


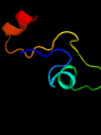




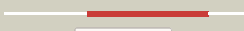
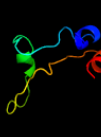





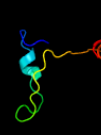








Phyre2

| | |
|---------------|-------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD3353c_(-)_3768907_3769167 |
| Date | Thu Aug 8 16:20:56 BST 2019 |
| Unique Job ID | ca119aae5967f88a |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|--|
| 1 | c3w8wA_ |  Alignment |  | 98.7 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative fad-dependent oxygenase encm; PDBTitle: the crystal structure of encm |
| 2 | c2y3rC_ |  Alignment |  | 98.6 | 17 | PDB header: oxidoreductase Chain: C: PDB Molecule: taml; PDBTitle: structure of the tirandamycin-bound fad-dependent tirandamycin oxidase2 taml in p21 space group |
| 3 | c2bvfA_ |  Alignment |  | 98.6 | 29 | PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1) |
| 4 | c5i1wD_ |  Alignment |  | 98.5 | 20 | PDB header: oxidoreductase Chain: D: PDB Molecule: crmk; PDBTitle: crystal structure of crmk, a flavoenzyme involved in the shunt product2 recycling mechanism in caerulomycin biosynthesis |
| 5 | c6eo5A_ |  Alignment |  | 98.3 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: ppbbe-like 1 d396n; PDBTitle: physcomitrella patens bbe-like 1 variant d396n |
| 6 | c1zr6A_ |  Alignment |  | 98.2 | 19 | PDB header: oxidoreductase Chain: A: PDB Molecule: glucoligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucoligosaccharide2 oxidase reveals a novel flavinylation |
| 7 | c2wdwB_ |  Alignment |  | 98.2 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis |
| 8 | c3popD_ |  Alignment |  | 98.1 | 13 | PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis |
| 9 | c2ipiD_ |  Alignment |  | 98.0 | 25 | PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase |
| 10 | c3rjaA_ |  Alignment |  | 98.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: carbohydrate oxidase; PDBTitle: crystal structure of carbohydrate oxidase from microdochium nivale in2 complex with substrate analogue |
| 11 | c3tjsA_ |  Alignment |  | 97.9 | 20 | PDB header: allergen, oxidoreductase Chain: A: PDB Molecule: pollen allergen phi p 4; PDBTitle: crystal structure of phi p 4, a grass pollen allergen with glucose2 dehydrogenase activity |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| 12 | c3vteA_ | Alignment | | 97.5 | 18 | PDB header: oxidoreductase Chain: A; PDB Molecule: tetrahydrocannabinolic acid synthase; PDBTitle: crystal structure of tetrahydrocannabinolic acid synthase from2 cannabis sativa |
| 13 | c3fwaA_ | Alignment | | 97.4 | 13 | PDB header: flavoprotein Chain: A; PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline |
| 14 | c3d2hA_ | Alignment | | 97.3 | 14 | PDB header: oxidoreductase Chain: A; PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form |
| 15 | c5l6fA_ | Alignment | | 97.2 | 22 | PDB header: oxidoreductase Chain: A; PDB Molecule: fad linked oxidase-like protein; PDBTitle: xylooligosaccharide oxidase from myceliophthora thermophila c1 in2 complex with xylobiose |
| 16 | c6f74B_ | Alignment | | 97.1 | 20 | PDB header: flavoprotein Chain: B; PDB Molecule: alcohol oxidase; PDBTitle: crystal structure of vao-type flavoprotein mtvao713 from2 myceliophthora thermophila c1 |
| 17 | c5d79B_ | Alignment | | 97.1 | 17 | PDB header: oxidoreductase Chain: B; PDB Molecule: berberine bridge enzyme-like protein; PDBTitle: structure of bbe-like #28 from arabidopsis thaliana |
| 18 | c6f73B_ | Alignment | | 97.0 | 33 | PDB header: flavoprotein Chain: B; PDB Molecule: mtvao615; PDBTitle: crystal structure of vao-type flavoprotein mtvao615 at ph 5.0 from2 myceliophthora thermophila c1 |
| 19 | c5fxpA_ | Alignment | | 96.8 | 15 | PDB header: oxidoreductase Chain: A; PDB Molecule: eugenol oxidase; PDBTitle: crystal structure of eugenol oxidase in complex with2 vanillin |
| 20 | c2exrA_ | Alignment | | 96.8 | 30 | PDB header: oxidoreductase Chain: A; PDB Molecule: cytokinin dehydrogenase 7; PDBTitle: x-ray structure of cytokinin oxidase/dehydrogenase (ckx) from2 arabidopsis thaliana at5g21482 |
| 21 | cli19B_ | Alignment | not modelled | 96.6 | 18 | PDB header: oxidoreductase Chain: B; PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum |
| 22 | c1wveB_ | Alignment | not modelled | 96.5 | 18 | PDB header: oxidoreductase Chain: B; PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit |
| 23 | c3pm9A_ | Alignment | not modelled | 96.2 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodospseudomonas palustris cga009 at 2.57 a resolution |
| 24 | c3js8A_ | Alignment | not modelled | 96.0 | 13 | PDB header: oxidoreductase Chain: A; PDB Molecule: cholesterol oxidase; PDBTitle: solvent-stable cholesterol oxidase |
| 25 | c4oa1B_ | Alignment | not modelled | 96.0 | 24 | PDB header: oxidoreductase Chain: B; PDB Molecule: cytokinin dehydrogenase 4; PDBTitle: crystal structure of maize cytokinin oxidase/dehydrogenase 4 (zmcko4)2 in complex with phenylurea inhibitor cppu in alternative spacegroup |
| 26 | c6c80B_ | Alignment | not modelled | 96.0 | 23 | PDB header: immune system Chain: B; PDB Molecule: cytokinin oxidase luckx1.1; PDBTitle: crystal structure of a flax cytokinin oxidase |
