | d1reoa1 | Alignment | not modelled | 99.9 | 19 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 57 | c4qi6A | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: cellobiose dehydrogenase from myriococcum thermophilum, mtc dh |
| 58 | c4udpA | Alignment | not modelled | 99.9 | 14 PDB header: oxidoreductase Chain: A: PDB Molecule: glucose-methanol-choline oxidoreductase; PDBTitle: crystal structure of 5-hydroxymethylfurfural oxidase (hmfo) in the2 oxidized state |
| 59 | c1coyA | Alignment | not modelled | 99.9 | 14 PDB header: oxidoreductase(oxygen receptor) Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase complexed with a steroid2 substrate. implications for fad dependent alcohol oxidases |
| 60 | c1cf3A | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from aspergillus niger |
| 61 | c4yntA | Alignment | not modelled | 99.9 | 11 PDB header: oxidoreductase Chain: A: PDB Molecule: glucose oxidase, putative; PDBTitle: crystal structure of aspergillus flavus fad glucose dehydrogenase |
| 62 | c4qi4A | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase Chain: A: PDB Molecule: cellobiose dehydrogenase; PDBTitle: dehydrogenase domain of myriococcum thermophilum cellobiose2 dehydrogenase, mtdh |
| 63 | c1gpeA | Alignment | not modelled | 99.9 | 11 PDB header: oxidoreductase(flavoprotein) Chain: A: PDB Molecule: protein (glucose oxidase); PDBTitle: glucose oxidase from penicillium amagasakiense |
| 64 | c2jbvA | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: A: PDB Molecule: choline oxidase; PDBTitle: crystal structure of choline oxidase reveals insights into the2 catalytic mechanism |
| 65 | d2iida1 | Alignment | not modelled | 99.9 | 15 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 66 | c4migC | Alignment | not modelled | 99.9 | 17 PDB header: oxidoreductase Chain: C: PDB Molecule: pyranose 2-oxidase; PDBTitle: pyranose 2-oxidase from phanerochaete chrysosporium, recombinant wild2 type |
| 67 | c3fimB | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: B: PDB Molecule: aryl-alcohol oxidase; PDBTitle: crystal structure of aryl-alcohol-oxidase from pleurotus eryngii |
| 68 | c2gewA | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo) |
| 69 | c4h7uA | Alignment | not modelled | 99.9 | 11 PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose dehydrogenase; PDBTitle: crystal structure of pyranose dehydrogenase from agaricus meleagris,2 wildtype |
| 70 | c6h3gC | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: C: PDB Molecule: alcohol oxidase; PDBTitle: alcohol oxidase from phanerochaete chrysosporium |
| 71 | c5nccB | Alignment | not modelled | 99.9 | 13 PDB header: oxidoreductase Chain: B: PDB Molecule: fatty acid photodecarboxylase; PDBTitle: structure of fatty acid photodecarboxylase in complex with fad and2 palmitic acid |
| 72 | c2yr6A | Alignment | not modelled | 99.9 | 14 PDB header: oxidoreductase Chain: A: PDB Molecule: pro-enzyme of l-phenylalanine oxidase; PDBTitle: crystal structure of l-phenylalanine oxidase from psuedomonas sp.p501 |
| 73 | c3q9tB | Alignment | not modelled | 99.9 | 11 PDB header: oxidoreductase Chain: B: PDB Molecule: choline dehydrogenase and related flavoproteins; PDBTitle: crystal structure analysis of formate oxidase |
| 74 | c2f5vA | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase Chain: A: PDB Molecule: pyranose 2-oxidase; PDBTitle: reaction geometry and thermostability mutant of pyranose 2-oxidase2 from the white-rot fungus peniophora sp. |
| 75 | c5hsaG | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase Chain: G: PDB Molecule: alcohol oxidase 1; PDBTitle: alcohol oxidase aox1 from pichia pastoris |
| 76 | d1kdga1 | Alignment | not modelled | 99.9 | 17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 77 | c2igoG | Alignment | not modelled | 99.9 | 12 PDB header: oxidoreductase Chain: G: PDB Molecule: pyranose oxidase; PDBTitle: crystal structure of pyranose 2-oxidase h167a mutant with 2-fluoro-2-2 deoxy-d-glucose |
| 78 | c4at2A | Alignment | not modelled | 99.9 | 16 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-ketosteroid-delta4-5alpha-dehydrogenase; PDBTitle: the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione |
| 79 | c1ju2A | Alignment | not modelled | 99.9 | 11 PDB header: lyase Chain: A: PDB Molecule: hydroxynitrile lyase; PDBTitle: crystal structure of the hydroxynitrile lyase from almond |
| 80 | d1b5qa1 | Alignment | not modelled | 99.9 | 17 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 81 | c2e1mA | Alignment | not modelled | 99.9 | 15 PDB header: oxidoreductase Chain: A: PDB Molecule: l-glutamate oxidase; PDBTitle: crystal structure of l-glutamate oxidase from |

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|-----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | streptomyces sp. x-119-6 |
| 82 | c3nlcA | Alignment | not modelled | 99.9 | 16 | 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 |
| 83 | d1cf3a1 | Alignment | not modelled | 99.9 | 14 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 84 | c4c3yF | Alignment | not modelled | 99.9 | 18 | PDB header: oxidoreductase Chain: F: PDB Molecule: 3-ketosteroid dehydrogenase; PDBTitle: crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione |
