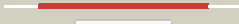



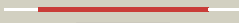






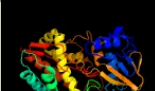












Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD1880c_cyp140_2130548_2131864 |
| Date | Fri Aug 2 13:30:49 BST 2019 |
| Unique Job ID | 7b4f104681072954 |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c4I0eA_ |  Alignment |  | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: p450 monooxygenase; PDBTitle: structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis (heme-coordinated expression tag) |
| 2 | c2wivA_ |  Alignment |  | 100.0 | 24 | PDB header: electron transport Chain: A: PDB Molecule: cytochrome p450-like protein xpla; PDBTitle: cytochrome-p450 xpla heme domain p21 |
| 3 | c3p3oA_ |  Alignment |  | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of the cytochrome p450 monooxygenase aurh (ntermil)2 from streptomyces thioluteus |
| 4 | d1cpta_ |  Alignment |  | 100.0 | 26 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 5 | c3bujA_ |  Alignment |  | 100.0 | 28 | PDB header: metal binding protein Chain: A: PDB Molecule: calo2; PDBTitle: crystal structure of calo2 |
| 6 | c5fyfA_ |  Alignment |  | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure of cyp153a from marinobacter aquaeolei |
| 7 | c3tktA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of cyp108d1 from novosphingobium aromaticivorans2 dsm12444 |
| 8 | c5hdiA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 144; PDBTitle: structural characterization of cyp144a1, a mycobacterium tuberculosis2 cytochrome p450 |
| 9 | c6giiA_ |  Alignment |  | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of tepidiphilus thermophilus p450 heme domain |
| 10 | c2fr7A_ |  Alignment |  | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450; PDBTitle: crystal structure of cytochrome p450 cyp199a2 |
| 11 | c6hqdB_ |  Alignment |  | 100.0 | 19 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from pseudomonas sp. 19-rlim |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | d1q5da_ | Alignment | | 100.0 | 29 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 13 | c4l36B_ | Alignment | | 100.0 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative p450-like protein; PDBTitle: crystal structure of the cytochrome p450 enzyme txtx |
| 14 | c5li8A_ | Alignment | | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 126; PDBTitle: crystal structure of mycobacterium tuberculosis cyp126a1 in complex2 with ketoconazole |
| 15 | c5gweB_ | Alignment | | 100.0 | 25 | PDB header: electron transport Chain: B: PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450 crej |
| 16 | c2xkrA_ | Alignment | | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 142; PDBTitle: crystal structure of mycobacterium tuberculosis cyp142: a novel2 cholesterol oxidase |
| 17 | c6bldA_ | Alignment | | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 268a2 cyp268a2; PDBTitle: mycobacterium marinum cytochrome p450 cyp268a2 in complex with2 pseudoionone |
| 18 | c3mgxB_ | Alignment | | 100.0 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: putative p450 monooxygenase; PDBTitle: crystal structure of p450 oxyd that is involved in the biosynthesis of2 vancomycin-type antibiotics |
| 19 | c6gk5A_ | Alignment | | 100.0 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 cyp267b1 protein; PDBTitle: crystal structure of cytochrome p450 cyp267b1 from sorangium2 cellulosum so ce56 |
| 20 | c6hqwA_ | Alignment | | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from novosphingobium aromaticivorans |
| 21 | c6g71A_ | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure of cyp1232a24 from arthrobacter sp. |
| 22 | c5foiB_ | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: B: PDB Molecule: mycinamicin viii c21 methyl hydroxylase; PDBTitle: crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii |
| 23 | c3lxiB_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of camphor-bound cyp101d1 |
| 24 | c2wm5A_ | Alignment | not modelled | 100.0 | 24 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 124; PDBTitle: x-ray structure of the substrate-free mycobacterium tuberculosis2 cytochrome p450 cyp124 |
