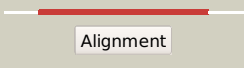

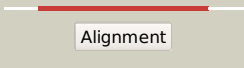

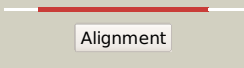
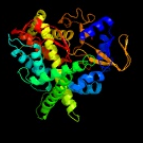
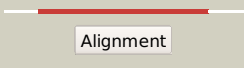

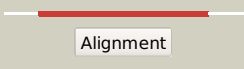

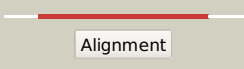

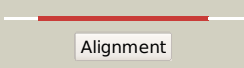

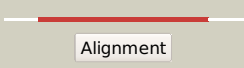

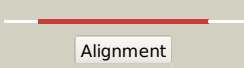

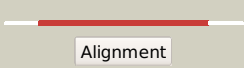

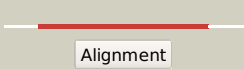









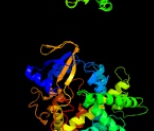


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1666c_cyp139_1892277_1893569
Date	Fri Aug 2 13:30:26 BST 2019
Unique Job ID	efce0682185cc262

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3pm0A_</a>			100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 1b1; <b>PDBTitle:</b> structural characterization of the complex between alpha-2 naphthoflavone and human cytochrome p450 1b1 (cyp1b1)
2	<a href="#">c2ve3A_</a>			100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 120; <b>PDBTitle:</b> retinoic acid bound cyanobacterial cyp120a1
3	<a href="#">c2q9fA_</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 46a1; <b>PDBTitle:</b> crystal structure of human cytochrome p450 46a1 in complex with2 cholesterol-3-sulphate
4	<a href="#">c2x2nB_</a>			100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lanosterol 14-alpha-demethylase; <b>PDBTitle:</b> x-ray structure of cyp51 from trypanosoma brucei in complex2 with posaconazole in two different conformations
5	<a href="#">d1tqna_</a>			100.0	18	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
6	<a href="#">c6mcwA_</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 51; <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
7	<a href="#">c6a18A_</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 90b1; <b>PDBTitle:</b> crystal structure of cyp90b1 in complex with 1,6-hexandiol
8	<a href="#">c3juvA_</a>			100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lanosterol 14-alpha demethylase; <b>PDBTitle:</b> crystal structure of human lanosterol 14alpha-demethylase (cyp51)
9	<a href="#">c6n6qC_</a>			100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome p450 (cyp102l1); <b>PDBTitle:</b> crystal structure of a cytochrome p450 (cyp102l1)
10	<a href="#">c3na0B_</a>			100.0	16	<b>PDB header:</b> oxidoreductase, electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cholesterol side-chain cleavage enzyme, mitochondrial; <b>PDBTitle:</b> crystal structure of human cyp11a1 in complex with 20,22-2 dihydroxycholesterol
11	<a href="#">c3e4eA_</a>			100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 2e1; <b>PDBTitle:</b> human cytochrome p450 2e1 in complex with the inhibitor 4-2 methylpyrazole

12	<a href="#">c5fsaA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyp51 variant1; <b>PDBTitle:</b> crystal structure of sterol 14-alpha demethylase (cyp51) from a2 pathogenic yeast candida albicans in complex with the antifungal drug3 posaconazole
13	<a href="#">c4lxjA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lanosterol 14-alpha demethylase; <b>PDBTitle:</b> saccharomyces cerevisiae lanosterol 14-alpha demethylase with2 lanosterol bound
14	<a href="#">c3daxB</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 7a1; <b>PDBTitle:</b> crystal structure of human cyp7a1
15	<a href="#">d1r9oa</a>	Alignment		100.0	16	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
16	<a href="#">c6b82B</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450, family 17, subfamily a, polypeptide 1; <b>PDBTitle:</b> zebra fish cyp-450 17a1 mutant abiraterone complex
17	<a href="#">c2iagA</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> prostacyclin synthase; <b>PDBTitle:</b> crystal structure of human prostacyclin synthase
18	<a href="#">c2f9qA</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 2d6; <b>PDBTitle:</b> crystal structure of human cytochrome p450 2d6
19	<a href="#">c3rukD</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> steroid 17-alpha-hydroxylase/17,20 lyase; <b>PDBTitle:</b> human cytochrome p450 cyp17a1 in complex with abiraterone
20	<a href="#">c6fyjA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty-acid peroxygenase; <b>PDBTitle:</b> cytochrome p450 peroxygenase cyp152k6 in complex with myristic acid
21	<a href="#">c4fdhA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 11b2, mitochondrial; <b>PDBTitle:</b> structure of human aldosterone synthase, cyp11b2, in complex with2 fadrozole
22	<a href="#">d3czha1</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
23	<a href="#">c2hi4A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 1a2; <b>PDBTitle:</b> crystal structure of human microsomal p450 1a2 in complex with alpha-2 naphthoflavone
24	<a href="#">d1nr6a</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
25	<a href="#">c4r21B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 family 17 polypeptide 2; <b>PDBTitle:</b> zebra fish cytochrome p450 17a2 with progesterone
26	<a href="#">c5fyfA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> structure of cyp153a from marinobacter aquaeolei
27	<a href="#">c3k9vB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1,25-dihydroxyvitamin d(3) 24-hydroxylase, mitochondrial; <b>PDBTitle:</b> crystal structure of rat mitochondrial p450 24a1 s57d in complex with2 chaps
28	<a href="#">c3hf2A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional p-450/nadph-p450 reductase; <b>PDBTitle:</b> crystal structure of the i401p mutant of cytochrome p450 bm3
						<b>Fold:</b> Cytochrome P450

