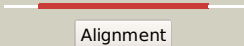

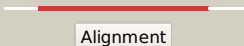

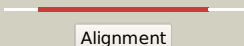







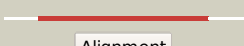











Phyre2

| | |
|------------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1751 (-)_1979628_1981010 |
| Date | Fri Aug 2 13:30:35 BST 2019 |
| Unique Job ID | 661ad16471773dfa |

Detailed template
information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2qa2A_ |  Alignment |  | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase cabe; PDBTitle: crystal structure of cabe, an aromatic hydroxylase from angucycline2 biosynthesis, determined to 2.7 a resolution |
| 2 | c2qa1A_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis |
| 3 | c6j0zC_ |  Alignment |  | 100.0 | 20 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative angucycline-like polyketide oxygenase; PDBTitle: crystal structure of alpk |
| 4 | c2dkhA_ |  Alignment |  | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate |
| 5 | c4k2xB_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus |
| 6 | c3fmwC_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxygenase; PDBTitle: the crystal structure of mtmoiv, a baeyer-villiger monooxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus. |
| 7 | c5kowA_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: pentachlorophenol 4-monooxygenase; PDBTitle: structure of rifampicin monooxygenase |
| 8 | c6c6rA_ |  Alignment |  | 100.0 | 14 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad |
| 9 | c5xgvB_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: pyre3; PDBTitle: the structure of diels-alderase pyre3 in the biosynthetic pathway of2 pyrroindomycins |
| 10 | c3i3IA_ |  Alignment |  | 100.0 | 20 | PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase |
| 11 | c1pn0A_ |  Alignment |  | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c3ihgA_ | Alignment | | 100.0 | 18 | PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone |
| 13 | c2r0gB_ | Alignment | | 100.0 | 22 | PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c |
| 14 | c3nixF_ | Alignment | | 100.0 | 15 | PDB header: oxidoreductase Chain: F: PDB Molecule: flavoprotein/dehydrogenase; PDBTitle: crystal structure of flavoprotein/dehydrogenase from cytophaga2 hutchinsonii. northeast structural genomics consortium target chr43. |
| 15 | c5fn0C_ | Alignment | | 100.0 | 18 | PDB header: oxidoreductase Chain: C: PDB Molecule: kynurenine 3-monoxygenase; PDBTitle: crystal structure of pseudomonas fluorescens kynurenine-3-2 monoxygenase (kmo) in complex with gsk180 |
| 16 | c3e1tA_ | Alignment | | 100.0 | 16 | 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 |
| 17 | c5tulA_ | Alignment | | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: tetracycline destructase tet(55); PDBTitle: crystal structure of tetracycline destructase tet(55) |
| 18 | c4k22A_ | Alignment | | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: protein visc; PDBTitle: structure of the c-terminal truncated form of e.coli c5-hydroxylase2 ubii involved in ubiquinone (q8) biosynthesis |
| 19 | c6bznA_ | Alignment | | 100.0 | 16 | PDB header: flavoprotein Chain: A: PDB Molecule: halogenase pltm; PDBTitle: crystal structure of halogenase pltm |
| 20 | c1phhA_ | Alignment | | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: p-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate |
| 21 | c6aioA_ | Alignment | not modelled | 100.0 | 20 | PDB header: flavoprotein Chain: A: PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monoxygenase pnpa from2 pseudomonas putida dll-e4 |
| 22 | c5dbjA_ | Alignment | not modelled | 100.0 | 17 | PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta |
| 23 | c3gmbB_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase |
| 24 | c4n9xA_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative monoxygenase; PDBTitle: crystal structure of the octaprenyl-methyl-methoxy-benzo molecule from2 erwina carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161 |
| 25 | c3allA_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a |
| 26 | c5tukC_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: C: PDB Molecule: tetracycline destructase tet(51); PDBTitle: crystal structure of tetracycline destructase tet(51) |
| 27 | c2rgiA_ | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monoxygenase; PDBTitle: crystal structure of flavin-containing monoxygenase phzs |
| | | | | | | PDB header: oxidoreductase |