| 25 | c2uvnB_ | Alignment | not modelled | 100.0 | 28 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 130; PDBTitle: crystal structure of econazole-bound cyp130 from mycobacterium2 tuberculosis |
| 26 | c6dcdA_ | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 150a6 cyp150a6; PDBTitle: mycobacterium marinum cytochrome p450 cyp150a6 in the substrate-free2 form |
| 27 | c3wvsA_ | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of cytochrome p450revi |
| 28 | d1re9a_ | Alignment | not modelled | 100.0 | 24 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |

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|----|-------------------------|-----------|--------------|-------|----|--|
| 29 | c3rwlA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 alkane hydroxylase 1 cyp153a7; PDBTitle: structure of p450pyr hydroxylase |
| 30 | c3r9cA | Alignment | not modelled | 100.0 | 34 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 164a2; PDBTitle: crystal structure of mycobacterium smegmatis cyp164a2 with econazole2 bound |
| 31 | c5h1zA | Alignment | not modelled | 100.0 | 25 | PDB header: hydrolase Chain: A: PDB Molecule: putative cyp alkane hydroxylase cyp153d17; PDBTitle: cyp153d17 from sphingomonas sp. pamc 26605 |
| 32 | c2z36A | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 type compactin 3",4"- PDBTitle: crystal structure of cytochrome p450 moxa from nonomuraea2 recticata (cyp105) |
| 33 | c4mm0B | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: B: PDB Molecule: p450-like monooxygenase; PDBTitle: crystal structure analysis of the putative thioether synthase sgvp2 involved in the tailoring step of griseoviridin |
| 34 | c5livC | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome p450 cyp260a1,cytochrome p450 cyp260a1; PDBTitle: crystal structure of myxobacterial cyp260a1 |
| 35 | c2xbkA | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: pimd protein; PDBTitle: x-ray structure of the substrate-bound cytochrome p450 pimd - a2 polyene macrolide antibiotic pimaricin epoxidase |
| 36 | c3a4hA | Alignment | not modelled | 100.0 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: vitamin d hydroxylase; PDBTitle: structure of cytochrome p450 vdh from pseudonocardia autotrophica2 (orthorhombic crystal form) |
| 37 | c3e5kA | Alignment | not modelled | 100.0 | 35 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 (cytochrome p450 hydroxylase); PDBTitle: crystal structure of cyp105p1 wild-type 4-phenylimidazole complex |
| 38 | c5ncbA | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of amycolatopsis cytochrome p450 goa in complex2 with guaicol. |
| 39 | c2zbxA | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450-su1; PDBTitle: crystal structure of vitamin d hydroxylase cytochrome p4502 105a1 (wild type) with imidazole bound |
| 40 | c3abbA | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of cyp105d6 |
| 41 | c6hqgB | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from phenylobacterium zucineum |
| 42 | c5hh3C | Alignment | not modelled | 100.0 | 28 | PDB header: oxidoreductase Chain: C: PDB Molecule: oxya protein; PDBTitle: oxa from actinoplanes teichomyceticus |
| 43 | d1lfka | Alignment | not modelled | 100.0 | 29 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 44 | c2z3tD | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of substrate free cytochrome p450 stap2 (cyp245a1) |
| 45 | d1gwia | Alignment | not modelled | 100.0 | 28 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 46 | c3ejdD | Alignment | not modelled | 100.0 | 33 | PDB header: oxidoreductase/lipid transport Chain: D: PDB Molecule: biotin biosynthesis cytochrome p450-like enzyme; PDBTitle: crystal structure of p450bio in complex with hexadec-9z-enoic acid2 ligated acyl carrier protein |
| 47 | d1z8oa1 | Alignment | not modelled | 100.0 | 35 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 48 | c4z5pB | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of the Inma cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.9 a resolution |
| 49 | c3nc7A | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 cypx; PDBTitle: cyp134a1 2-phenylimidazole bound structure |
| 50 | d1ueda | Alignment | not modelled | 100.0 | 27 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 51 | c4e2pA | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 107b1 (p450cviib1); PDBTitle: crystal structure of a post-tailoring hydroxylase (hmtn) involved in2 the himastatin biosynthesis |
