

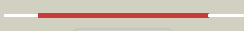












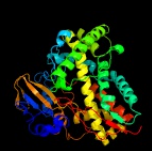

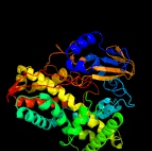





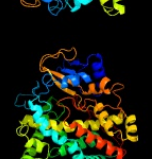

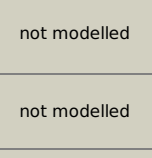


# Phyre2

|               |                                  |
|---------------|----------------------------------|
| Email         | mdejesus@rockefeller.edu         |
| Description   | RVBD1256c_cyp130_1403392_1404609 |
| Date          | Wed Jul 31 22:05:34 BST 2019     |
| Unique Job ID | 930b3429ab0a9b98                 |

Detailed template information

| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c2uvnB_</a> | <br>Alignment   |    | 100.0      | 100    | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 130;<br><b>PDBTitle:</b> crystal structure of econazole-bound cyp130 from mycobacterium2 tuberculosis                                       |
| 2  | <a href="#">c4l0eA_</a> | <br>Alignment   |    | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> p450 monooxygenase;<br><b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis (heme-coordinated expression tag) |
| 3  | <a href="#">c6gk5A_</a> | <br>Alignment   |    | 100.0      | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cyp267b1 protein;<br><b>PDBTitle:</b> crystal structure of cytochrome p450 cyp267b1 from sorangium2 cellulosum so ce56                      |
| 4  | <a href="#">c3buja_</a> | <br>Alignment   |   | 100.0      | 27     | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> calo2;<br><b>PDBTitle:</b> crystal structure of calo2  |
| 5  | <a href="#">c5li8A_</a> | <br>Alignment |  | 100.0      | 30     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 126;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyp126a1 in complex2 with ketoconazole                    |
| 6  | <a href="#">c6hqdB_</a> | <br>Alignment |  | 100.0      | 23     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450-153 from pseudomonas sp. 19-rlim   |
| 7  | <a href="#">c3mgxB_</a> | <br>Alignment |  | 100.0      | 27     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative p450 monooxygenase;<br><b>PDBTitle:</b> crystal structure of p450 oxyd that is involved in the biosynthesis of 2 vancomycin-type antibiotics       |
| 8  | <a href="#">c6giiA_</a> | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> the crystal structure of tepidiphilus thermophilus p450 heme domain  |
| 9  | <a href="#">c3tktA_</a> | <br>Alignment |  | 100.0      | 29     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of cyp108d1 from novosphingobium aromaticivorans2 dsm12444   |
| 10 | <a href="#">c2wivA_</a> | <br>Alignment |  | 100.0      | 24     | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450-like protein xpla;<br><b>PDBTitle:</b> cytochrome-p450 xpla heme domain p21   |
| 11 | <a href="#">c3a4hA_</a> | <br>Alignment |  | 100.0      | 36     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> vitamin d hydroxylase;<br><b>PDBTitle:</b> structure of cytochrome p450 vdh from pseudonocardia autotrophica2 (orthorhombic crystal form)                   |