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|----|-------------------------|-----------|--------------|-------|----|---|
| 28 | c4bk2A | Alignment | not modelled | 100.0 | 19 | Chain: A; PDB Molecule: probable salicylate monooxygenase; PDBTitle: crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for3 regioselective aromatic hydroxylation: q301e mutant |
| 29 | c5bulA | Alignment | not modelled | 100.0 | 15 | PDB header: hydrolase Chain: A; PDB Molecule: flavin-dependent halogenase triple mutant; PDBTitle: structure of flavin-dependent brominase bmp2 triple mutant y302s f306v2 a345w |
| 30 | c5bukA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: fadh2-dependent halogenase; PDBTitle: structure of flavin-dependent chlorinase mpy16 |
| 31 | c5wgyA | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A; PDB Molecule: flavin-dependent halogenase; PDBTitle: crystal structure of mala' c112s/c128s, malbrancheamide b complex |
| 32 | c5tueB | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: B; PDB Molecule: tetracycline destructase tet(50); PDBTitle: crystal structure of tetracycline destructase tet(50) |
| 33 | c4cy8A | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: 2-hydroxybiphenyl 3-monooxygenase; PDBTitle: 2-hydroxybiphenyl 3-monooxygenase (hbpa) in complex with fad |
| 34 | c5x68B | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B; PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of human kmo |
| 35 | c6bz5B | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: B; PDB Molecule: salicylate hydroxylase; PDBTitle: structure and mechanism of salicylate hydroxylase from pseudomonas2 putida g7 |
| 36 | c2x3nA | Alignment | not modelled | 100.0 | 20 | PDB header: oxidoreductase Chain: A; PDB Molecule: probable fad-dependent monooxygenase; PDBTitle: crystal structure of pqsl, a probable fad-dependent monooxygenase from2 pseudomonas aeruginosa |
| 37 | c3rp7A | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpox complexed with fad and2 uric acid |
| 38 | c5evyX | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: X; PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex |
| 39 | c5eowA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: 6-hydroxynicotinate 3-monooxygenase; PDBTitle: crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440 |
| 40 | c4j33B | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: B; PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of kynurenine 3-monooxygenase (kmo-394) |
| 41 | c3c4aA | Alignment | not modelled | 100.0 | 13 | PDB header: oxidoreductase Chain: A; PDB Molecule: probable tryptophan hydroxylase viod; PDBTitle: crystal structure of viod hydroxylase in complex with fad from2 chromobacterium violaceum. northeast structural genomics consortium3 target cvr158 |
| 42 | d1k0ia1 | 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 |
| 43 | c3cgvA | Alignment | not modelled | 100.0 | 18 | PDB header: structural genomics, unknown function Chain: A; PDB Molecule: geranylgeranyl reductase related protein; PDBTitle: crystal structure of geranylgeranyl bacteriochlorophyll reductase-like2 fixc homolog (np_393992.1) from thermoplasma acidophilum at 1.60 a3 resolution |
| 44 | c3atrA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand |
| 45 | c2vouA | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A; PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans |
| 46 | d3c96a1 | Alignment | not modelled | 100.0 | 25 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 47 | c2bryA | Alignment | not modelled | 100.0 | 17 | PDB header: transport Chain: A; PDB Molecule: nedd9 interacting protein with calponin homology PDBTitle: crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution |
| 48 | d1pn0a1 | Alignment | not modelled | 100.0 | 13 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 49 | c2xdoC | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: C; PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron |
| 50 | c4hb9A | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A; PDB Molecule: similarities with probable monooxygenase; PDBTitle: crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791) |
| 51 | c5uaoA | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: tryptophane-5-halogenase; PDBTitle: crystal structure of mibh, a lathipeptide tryptophan 5-halogenase |
| 52 | c4txkA | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: protein-methionine sulfoxide oxidase mical1; PDBTitle: construct of mical-1 containing the monooxygenase and |