| 52 | d1s1fa | Alignment | not modelled | 100.0 | 31 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 53 | c1t2bA | Alignment | not modelled | 100.0 | 21 | PDB header: unknown function Chain: A: PDB Molecule: p450cin; PDBTitle: crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole |
| 54 | c5l1sA | Alignment | not modelled | 100.0 | 28 | PDB header: oxidoreductase Chain: A: PDB Molecule: pentalenolactone synthase; PDBTitle: x-ray structure of f232l mutant of cytochrome p450 pntm |

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|----|------------------------|-----------|--------------|-------|----|---|
| | | | | | | with2 pentalenolactone f PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 113a1; PDBTitle: structure of cytochrome p450 eryk in complex with its2 natural substrate erd |
| 55 | c2jjoA | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of camphor-bound cyp101d2 |
| 56 | c3nv6A | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structures of cyp101d2 y96a mutant |
| 57 | c4dxyA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p-450; PDBTitle: olep, the cytochrome p450 epoxidase from streptomyces antibioticus2 involved in oleandomycin biosynthesis: functional analysis and3 crystallographic structure in complex with clotrimazole. |
| 58 | c4xe3B | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: C: PDB Molecule: putative cytochrome p450; PDBTitle: crystal structure of cyp105n1 from streptomyces coelicolor a3(2) |
| 59 | c3tywC | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450(meg); PDBTitle: cyp106a2 |
| 60 | c4yt3B | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of gfsf |
| 61 | c5y1iA | Alignment | not modelled | 100.0 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 cyp125; PDBTitle: crystal structure of mycobacterium tuberculosis cytochrome p4502 cyp125, p212121 crystal form |
| 62 | c3ivyA | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: 20-oxo-5-o-mycaminosyltylactone 23-monooxygenase; PDBTitle: tylhi in complex with native substrate 23-deoxy-5-o-mycaminosyl-2 tylenolide (23-dmtl) |
| 63 | c6b11B | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 hydroxylase; PDBTitle: structure of cytochrome p450 cyp109q5 from chondromyces apiculatus |
| 64 | c6gmfA | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: D: PDB Molecule: cyp101j2; PDBTitle: crystal structure of cyp101j2 |
| 65 | c5kyoD | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure of p450 raua (cyp1050a1) complexed with a biosynthetic2 intermediate of aurachin re |
| 66 | c3wecA | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxyb; PDBTitle: oxyb from actinoplanes teichomyceticus |
| 67 | c4tvfA | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: pentalenic acid synthase; PDBTitle: the crystal structure of cytochrome p450 105d7 from streptomyces2 avermitilis in complex with diclofenac |
| 68 | c4ubsA | Alignment | not modelled | 100.0 | 35 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: crystal structure of yc-17-bound cytochrome p450 pikc2 (cyp107l1) |
| 69 | c2c6hB | Alignment | not modelled | 100.0 | 35 | PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide biosynthesis cytochrome p450 pkss; PDBTitle: bacillus subtilis 168 bacillaene polyketide synthase (pks) cytochrome2 p450 pkss |
| 70 | c4yzzA | Alignment | not modelled | 100.0 | 34 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxy protein; PDBTitle: structure of oxye (cyp165d3), a cytochrome p450 involved in2 teicoplanin biosynthesis |
| 71 | c3o1aA | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2) |
| 72 | c2dkkA | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: cytochrome p450 txtc employs substrate conformational switching for2 sequential aliphatic and aromatic thaxtomin hydroxylation |
| 73 | c6f0bA | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the structure of a carbohydrate active p450 |
| 74 | c6g5gA | Alignment | not modelled | 100.0 | 23 | PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of cytochrome p450 cyp101c1 |
| 75 | c3ofuE | Alignment | not modelled | 100.0 | 25 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of cytochrome p450 cyp107w1 from streptomyces2 avermitilis |