|    |                        |           |   |       |    |  |
|----|------------------------|-----------|---|-------|----|--|
| 12 | <a href="#">c2z3tD</a> | Alignment |     | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)   |
| 13 | <a href="#">c5fyfA</a> | Alignment |    | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> structure of cyp153a from marinobacter aquaeolei   |
| 14 | <a href="#">c6bldA</a> | Alignment |    | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 268a2 cyp268a2;<br><b>PDBTitle:</b> mycobacterium marinum cytochrome p450 cyp268a2 in complex with2 pseudoionone                    |
| 15 | <a href="#">d1q5da</a> | Alignment |    | 100.0 | 22 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 16 | <a href="#">d1cpta</a> | Alignment |    | 100.0 | 30 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 17 | <a href="#">c5hdiA</a> | Alignment |   | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 144;<br><b>PDBTitle:</b> structural characterization of cyp144a1, a mycobacterium tuberculosis2 cytochrome p450                     |
| 18 | <a href="#">c2fr7A</a> | Alignment |  | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450;<br><b>PDBTitle:</b> crystal structure of cytochrome p450 cyp199a2   |
| 19 | <a href="#">c6hqwA</a> | Alignment |  | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans   |
| 20 | <a href="#">c4yztA</a> | Alignment |  | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis cytochrome p450 pkss;<br><b>PDBTitle:</b> bacillus subtilis 168 bacillaene polyketide synthase (pks) cytochrome2 p450 pkss  |
| 21 | <a href="#">c5h1zA</a> | Alignment | not modelled  | 100.0 | 25 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cyp alkane hydroxylase cyp153d17;<br><b>PDBTitle:</b> cyp153d17 from sphingomonas sp. pamc 26605  |
| 22 | <a href="#">c3lxiB</a> | Alignment | not modelled  | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of camphor-bound cyp101d1  |
| 23 | <a href="#">c6gmfA</a> | Alignment | not modelled  | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> structure of cytochrome p450 cyp109q5 from chondromyces apiculatus                        |
| 24 | <a href="#">c2xkrA</a> | Alignment | not modelled  | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 142;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyp142: a novel2 cholesterol oxidase              |
| 25 | <a href="#">c2xbkA</a> | Alignment | not modelled  | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pimd protein;<br><b>PDBTitle:</b> x-ray structure of the substrate-bound cytochrome p450 pimd - a2 polyene macrolide antibiotic pimaricin epoxidase |
| 26 | <a href="#">c5ncbA</a> | Alignment | not modelled  | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of amycolatopsis cytochrome p450 goa in complex2 with guaicol.                               |
| 27 | <a href="#">c2wm5A</a> | Alignment | not modelled  | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 124;<br><b>PDBTitle:</b> x-ray structure of the substrate-free mycobacterium tuberculosis2 cytochrome p450 cyp124          |
| 28 | <a href="#">c3rwlA</a> | Alignment | not modelled  | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 alkane hydroxylase 1 cyp153a7;<br><b>PDBTitle:</b> structure of p450pyr hydroxylase   |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
| 29 | <a href="#">d1re9a_</a> | Alignment | not modelled | 100.0 | 27 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 30 | <a href="#">c4dxyA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structures of cyp101d2 y96a mutant  |
| 31 | <a href="#">c3nc7A_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cypx;<br><b>PDBTitle:</b> cyp134a1 2-phenylimidazole bound structure   |
| 32 | <a href="#">c3ivyA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cyp125;<br><b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cytochrome p4502 cyp125, p212121 crystal form  |
| 33 | <a href="#">c3p3oA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of the cytochrome p450 monooxygenase aurh (ntermii)2 from streptomyces thioluteus   |
| 34 | <a href="#">c4l36B_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> putative p450-like protein;<br><b>PDBTitle:</b> crystal structure of the cytochrome p450 enzyme txtc   |
| 35 | <a href="#">c3nv6A_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of camphor-bound cyp101d2   |
| 36 | <a href="#">c2z36A_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 type compactin 3",4"-<br><b>PDBTitle:</b> crystal structure of cytochrome p450 moxa from nonomuraea2 recticataena (cyp105)   |
| 37 | <a href="#">c5gweB_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450 crej  |
| 38 | <a href="#">c5kyoD_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> cyp101j2;<br><b>PDBTitle:</b> crystal structure of cyp101j2  |
| 39 | <a href="#">c6g71A_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> structure of cyp1232a24 from arthrobacter sp.   |
| 40 | <a href="#">c5foiB_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin viii c21 methyl hydroxylase;<br><b>PDBTitle:</b> crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii                  |
| 41 | <a href="#">c2c6hB_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 monooxygenase;<br><b>PDBTitle:</b> crystal structure of yc-17-bound cytochrome p450 pikc2 (cyp107l1)   |
| 42 | <a href="#">c3e5kA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 (cytochrome p450 hydroxylase);<br><b>PDBTitle:</b> crystal structure of cyp105p1 wild-type 4-phenylimidazole complex   |
| 43 | <a href="#">c6hqqB_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450-153 from phenylobacterium zucineum  |
| 44 | <a href="#">c5cjeA_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> structure of cyp107l2   |
| 45 | <a href="#">c4mm0B_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> p450-like monooxygenase;<br><b>PDBTitle:</b> crystal structure analysis of the putative thioether synthase sgvp2 involved in the tailoring step of griseoviridin   |
| 46 | <a href="#">c6dcdA_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 150a6 cyp150a6;<br><b>PDBTitle:</b> mycobacterium marinum cytochrome p450 cyp150a6 in the substrate-free2 form   |
| 47 | <a href="#">d1z8oa1</a> | Alignment | not modelled | 100.0 | 30 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 48 | <a href="#">c5hh3C_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> oxya protein;<br><b>PDBTitle:</b> oxa from actinoplanes teichomyceticus  |
| 49 | <a href="#">c3r9cA_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 164a2;<br><b>PDBTitle:</b> crystal structure of mycobacterium smegmatis cyp164a2 with econazole2 bound   |
| 50 | <a href="#">c5l1sA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pentalenolactone synthase;<br><b>PDBTitle:</b> x-ray structure of f232l mutant of cytochrome p450 pntm with2 pentalenolactone f  |
| 51 | <a href="#">c3ejdD_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> oxidoreductase/lipid transport<br><b>Chain:</b> D: <b>PDB Molecule:</b> biotin biosynthesis cytochrome p450-like enzyme;<br><b>PDBTitle:</b> crystal structure of p450bioi in complex with hexadec-9z-enoic acid2 ligated acyl carrier protein                       |
| 52 | <a href="#">c4z5pB_</a> | Alignment | not modelled | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> crystal structure of the lma cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.9 a resolution |
| 53 | <a href="#">c3wvsA_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase;<br><b>PDBTitle:</b> crystal structure of cytochrome p450revi   |
| 54 | <a href="#">c2zbxA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450-su1;<br><b>PDBTitle:</b> crystal structure of vitamin d hydroxylase cytochrome   |