29	<a href="#">d2ij2a1</a>	Alignment	not modelled	100.0	22	<b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
30	<a href="#">c4l54A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> terminal olefin-forming fatty acid decarboxylase; <b>PDBTitle:</b> structure of cytochrome p450 olet, ligand-free
31	<a href="#">d1po5a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
32	<a href="#">c3eqmA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 19a1; <b>PDBTitle:</b> crystal structure of human placental aromatase cytochrome p450 in2 complex with androstenedione
33	<a href="#">c5t6qA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 4b1; <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
34	<a href="#">c3el3A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450; <b>PDBTitle:</b> distinct monooxygenase and farnesene synthase active sites2 in cytochrome p450 170a1
35	<a href="#">c4r1zB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cyp17a1 protein; <b>PDBTitle:</b> zebra fish cytochrome p450 17a1 with abiraterone
36	<a href="#">c3qz1D_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> steroid 21-hydroxylase; <b>PDBTitle:</b> crystal structure of bovine steroid of 21-hydroxylase (p450c21)
37	<a href="#">d2nnja1</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
38	<a href="#">c3ebsA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 2a6; <b>PDBTitle:</b> human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin
39	<a href="#">c3lxiB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of camphor-bound cyp101d1
40	<a href="#">c3a4hA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> vitamin d hydroxylase; <b>PDBTitle:</b> structure of cytochrome p450 vdh from pseudonocardia autotrophica2 (orthorhombic crystal form)
41	<a href="#">c3g1qC_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> sterol 14-alpha-demethylase; <b>PDBTitle:</b> crystal structure of sterol 14-alpha demethylase (cyp51) from2 trypanosoma brucei in ligand free state
42	<a href="#">d2ciba1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
43	<a href="#">c5tl8A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein cyp51; <b>PDBTitle:</b> naegleria fowleri cyp51-positaconazole complex
44	<a href="#">d1lzoa_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
45	<a href="#">c5ylwA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferruginol synthase; <b>PDBTitle:</b> cyp76ah1 from salvia miltiorrhiza
46	<a href="#">c2zbxA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450-su1; <b>PDBTitle:</b> crystal structure of vitamin d hydroxylase cytochrome p4502 105a1 (wild type) with imidazole bound
47	<a href="#">c4l0eA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p450 monooxygenase; <b>PDBTitle:</b> structure of p450sky (cyp163b3), a cytochrome p450 from skyllamycin2 biosynthesis (heme-coordinated expression tag)
48	<a href="#">c2jjoA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 113a1; <b>PDBTitle:</b> structure of cytochrome p450 eryk in complex with its2 natural substrate erd
49	<a href="#">c2xkrA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 142; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyp142: a novel2 cholesterol oxidase
50	<a href="#">c3awmA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid alpha-hydroxylase; <b>PDBTitle:</b> cytochrome p450sp alpha (cyp152b1) wild-type with palmitic acid
51	<a href="#">d1re9a_</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
52	<a href="#">c4uy1B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 14-alpha sterol demethylase; <b>PDBTitle:</b> crystal structure of sterol 14-alpha demethylase (cyp51b) from a2 pathogenic filamentous fungus aspergillus fumigatus in complex3 with vni
53	<a href="#">d1n97a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
54	<a href="#">c2wivA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450-like protein xpla; <b>PDBTitle:</b> cytochrome-p450 xpla heme domain p21
						<b>PDB header:</b> metal binding protein