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|----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | calponin2 homology domains 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 |
| 53 | c2ardA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 6-halogenase; PDBTitle: crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini |
| 54 | c5hy5A_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: styrene monooxygenase a; PDBTitle: structure of the oxygenase component of a pseudomonas styrene2 monooxygenase |
| 55 | c3ihmB_ | Alignment | not modelled | 100.0 | 16 | PDB header: flavoprotein Chain: A: PDB Molecule: tryptophan halogenase superfamily; PDBTitle: brvh, a flavin-dependent halogenase from brevundimonas sp. bal3 |
| 56 | c6fr1A_ | Alignment | not modelled | 100.0 | 16 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 57 | d2voua1 | Alignment | not modelled | 100.0 | 25 | PDB header: antifungal protein Chain: D: PDB Molecule: tryptophan 5-halogenase; PDBTitle: crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan |
| 58 | c2weuD_ | Alignment | not modelled | 100.0 | 21 | PDB header: flavoprotein Chain: B: PDB Molecule: tryptophan 6-halogenase; PDBTitle: mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5) |
| 59 | c6ib5B_ | Alignment | not modelled | 100.0 | 17 | PDB header: biosynthetic protein, flavoprotein Chain: B: PDB Molecule: tryptophan halogenase; PDBTitle: rebh with bound l-trp |
| 60 | c2e4gB_ | Alignment | not modelled | 100.0 | 18 | 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 |
| 61 | c2pyxA_ | Alignment | not modelled | 100.0 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 62 | d2gmha1 | Alignment | not modelled | 100.0 | 17 | 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 |
| 63 | c2gmhA_ | Alignment | not modelled | 100.0 | 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 |
| 64 | c3nrnA_ | Alignment | not modelled | 99.9 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structurure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10. |
| 65 | c1yvVB_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: flavoenzyme pa4991; PDBTitle: crystal structure of the fad dependent oxidoreductase pa4991 from2 pseudomonas aeruginosa |
| 66 | c5ez7A_ | Alignment | not modelled | 99.8 | 18 | 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. |
| 67 | c3da1A_ | Alignment | not modelled | 99.8 | 13 | PDB header: oxidoreductase Chain: A: PDB Molecule: renalase; PDBTitle: crystal structure of human renalase (isoform 1) |
| 68 | c3qj4A_ | Alignment | not modelled | 99.7 | 12 | PDB header: oxidoreductase Chain: B: PDB Molecule: sarcosine oxidase; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii |
| 69 | c1y56B_ | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-arginine dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa d-arginine dehydrogenase2 in complex with imino-arginine |
| 70 | c3nyeA_ | Alignment | not modelled | 99.7 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208 |
| 71 | c3ka7A_ | 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 |
| 72 | c4p9sA_ | Alignment | not modelled | 99.7 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted glycerol-3-2 phosphate dehydrogenase in complex with dhap |
| 73 | c2r4jA_ | Alignment | not modelled | 99.7 | 17 | 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 |
| 74 | c2olnA_ | Alignment | not modelled | 99.7 | 16 | PDB header: oxidoreductase/inhibitor Chain: A: PDB Molecule: fad-dependent glycine oxydase; PDBTitle: crystal structure of cmis2 with inhibitor |
| 75 | c6j39A_ | Alignment | not modelled | 99.6 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: monomeric sarcosine oxidase; PDBTitle: crystal structure of r49k mutant of monomeric sarcosine oxidase2 crystallized in phosphate as precipitant |
| 76 | c3bhkA_ | Alignment | not modelled | 99.6 | 16 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 77 | d2ivda1 | Alignment | not modelled | 99.6 | 26 | |