|    |                         |           |              |       |    |   |
|----|-------------------------|-----------|--------------|-------|----|---|
|    |                         |           |              |       |    | p4502 105a1 (wild type) with imidazole bound<br><b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 107b1 (p450cviib1);<br><b>PDBTitle:</b> crystal structure of a post-tailoring hydroxylase (hmtn) involved in2 the himastatin biosynthesis                          |
| 55 | <a href="#">c4e2pA_</a> | Alignment | not modelled | 100.0 | 32 |   |
| 56 | <a href="#">d1jfa_</a>  | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 57 | <a href="#">c1t2bA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> p450cin;<br><b>PDBTitle:</b> crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole   |
| 58 | <a href="#">d1lfka_</a> | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 59 | <a href="#">c4xe3B_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p-450;<br><b>PDBTitle:</b> olep, the cytochrome p450 epoxidase from streptomyces antibioticus2 involved in oleandomycin biosynthesis: functional analysis and3 crystallographic structure in complex with clotrimazole. |
| 60 | <a href="#">c6f0bA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 monooxygenase;<br><b>PDBTitle:</b> cytochrome p450 txtc employs substrate conformational switching for2 sequential aliphatic and aromatic thaxtomin hydroxylation  |
| 61 | <a href="#">c3tywC_</a> | Alignment | not modelled | 100.0 | 29 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> putative cytochrome p450;<br><b>PDBTitle:</b> crystal structure of cyp105n1 from streptomyces coelicolor a3(2)   |
| 62 | <a href="#">c5ofqD_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of substrate-free cyp109a2 from bacillus megaterium   |
| 63 | <a href="#">c6b11B_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> 20-oxo-5-o-mycaminosyltylactone 23-monooxygenase;<br><b>PDBTitle:</b> tylhi in complex with native substrate 23-deoxy-5-o-mycaminosyl-2 tylonolide (23-dmtl)   |
| 64 | <a href="#">c3abbA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> crystal structure of cyp105d6   |
| 65 | <a href="#">c5l90B_</a> | Alignment | not modelled | 100.0 | 31 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> the crystal structure of substrate-free cyp109e1 from bacillus2 megaterium at 2.55 angstrom resolution  |
| 66 | <a href="#">d1s1fa_</a> | Alignment | not modelled | 100.0 | 28 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 67 | <a href="#">c3wecA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> structure of p450 raua (cyp1050a1) complexed with a biosynthetic2 intermediate of aurachin re   |
| 68 | <a href="#">d1gwia_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 69 | <a href="#">c4yt3B_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450(meg);<br><b>PDBTitle:</b> cyp106a2   |
| 70 | <a href="#">d1ueda_</a> | Alignment | not modelled | 100.0 | 29 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 71 | <a href="#">c3ofuE_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of cytochrome p450 cyp101c1   |
| 72 | <a href="#">c5y1iA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> the crystal structure of gfsf   |
| 73 | <a href="#">c5livC_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome p450 cyp260a1,cytochrome p450 cyp260a1;<br><b>PDBTitle:</b> crystal structure of myxobacterial cyp260a1   |
| 74 | <a href="#">c2y46B_</a> | Alignment | not modelled | 100.0 | 33 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> p-450-like protein;<br><b>PDBTitle:</b> structure of the mixed-function p450 mycg in complex with mycinamicin2 iv in c 2 2 21 space group  |
| 75 | <a href="#">c4ubsA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> pentalenic acid synthase;<br><b>PDBTitle:</b> the crystal structure of cytochrome p450 105d7 from streptomyces2 avermitilis in complex with diclofenac   |
| 76 | <a href="#">c6g5qA_</a> | Alignment | not modelled | 100.0 | 23 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> the structure of a carbohydrate active p450   |
| 77 | <a href="#">c2dkkA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)   |
| 78 | <a href="#">c2jioA_</a> | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 113a1;<br><b>PDBTitle:</b> structure of cytochrome p450 eryk in complex with its2 natural substrate erd  |
| 79 | <a href="#">c4wpzA_</a> | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure of cytochrome p450 cyp107w1 from streptomyces2 avermitilis  |
|    |                         |           |              |       |    | <b>PDB header:</b> oxidoreductase   |