| 27 | c4bc9C_ | Alignment | not modelled | 95.9 | 17 | PDB header: transferase Chain: C; PDB Molecule: alkyldihydroxyacetonephosphate synthase, peroxisomal; PDBTitle: mammalian alkyldihydroxyacetonephosphate synthase: wild-type, adduct2 with cyanoethyl |
| 28 | d1w1oa2 | Alignment | not modelled | 95.6 | 23 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| | | | | | | Family: FAD-linked oxidases, N-terminal domain |
| 29 | c4ml8C_ | Alignment | not modelled | 95.6 | 23 | PDB header: oxidoreductase Chain: C: PDB Molecule: cytokinin oxidase 2; PDBTitle: structure of maize cytokinin oxidase/dehydrogenase 2 (zmcko2) |
| 30 | c3bw7A_ | Alignment | not modelled | 94.8 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytokinin dehydrogenase 1; PDBTitle: maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1 |
| 31 | d1wvfa2 | Alignment | not modelled | 94.0 | 20 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 32 | c2uuvC_ | Alignment | not modelled | 93.9 | 17 | PDB header: transferase Chain: C: PDB Molecule: alkyldihydroxyacetonephosphate synthase; PDBTitle: alkyldihydroxyacetonephosphate synthase in p1 |
| 33 | d2i0ka2 | Alignment | not modelled | 93.4 | 18 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 34 | c4ud8B_ | Alignment | not modelled | 93.2 | 16 | PDB header: oxidoreductase Chain: B: PDB Molecule: fad-binding and bbe domain-containing protein; PDBTitle: atbbe15 |
| 35 | d1e8ga2 | Alignment | not modelled | 91.7 | 16 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 36 | c2vfvA_ | Alignment | not modelled | 85.4 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: xylitol oxidase; PDBTitle: alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite |
| 37 | c1ahuB_ | Alignment | not modelled | 77.5 | 18 | PDB header: flavoenzyme Chain: B: PDB Molecule: vanillyl-alcohol oxidase; PDBTitle: structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol |
| 38 | d1f0xa2 | Alignment | not modelled | 71.5 | 18 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain |
| 39 | d2cja1 | Alignment | not modelled | 65.8 | 14 | Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein |
| 40 | c2pq4B_ | Alignment | not modelled | 63.7 | 31 | PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide |
| 41 | c4fdoA_ | Alignment | not modelled | 62.6 | 8 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: oxidoreductase dpre1; PDBTitle: mycobacterium tuberculosis dpre1 in complex with ct319 |
| 42 | c1f0xA_ | Alignment | not modelled | 61.1 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral membrane2 respiratory enzyme. |
| 43 | d2giba1 | Alignment | not modelled | 60.5 | 14 | Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein |
| 44 | c2e76D_ | Alignment | not modelled | 58.1 | 16 | PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus |
| 45 | c4pytA_ | Alignment | not modelled | 56.5 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: udp-n-acetylenolpyruvoylglucosamine reductase; PDBTitle: crystal structure of a murb family ep-udp-n-acetylglucosamine2 reductase |
| 46 | d2ge7a1 | Alignment | not modelled | 48.2 | 14 | Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein |
| 47 | c2fynO_ | Alignment | not modelled | 42.9 | 24 | PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex |
| 48 | c2fyuE_ | Alignment | not modelled | 37.0 | 9 | PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor |
| 49 | c6g13B_ | Alignment | not modelled | 28.8 | 11 | PDB header: viral protein Chain: B: PDB Molecule: nucleoprotein; PDBTitle: c-terminal domain of mers-cov nucleocapsid |
| 50 | c1p84E_ | Alignment | not modelled | 27.3 | 14 | PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex |
| 51 | d1uxya1 | Alignment | not modelled | 22.7 | 15 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvyglucosamine reductase (MurB), N-terminal domain |
| 52 | c6fo2R_ | Alignment | not modelled | 19.9 | 10 | PDB header: membrane protein Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound |
| 53 | d1hska1 | Alignment | not modelled | 15.0 | 22 | Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvyglucosamine |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|--|
| | | | | | | reductase (MurB), N-terminal domain |
| 54 | d2ca1a1 | Alignment | not modelled | 13.0 | 12 | Fold: Nucleocapsid protein dimerization domain Superfamily: Nucleocapsid protein dimerization domain Family: Coronavirus nucleocapsid protein |
| 55 | c6f0gD_ | Alignment | not modelled | 10.7 | 40 | PDB header: chaperone Chain: D: PDB Molecule: ip3; PDBTitle: crystal structure asf1-ip3 |
| 56 | c6f0gC_ | Alignment | not modelled | 10.7 | 40 | PDB header: chaperone Chain: C: PDB Molecule: ip3; PDBTitle: crystal structure asf1-ip3 |
| 57 | c2l5aA_ | Alignment | not modelled | 8.8 | 32 | PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3 |
| 58 | d1nbaa_ | Alignment | not modelled | 7.7 | 35 | Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases |
| 59 | c5whaF_ | Alignment | not modelled | 7.3 | 5 | PDB header: protein binding Chain: F: PDB Molecule: miniprotein 225-11; PDBTitle: kras g12v, bound to gdp and miniprotein 225-11 |
| 60 | d2cwja1 | Alignment | not modelled | 6.0 | 12 | Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP |
| 61 | c5aj3i_ | Alignment | not modelled | 5.8 | 20 | PDB header: ribosome Chain: I: PDB Molecule: mitoribosomal protein us9m, mrps9; PDBTitle: structure of the small subunit of the mammalian mitoribosome |