| 76 | c4wpzA | Alignment | not modelled | 100.0 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: putative p450-like enzyme; PDBTitle: identification of the functions of unusual cytochrome p450-like2 monooxygenases involved in microbial secondary metabolism |
| 77 | c5z9jA | Alignment | not modelled | 100.0 | 26 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 78 | d1jfbA | Alignment | not modelled | 100.0 | 25 | PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cytochrome p450 hydroxylase; |
| 79 | c6m7IA | Alignment | not modelled | 100.0 | 33 | |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| | | | | | | PDBTitle: complex of oxa with the x-domain from gpa biosynthesis |
| 80 | c2y46B_ | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: B: PDB Molecule: p-450-like protein; PDBTitle: structure of the mixed-function p450 mycg in complex with mycinamicin2 iv in c 2 2 21 space group |
| 81 | c5ofqD_ | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of substrate-free cyp109a2 from bacillus megaterium |
| 82 | c5I90B_ | Alignment | not modelled | 100.0 | 27 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of substrate-free cyp109e1 from bacillus2 megaterium at 2.55 angstrom resolution |
| 83 | c5hiwA_ | Alignment | not modelled | 100.0 | 22 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 cyp260b1; PDBTitle: sorangium cellulosum so ce56 cytochrome p450 260b1 |
| 84 | c4oqrA_ | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: cyp105as1; PDBTitle: structure of a cyp105as1 mutant in complex with compactin |
| 85 | c4jbtB_ | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase/substrate Chain: B: PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: the 2.2 a crystal structure of cyp154c5 from nocardia farcinica in2 complex with androstenedione |
| 86 | d1n40a_ | Alignment | not modelled | 100.0 | 24 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 87 | c5nwsA_ | Alignment | not modelled | 100.0 | 33 | PDB header: biosynthetic protein Chain: A: PDB Molecule: saacmm; PDBTitle: crystal structure of saacmm involved in actinomycin biosynthesis |
| 88 | d1odoa_ | Alignment | not modelled | 100.0 | 32 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 89 | c4ggvA_ | Alignment | not modelled | 100.0 | 31 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 superfamily protein; PDBTitle: crystal structure of hmtt involved in himastatin biosynthesis |
| 90 | c3oo3A_ | Alignment | not modelled | 100.0 | 29 | PDB header: oxidoreductase Chain: A: PDB Molecule: oxy protein; PDBTitle: crystal structure of the orf6* (cyp165d3) monooxygenase involved in2 teicoplanin biosynthesis |
| 91 | c4rm4A_ | Alignment | not modelled | 100.0 | 31 | PDB header: electron transport Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of the versatile cytochrome p450 enzyme cyp109b12 from bacillus subtilis |
| 92 | d1io7a_ | Alignment | not modelled | 100.0 | 27 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 93 | c5cjeA_ | Alignment | not modelled | 100.0 | 37 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: structure of cyp107i2 |
| 94 | c5vwsA_ | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: ligand free structure of cytochrome p450 tbjt1 |
| 95 | c5ysmA_ | Alignment | not modelled | 100.0 | 33 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: crystal structure analysis of rif16 |
| 96 | d1ue8a_ | Alignment | not modelled | 100.0 | 26 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 97 | c6hqwb_ | Alignment | not modelled | 100.0 | 30 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from novosphingobium aromaticivorans |
| 98 | c4z5qA_ | Alignment | not modelled | 100.0 | 32 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of the lmz cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.8 a resolution |
| 99 | c4I54A_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A: PDB Molecule: terminal olefin-forming fatty acid decarboxylase; PDBTitle: structure of cytochrome p450 olet, ligand-free |
| 100 | c6fyjA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A: PDB Molecule: fatty-acid peroxygenase; PDBTitle: cytochrome p450 peroxygenase cyp152k6 in complex with myristic acid |