|     |                         |           |              |       |    |  |
|-----|-------------------------|-----------|--------------|-------|----|--|
| 80  | <a href="#">c4tvfA_</a> | Alignment | not modelled | 100.0 | 31 | <b>Chain:</b> A: <b>PDB Molecule:</b> oxyb;<br><b>PDBTitle:</b> oxyb from actinoplanes teichomyceticus   |
| 81  | <a href="#">c5z9jA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative p450-like enzyme;<br><b>PDBTitle:</b> identification of the functions of unusual cytochrome p450-like2 monooxygenases involved in microbial secondary metabolism                                     |
| 82  | <a href="#">c3o1aA_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxy protein;<br><b>PDBTitle:</b> structure of oxye (cyp165d3), a cytochrome p450 involved in2 teicoplanin biosynthesis  |
| 83  | <a href="#">c5nwsA_</a> | Alignment | not modelled | 100.0 | 28 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> isaacmm;<br><b>PDBTitle:</b> crystal structure of saacmm involved in actinomycin biosynthesis   |
| 84  | <a href="#">d1n40a_</a> | Alignment | not modelled | 100.0 | 22 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 85  | <a href="#">c4oqrA_</a> | Alignment | not modelled | 100.0 | 24 | <b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> cyp105as1;<br><b>PDBTitle:</b> structure of a cyp105as1 mutant in complex with compactin   |
| 86  | <a href="#">c6m7lA_</a> | Alignment | not modelled | 100.0 | 25 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis  |
| 87  | <a href="#">c4jbtB_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase/substrate<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 monooxygenase;<br><b>PDBTitle:</b> the 2.2 a crystal structure of cyp154c5 from nocardia farcinica in2 complex with androstenedione   |
| 88  | <a href="#">c5hiwA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cyp260b1;<br><b>PDBTitle:</b> sorangium cellulosum so ce56 cytochrome p450 260b1  |
| 89  | <a href="#">d1odoa_</a> | Alignment | not modelled | 100.0 | 26 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 90  | <a href="#">c4ggvA_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 superfamily protein;<br><b>PDBTitle:</b> crystal structure of hmtt involved in himastatin biosynthesis  |
| 91  | <a href="#">c4rm4A_</a> | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> electron transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> the crystal structure of the versatile cytochrome p450 enzyme cyp109b12 from bacillus subtilis   |
| 92  | <a href="#">d1io7a_</a> | Alignment | not modelled | 100.0 | 25 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 93  | <a href="#">c3oo3A_</a> | Alignment | not modelled | 100.0 | 26 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> oxy protein;<br><b>PDBTitle:</b> crystal structure of the orf6* (cyp165d3) monooxygenase involved in2 teicoplanin biosynthesis  |
| 94  | <a href="#">c5vwsA_</a> | Alignment | not modelled | 100.0 | 32 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> ligand free structure of cytochrome p450 tbtj1   |
| 95  | <a href="#">c6hqwb_</a> | Alignment | not modelled | 100.0 | 35 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans   |
| 96  | <a href="#">c5ysmA_</a> | Alignment | not modelled | 100.0 | 30 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> crystal structure analysis of rif16  |
| 97  | <a href="#">d1ue8a_</a> | Alignment | not modelled | 100.0 | 24 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 98  | <a href="#">c4l54A_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> terminal olefin-forming fatty acid decarboxylase;<br><b>PDBTitle:</b> structure of cytochrome p450 olet, ligand-free  |
| 99  | <a href="#">c4z5qA_</a> | Alignment | not modelled | 100.0 | 27 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase;<br><b>PDBTitle:</b> crystal structure of the lnmz cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.8 a resolution |
| 100 | <a href="#">c6fyjA_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty-acid peroxygenase;<br><b>PDBTitle:</b> cytochrome p450 peroxygenase cyp152k6 in complex with myristic acid  |
| 101 | <a href="#">c3awmA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid alpha-hydroxylase;<br><b>PDBTitle:</b> cytochrome p450sp alpha (cyp152b1) wild-type with palmitic acid   |
| 102 | <a href="#">d1lzoa_</a> | Alignment | not modelled | 100.0 | 13 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450  |
| 103 | <a href="#">c2x2nB_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> lanosterol 14-alpha-demethylase;<br><b>PDBTitle:</b> x-ray structure of cyp51 from trypanosoma brucei in complex2 with posaconazole in two different conformations  |
| 104 | <a href="#">c2rfcB_</a> | Alignment | not modelled | 100.0 | 21 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> ligand bound (4-phenylimidazole) crystal structure of a2 cytochrome p450 from the thermoacidophilic archaeon3 picrophilus torridus                                       |
| 105 | <a href="#">c5yhjB_</a> | Alignment | not modelled | 100.0 | 12 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450;<br><b>PDBTitle:</b> cytochrome p450ex alpha (cyp152n1) wild-type with myristic acid  |