| 85 | c4ia6B | Alignment | not modelled | 99.8 | 13 | PDB header: immune system Chain: B: PDB Molecule: myosin-crossreactive antigen; PDBTitle: hydratase from lactobacillus acidophilus in a ligand bound form (la2 lah) |
| 86 | d2ivda1 | Alignment | not modelled | 99.8 | 18 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 87 | c4z24A | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: gmc-type oxidoreductase r135; PDBTitle: mimivirus r135 (residues 51-702) |
| 88 | c6n56A | Alignment | not modelled | 99.8 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase, flavo protein subunit; PDBTitle: crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27 |
| 89 | c1yvvB | Alignment | not modelled | 99.8 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10. |
| 90 | c3qj4A | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1) |
| 91 | c4xwzA | Alignment | not modelled | 99.8 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: fructosyl amine:oxygen oxidoreductase; PDBTitle: the crystal structure of fructosyl amine: oxygen oxidoreductase2 (amadoriase i) from aspergillus fumigatus in complex with the3 substrate fructosyl lysine |
| 92 | c3g05B | Alignment | not modelled | 99.8 | 20 | 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 mnmg |
| 93 | d2f5va1 | Alignment | not modelled | 99.8 | 15 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 94 | d3coxa1 | Alignment | not modelled | 99.8 | 14 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 95 | c3djeA | Alignment | not modelled | 99.8 | 17 | 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 |
| 96 | c3cp2A | Alignment | not modelled | 99.8 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli |
| 97 | c2zxiC | Alignment | not modelled | 99.8 | 18 | PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: structure of aquifex aeolicus gida in the form ii crystal |
| 98 | c1qo8A | Alignment | not modelled | 99.8 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome c32 fumarate reductase |
| 99 | d1seza1 | Alignment | not modelled | 99.8 | 22 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 100 | c5glgA | Alignment | not modelled | 99.8 | 12 | PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase 2; PDBTitle: the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast |
| 101 | c4x9mA | Alignment | not modelled | 99.7 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound |
| 102 | c3cesB | Alignment | not modelled | 99.7 | 19 | PDB header: rna binding protein Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme |
| 103 | d1gpea1 | Alignment | not modelled | 99.7 | 15 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 104 | c3cp8C | Alignment | not modelled | 99.7 | 16 | PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum |
| 105 | c5fjnB | Alignment | not modelled | 99.7 | 15 | PDB header: hydrolase Chain: B: PDB Molecule: l-amino acid deaminase; PDBTitle: structure of l-amino acid deaminase from proteus myxofaciens2 in complex with anthranilate |
| | | | | | | PDB header: oxidoreductase(flavoenzyme) |

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|-----|-------------------------|-----------|--------------|------|----|---|
| 106 | c1geuA | Alignment | not modelled | 99.7 | 12 | Chain: A; PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site |
| 107 | c4rsIA | Alignment | not modelled | 99.7 | 13 | PDB header: oxidoreductase Chain: A; PDB Molecule: fructosyl peptide oxidase; PDBTitle: structure of fructosyl peptide oxidase from e. terrenum |
| 108 | c3vr8E | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: E; PDB Molecule: flavoprotein subunit of complex ii; PDBTitle: mitochondrial rhoquinol-fumarate reductase from the parasitic2 nematode ascaris suum |
| 109 | c5hxwF | Alignment | not modelled | 99.7 | 17 | PDB header: oxidoreductase Chain: F; PDB Molecule: l-amino acid deaminase; PDBTitle: l-amino acid deaminase from proteus vulgaris |
| 110 | c1pj6A | Alignment | not modelled | 99.7 | 13 | 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 |
| 111 | c1yq4A | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone |
| 112 | c3axbA | Alignment | not modelled | 99.7 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: structure of a dye-linked l-proline dehydrogenase from the aerobic2 hyperthermophilic archaeon, aeropyrum pernix |
| 113 | c2eq7B | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: B; PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo |
| 114 | c6gg2A | Alignment | not modelled | 99.7 | 13 | PDB header: oxidoreductase Chain: A; PDB Molecule: amino acid oxidase fmpa; PDBTitle: the structure of fsqb from aspergillus fumigatus, a flavoenzyme of the2 amine oxidase family |
| 115 | c1zkaA | Alignment | not modelled | 99.7 | 12 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2 |
| 116 | c3dgzA | Alignment | not modelled | 99.7 | 12 | PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation |
| 117 | d1n4wa1 | Alignment | not modelled | 99.7 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 118 | c2rghA | Alignment | not modelled | 99.7 | 17 | 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 |
| 119 | c3atrA | Alignment | not modelled | 99.7 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand |
| 120 | c4p9sA | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: dimethylglycine dehydrogenase; PDBTitle: crystal structure of the mature form of rat dmgdh |