| 101 | c3awmA_ | Alignment | not modelled | 100.0 | 18 | PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid alpha-hydroxylase; PDBTitle: cytochrome p450sp alpha (cyp152b1) wild-type with palmitic acid |
| 102 | c2x2nB_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: B: PDB Molecule: lanosterol 14-alpha-demethylase; PDBTitle: x-ray structure of cyp51 from trypanosoma brucei in complex2 with posaconazole in two different conformations |
| 103 | d1izoa_ | Alignment | not modelled | 100.0 | 14 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 104 | c2rfcB_ | Alignment | not modelled | 100.0 | 26 | PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: ligand bound (4-phenylimidazole) crystal structure of a2 cytochrome p450 from the thermoacidophilic archaeon3 picophilus torridus |
| 105 | c6a18A_ | Alignment | not modelled | 100.0 | 17 | PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 90b1; |

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|-----|-------------------------|-----------|--------------|-------|----|---|
| 105 | c6a10A_ | Alignment | not modelled | 100.0 | 17 | PDBTitle: crystal structure of cyp90b1 in complex with 1,6-hexandiol PDB header: oxidoreductase |
| 106 | c5yhjB_ | Alignment | not modelled | 100.0 | 16 | Chain: B; PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450ex alpha (cyp152n1) wild-type with myristic acid |
| 107 | c2iagA_ | Alignment | not modelled | 100.0 | 16 | PDB header: isomerase Chain: A; PDB Molecule: prostacyclin synthase; PDBTitle: crystal structure of human prostacyclin synthase |
| 108 | c4lxjA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: lanosterol 14-alpha demethylase; PDBTitle: saccharomyces cerevisiae lanosterol 14-alpha demethylase with2 lanosterol bound |
| 109 | c3juvA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: lanosterol 14-alpha demethylase; PDBTitle: crystal structure of human lanosterol 14alpha-demethylase (cyp51) |
| 110 | c3na0B_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase, electron transport Chain: B; PDB Molecule: cholesterol side-chain cleavage enzyme, mitochondrial; PDBTitle: crystal structure of human cyp11a1 in complex with 20,22-2 dihydroxycholesterol |
| 111 | c3e4eA_ | Alignment | not modelled | 100.0 | 16 | PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 2e1; PDBTitle: human cytochrome p450 2e1 in complex with the inhibitor 4-2 methylpyrazole |
| 112 | c3g1qC_ | Alignment | not modelled | 100.0 | 14 | PDB header: oxidoreductase Chain: C; PDB Molecule: sterol 14-alpha-demethylase; PDBTitle: crystal structure of sterol 14-alpha demethylase (cyp51) from2 trypanosoma brucei in ligand free state |
| 113 | c2ve3A_ | Alignment | not modelled | 100.0 | 21 | PDB header: oxidoreductase Chain: A; PDB Molecule: putative cytochrome p450 120; PDBTitle: retinoic acid bound cyanobacterial cyp120a1 |
| 114 | c6mcwA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 51; PDBTitle: crystal structure of the p450 domain of the cyp51-ferredoxin fusion2 protein from methylococcus capsulatus, complex with the detergent3 anapoe-x-114 |
| 115 | c5fsaA_ | Alignment | not modelled | 100.0 | 15 | PDB header: oxidoreductase Chain: A; PDB Molecule: cyp51 variant1; PDBTitle: crystal structure of sterol 14-alpha demethylase (cyp51) from a2 pathogenic yeast candida albicans in complex with the antifungal drug3 posaconazole |
| 116 | c2rchA_ | Alignment | not modelled | 100.0 | 16 | PDB header: lyase Chain: A; PDB Molecule: cytochrome p450 74a; PDBTitle: crystal structure of arabidopsis thaliana allene oxide synthase (aos,2 cytochrome p450 74a, cyp74a) complexed with 13(s)-hod at 1.85 a3 resolution |
| 117 | d1tqna_ | Alignment | not modelled | 100.0 | 19 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 118 | d1r9oa_ | Alignment | not modelled | 100.0 | 16 | Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450 |
| 119 | c5t6qA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 4b1; PDBTitle: structure of cytochrome p450 4b1 (cyp4b1) complexed with octane: an n-2 alkane and fatty acid omega-hydroxylase with a covalently bound heme |
| 120 | c2q9fA_ | Alignment | not modelled | 100.0 | 19 | PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 46a1; PDBTitle: crystal structure of human cytochrome p450 46a1 in complex with2 cholesterol-3-sulphate |