|     |                         |           |              |       |    |   |
|-----|-------------------------|-----------|--------------|-------|----|---|
| 106 | <a href="#">c3juvA_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lanosterol 14-alpha demethylase;<br><b>PDBTitle:</b> crystal structure of human lanosterol 14alpha-demethylase (cyp51)   |
| 107 | <a href="#">c2rchA_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 74a;<br><b>PDBTitle:</b> crystal structure of arabidopsis thaliana allene oxide synthase (aos,2 cytochrome p450 74a, cyp74a) complexed with 13(s)-hod at 1.85 a3 resolution           |
| 108 | <a href="#">c2iaqA_</a> | Alignment | not modelled | 100.0 | 13 | <b>PDB header:</b> isomerase<br><b>Chain:</b> A: <b>PDB Molecule:</b> prostacyclin synthase;<br><b>PDBTitle:</b> crystal structure of human prostacyclin synthase   |
| 109 | <a href="#">c6a18A_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 90b1;<br><b>PDBTitle:</b> crystal structure of cyp90b1 in complex with 1,6-hexandiol   |
| 110 | <a href="#">c4lxjA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> lanosterol 14-alpha demethylase;<br><b>PDBTitle:</b> saccharomyces cerevisiae lanosterol 14-alpha demethylase with2 lanosterol bound   |
| 111 | <a href="#">c3hf2A_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional p-450/nadph-p450 reductase;<br><b>PDBTitle:</b> crystal structure of the i401p mutant of cytochrome p450 bm3  |
| 112 | <a href="#">c2ve3A_</a> | Alignment | not modelled | 100.0 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 120;<br><b>PDBTitle:</b> retinoic acid bound cyanobacterial cyp120a1  |
| 113 | <a href="#">c2q9fA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 46a1;<br><b>PDBTitle:</b> crystal structure of human cytochrome p450 46a1 in complex with2 cholesterol-3-sulphate  |
| 114 | <a href="#">c3na0B_</a> | Alignment | not modelled | 100.0 | 15 | <b>PDB header:</b> oxidoreductase, electron transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> cholesterol side-chain cleavage enzyme, mitochondrial;<br><b>PDBTitle:</b> crystal structure of human cyp11a1 in complex with 20,22-2 dihydroxycholesterol               |
| 115 | <a href="#">c6n6qC_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome p450 (cyp102I1);<br><b>PDBTitle:</b> crystal structure of a cytochrome p450 (cyp102I1)  |
| 116 | <a href="#">c5t6qA_</a> | Alignment | not modelled | 100.0 | 16 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 4b1;<br><b>PDBTitle:</b> structure of cytochrome p450 4b1 (cyp4b1) complexed with octane: an n-2 alkane and fatty acid omega-hydroxylase with a covalently bound heme        |
| 117 | <a href="#">c6mcwA_</a> | Alignment | not modelled | 100.0 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 51;<br><b>PDBTitle:</b> crystal structure of the p450 domain of the cyp51-ferredoxin fusion2 protein from methylococcus capsulatus, complex with the detergent3 anapoe-x-114 |
| 118 | <a href="#">c3danA_</a> | Alignment | not modelled | 100.0 | 14 | <b>PDB header:</b> lyase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 74a2;<br><b>PDBTitle:</b> crystal structure of allene oxide synthase  |
| 119 | <a href="#">d1n97a_</a> | Alignment | not modelled | 100.0 | 18 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |
| 120 | <a href="#">d1tqna_</a> | Alignment | not modelled | 100.0 | 16 | <b>Fold:</b> Cytochrome P450<br><b>Superfamily:</b> Cytochrome P450<br><b>Family:</b> Cytochrome P450   |