55	<a href="#">c3bujA_</a>	Alignment	not modelled	100.0	22	<b>Chain:</b> A: <b>PDB Molecule:</b> calo2; <b>PDBTitle:</b> crystal structure of calo2
56	<a href="#">c4yvrA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis cytochrome p450 pkss; <b>PDBTitle:</b> bacillus subtilis 168 bacillaene polyketide synthase (pks) cytochrome2 p450 pkss
57	<a href="#">c6hqdB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from pseudomonas sp. 19-rlim
58	<a href="#">c5I90B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of substrate-free cyp109e1 from bacillus2 megaterium at 2.55 angstrom resolution
59	<a href="#">c5nwsA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> saacmm; <b>PDBTitle:</b> crystal structure of saacmm involved in actinomycin biosynthesis
60	<a href="#">c2z36A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 type compactin 3",4"- <b>PDBTitle:</b> crystal structure of cytochrome p450 moxa from nonomuraea2 recticatena (cyp105)
61	<a href="#">d1cptA_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
62	<a href="#">c5yhjB_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450ex alpha (cyp152n1) wild-type with myristic acid
63	<a href="#">c5li8A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 126; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cyp126a1 in complex2 with ketoconazole
64	<a href="#">c3rwlA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 alkane hydroxylase 1 cyp153a7; <b>PDBTitle:</b> structure of p450pyr hydroxylase
65	<a href="#">c3tktA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of cyp108d1 from novosphingobium aromaticivorans2 dsm12444
66	<a href="#">c5ofqD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of substrate-free cyp109a2 from bacillus megaterium
67	<a href="#">c2fr7A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp199a2
68	<a href="#">c4dxY_A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structures of cyp101d2 y96a mutant
69	<a href="#">d1q5da_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
70	<a href="#">c6gk5A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cyp267b1 protein; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp267b1 from sorangium2 cellulosum so ce56
71	<a href="#">c4e2pA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 107b1 (p450cviib1); <b>PDBTitle:</b> crystal structure of a post-tailoring hydroxylase (hmtn) involved in2 the himastatin biosynthesis
72	<a href="#">c5h1zA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cyp alkane hydroxylase cyp153d17; <b>PDBTitle:</b> cyp153d17 from sphingomonas sp. pamc 26605
73	<a href="#">c5l1sA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pentalenolactone synthase; <b>PDBTitle:</b> x-ray structure of f232l mutant of cytochrome p450 pntm with2 pentalenolactone f
74	<a href="#">c5ncbA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of amycolatopsis cytochrome p450 gcoa in complex2 with guaiaacol.
75	<a href="#">d1z8oa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
76	<a href="#">c3nc7A_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cypx; <b>PDBTitle:</b> cyp134a1 2-phenylimidazole bound structure
77	<a href="#">c3mgxB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative p450 monooxygenase; <b>PDBTitle:</b> crystal structure of p450 oxyd that is involved in the biosynthesis of2 vancomycin-type antibiotics
78	<a href="#">c3b99B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> prostaglandin i2 synthase; <b>PDBTitle:</b> crystal structure of zebrafish prostacyclin synthase (cytochrome p4502 8a1) in complex with substrate analog u51605
79	<a href="#">c6giiA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of tepidiphilus thermophilus p450 heme domain
80	<a href="#">c4jbtB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase/substrate <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 monooxygenase; <b>PDBTitle:</b> the 2.2 a crystal structure of cyp154c5 from nocardia farcinica in2 complex with androstenedione
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin viii c21 methyl hydroxylase;