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|-----|-------------------------|-----------|--------------|------|----|--|
| 78 | c3ps9A_ | Alignment | not modelled | 99.6 | 18 | PDB header: transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of mnmc from e. coli |
| 79 | c3dmeB_ | Alignment | not modelled | 99.6 | 13 | PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved exported protein; PDBTitle: crystal structure of conserved exported protein from bordetella2 pertussis. northeast structural genomics target ber141 |
| 80 | c1pj6A_ | Alignment | not modelled | 99.6 | 20 | 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 |
| 81 | c5ttkB_ | Alignment | not modelled | 99.6 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase; PDBTitle: crystal structure of selenomethionine-incorporated nicotine2 oxidoreductase from pseudomonas putida |
| 82 | c5g3sB_ | Alignment | not modelled | 99.6 | 13 | 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 |
| 83 | c5twcA_ | Alignment | not modelled | 99.6 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: oxidoreductase iruo in the oxidized form |
| 84 | c2vvlD_ | Alignment | not modelled | 99.6 | 13 | 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. |
| 85 | c3axbA_ | Alignment | not modelled | 99.6 | 15 | 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 |
| 86 | c4x9mA_ | Alignment | not modelled | 99.6 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: l-alpha-glycerophosphate oxidase; PDBTitle: oxidized l-alpha-glycerophosphate oxidase from mycoplasma pneumoniae2 with fad bound |
| 87 | c2ivdA_ | Alignment | not modelled | 99.6 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen |
| 88 | d2gqfa1 | Alignment | not modelled | 99.6 | 21 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like |
| 89 | c3i6dA_ | Alignment | not modelled | 99.6 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: protoporphyrinogen oxidase; PDBTitle: crystal structure of ppo from bacillus subtilis with af |
| 90 | c6cr0A_ | Alignment | not modelled | 99.6 | 12 | 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 |
| 91 | c3f8rD_ | Alignment | not modelled | 99.6 | 19 | PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules |
| 92 | c3pvcA_ | Alignment | not modelled | 99.6 | 20 | PDB header: oxidoreductase, transferase Chain: A: PDB Molecule: trna 5-methylaminomethyl-2-thiouridine biosynthesis PDBTitle: crystal structure of apo mnmc from yersinia pestis |
| 93 | c5mogB_ | Alignment | not modelled | 99.6 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: phytoene dehydrogenase, chloroplastic/chromoplastic; PDBTitle: oryza sativa phytoene desaturase inhibited by norflurazon |
| 94 | c2gahB_ | Alignment | not modelled | 99.6 | 18 | PDB header: oxidoreductase Chain: B: PDB Molecule: heterotetrameric sarcosine oxidase beta-subunit; PDBTitle: heterotetrameric sarcosine: structure of a diflavin2 metalloenzyme at 1.85 a resolution |
| 95 | c4xwzA_ | Alignment | not modelled | 99.6 | 16 | 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 |
| 96 | c2rgoA_ | Alignment | not modelled | 99.6 | 18 | 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 |
| 97 | d1b5qa1 | Alignment | not modelled | 99.6 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain |
| 98 | d1kf6a2 | Alignment | not modelled | 99.6 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 99 | c6garB_ | Alignment | not modelled | 99.5 | 13 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus |
| 100 | c4y4nE_ | Alignment | not modelled | 99.5 | 25 | PDB header: biosynthetic protein Chain: E: PDB Molecule: putative ribose 1,5-bisphosphate isomerase; PDBTitle: thiazole synthase thi4 from methanococcus igneus |
| 101 | c1ryiB_ | Alignment | not modelled | 99.5 | 15 | PDB header: oxidoreductase Chain: B: PDB Molecule: glycine oxidase; PDBTitle: structure of glycine oxidase with bound inhibitor glycolate |
| 102 | d1reoa1 | 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 |
| | | | | | | PDB header: biosynthetic protein |

| | | | | | | |
|-----|-------------------------|-----------|--------------|------|----|--|
| 103 | c3jskN_ | Alignment | not modelled | 99.5 | 20 | Chain: N: PDB Molecule: cybpb37 protein; PDBTitle: thiazole synthase from neurospora crassa |
| 104 | c2rghA_ | Alignment | not modelled | 99.5 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from 2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase |
| 105 | d1neka2 | Alignment | not modelled | 99.5 | 13 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 106 | c4dgkA_ | Alignment | not modelled | 99.5 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: phytoene dehydrogenase; PDBTitle: crystal structure of phytoene desaturase crti from pantoea ananatis |
| 107 | c1c0iA_ | Alignment | not modelled | 99.5 | 14 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-amino acid oxidase; PDBTitle: crystal structure of d-amino acid oxidase in complex with two2 anthranilate molecules |
| 108 | c4repA_ | Alignment | not modelled | 99.5 | 22 | PDB header: oxidoreductase, flavoprotein Chain: A: PDB Molecule: gamma-carotene desaturase; PDBTitle: crystal structure of gamma-carotenoid desaturase |
| 109 | c1s3bB_ | Alignment | not modelled | 99.5 | 16 | 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 |
| 110 | c3ab1B_ | Alignment | not modelled | 99.5 | 17 | PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadh reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase |
| 111 | d2bs2a2 | Alignment | not modelled | 99.5 | 19 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 112 | c4i58A_ | Alignment | not modelled | 99.5 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexylamine oxidase; PDBTitle: cyclohexylamine oxidase from brevibacterium oxydans ih-35a |
| 113 | c2zxiC_ | Alignment | not modelled | 99.5 | 19 | 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 |
| 114 | c1f8sA_ | Alignment | not modelled | 99.5 | 15 | 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. |
| 115 | c3djeA_ | Alignment | not modelled | 99.5 | 16 | 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 |
| 116 | d1jnra2 | Alignment | not modelled | 99.5 | 17 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 117 | c5fjnB_ | Alignment | not modelled | 99.5 | 20 | 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 |
| 118 | d1qo8a2 | Alignment | not modelled | 99.5 | 18 | Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain |
| 119 | c4yshA_ | Alignment | not modelled | 99.4 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: glycine oxidase; PDBTitle: crystal structure of glycine oxidase from geobacillus kaustophilus |
| 120 | c3cp2A_ | Alignment | not modelled | 99.4 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from e. coli |