81	<a href="#">c5foiB_</a>	Alignment	not modelled	100.0	22	<b>PDBTitle:</b> crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii
82	<a href="#">c4yt3B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450(meg); <b>PDBTitle:</b> cyp106a2
83	<a href="#">c5hdiA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 144; <b>PDBTitle:</b> structural characterization of cyp144a1, a mycobacterium tuberculosis2 cytochrome p450
84	<a href="#">c3ejdD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase/lipid transport <b>Chain:</b> D: <b>PDB Molecule:</b> biotin biosynthesis cytochrome p450-like enzyme; <b>PDBTitle:</b> crystal structure of p450bioi in complex with hexadec-9z-enoic acid2 ligated acyl carrier protein
85	<a href="#">c6b11B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 20-oxo-5-o-mycaminosyltylactone 23-monooxygenase; <b>PDBTitle:</b> tylhi in complex with native substrate 23-deoxy-5-o-mycaminosyl-2 tylonolide (23-dmtl)
86	<a href="#">d1odoa_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
87	<a href="#">c2rchA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 74a; <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
88	<a href="#">c4mm0B_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> p450-like monooxygenase; <b>PDBTitle:</b> crystal structure analysis of the putative thioether synthase sgvp2 involved in the tailoring step of griseoviridin
89	<a href="#">c4z5pB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <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
90	<a href="#">d1gwia_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
91	<a href="#">c2z3tD_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)
92	<a href="#">c2c6hB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 monooxygenase; <b>PDBTitle:</b> crystal structure of yc-17-bound cytochrome p450 pikc2 (cyp107l1)
93	<a href="#">c3r9cA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 164a2; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis cyp164a2 with econazole2 bound
94	<a href="#">c3nv6A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of camphor-bound cyp101d2
95	<a href="#">c2y46B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> p-450-like protein; <b>PDBTitle:</b> structure of the mixed-function p450 mycg in complex with mycinamicin2 iv in c 2 2 21 space group
96	<a href="#">c4xe3B_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p-450; <b>PDBTitle:</b> olep, the cytochrome p450 epoxidase from streptomyces antibioticus2 involved in oleandomycin biosynthesis: functional analysis and3 crystallographic structure in complex with clotrimazole.
97	<a href="#">c3e5kA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 (cytochrome p450 hydroxylase); <b>PDBTitle:</b> crystal structure of cyp105p1 wild-type 4-phenylimidazole complex
98	<a href="#">c2uvmB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450 130; <b>PDBTitle:</b> crystal structure of econazole-bound cyp130 from mycobacterium2 tuberculosis
99	<a href="#">c3abbA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <b>PDBTitle:</b> crystal structure of cyp105d6
100	<a href="#">c5hh3C_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxya protein; <b>PDBTitle:</b> oxa from actinoplanes teichomyceticus
101	<a href="#">c6hqwA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans
102	<a href="#">d1lfka_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
103	<a href="#">c2xbkA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pimd protein; <b>PDBTitle:</b> x-ray structure of the substrate-bound cytochrome p450 pimd - a2 polyene macrolide antibiotic pimaricin epoxidase
104	<a href="#">c2wm5A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 124; <b>PDBTitle:</b> x-ray structure of the substrate-free mycobacterium tuberculosis2 cytochrome p450 cyp124
105	<a href="#">c3tywC_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative cytochrome p450; <b>PDBTitle:</b> crystal structure of cyp105n1 from streptomyces

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106	<a href="#">c4rm4A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of the versatile cytochrome p450 enzyme cyp109b12 from bacillus subtilis
107	<a href="#">c5cjeA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <b>PDBTitle:</b> structure of cyp107I2
108	<a href="#">c6f0bA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 monooxygenase; <b>PDBTitle:</b> cytochrome p450 txtc employs substrate conformational switching for 2 sequential aliphatic and aromatic thaxtomin hydroxylation
109	<a href="#">c5y1iA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of gfsf
110	<a href="#">c4ggvA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 superfamily protein; <b>PDBTitle:</b> crystal structure of hmtt involved in himastatin biosynthesis
111	<a href="#">d1jfbA_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
112	<a href="#">c6gmfA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 hydroxylase; <b>PDBTitle:</b> structure of cytochrome p450 cyp109q5 from chondromyces apiculatus
113	<a href="#">c5livC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome p450 cyp260a1,cytochrome p450 cyp260a1; <b>PDBTitle:</b> crystal structure of myxobacterial cyp260a1
114	<a href="#">c5kyoD_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cyp101j2; <b>PDBTitle:</b> crystal structure of cyp101j2
115	<a href="#">c1t2bA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> p450cin; <b>PDBTitle:</b> crystal structure of cytochrome p450cin complexed with its 2 substrate 1,8-cineole
116	<a href="#">c5z9jA_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative p450-like enzyme; <b>PDBTitle:</b> identification of the functions of unusual cytochrome p450-like 2 monooxygenases involved in microbial secondary metabolism
117	<a href="#">c5vwsA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> ligand free structure of cytochrome p450 tbtj1
118	<a href="#">c6dcdA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 150a6 cyp150a6; <b>PDBTitle:</b> mycobacterium marinum cytochrome p450 cyp150a6 in the substrate-free 2 form
119	<a href="#">c3ofuE_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp101c1
120	<a href="#">c4l36B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative p450-like protein; <b>PDBTitle:</b> crystal structure of the cytochrome p450 enzyme txtc