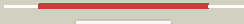



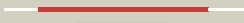



























# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3545c\_cyp125\_3984323\_3985624  
 Date Fri Aug 9 18:20:22 BST 2019  
 Unique Job ID 9eeaf508f9aeb372

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4l0eA_</a>	 Alignment		100.0	29	<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)
2	<a href="#">c3ivyA_</a>	 Alignment		100.0	96	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome p450 cyp125; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis cytochrome p4502 cyp125, p212121 crystal form
3	<a href="#">c2wm5A_</a>	 Alignment		100.0	39	<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
4	<a href="#">c5fyfA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> structure of cyp153a from marinobacter aquaeolei
5	<a href="#">c3mgxB_</a>	 Alignment		100.0	25	<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 of 2 vancomycin-type antibiotics
6	<a href="#">c6bldA_</a>	 Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome p450 268a2 cyp268a2; <b>PDBTitle:</b> mycobacterium marinum cytochrome p450 cyp268a2 in complex with 2 pseudoionone
7	<a href="#">c3tktA_</a>	 Alignment		100.0	27	<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
8	<a href="#">d1cptA_</a>	 Alignment		100.0	27	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
9	<a href="#">c2xkrA_</a>	 Alignment		100.0	29	<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 novel 2 cholesterol oxidase
10	<a href="#">c6hqdB_</a>	 Alignment		100.0	27	<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-riim
11	<a href="#">c5li8A_</a>	 Alignment		100.0	38	<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 complex 2 with ketoconazole

12	<a href="#">dlre9a_</a>	Alignment		100.0	25	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
13	<a href="#">c3lxiB_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of camphor-bound cyp101d1
14	<a href="#">c2wivA_</a>	Alignment		100.0	23	<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
15	<a href="#">c2z36A_</a>	Alignment		100.0	27	<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 nonomuraa2 recticataena (cyp105)
16	<a href="#">c1t2bA_</a>	Alignment		100.0	24	<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 its2 substrate 1,8-cineole
17	<a href="#">c3p3oA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of the cytochrome p450 monooxygenase aurb (intermii)2 from streptomyces thioluteus
18	<a href="#">c6hqwA_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans
19	<a href="#">c3rwiA_</a>	Alignment		100.0	30	<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
20	<a href="#">c4dxyA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structures of cyp101d2 y96a mutant
21	<a href="#">d1q5da_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
22	<a href="#">c3bujA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calo2; <b>PDBTitle:</b> crystal structure of calo2
23	<a href="#">c2fr7A_</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> crystal structure of cytochrome p450 cyp199a2
24	<a href="#">c5h1zA_</a>	Alignment	not modelled	100.0	28	<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
25	<a href="#">c6gk5A_</a>	Alignment	not modelled	100.0	28	<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
26	<a href="#">c2zbxA_</a>	Alignment	not modelled	100.0	24	<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
27	<a href="#">c3nv6A_</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 camphor-bound cyp101d2
28	<a href="#">c5foiB_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> mycinamicin viii c21 methyl hydroxylase; <b>PDBTitle:</b> crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii
29	<a href="#">c2uvnB_</a>	Alignment	not modelled	100.0	26	<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

30	<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
31	<a href="#">c3wvsA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of cytochrome p450revi
32	<a href="#">c3a4hA</a>	Alignment	not modelled	100.0	30	<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)
33	<a href="#">c6giiA</a>	Alignment	not modelled	100.0	21	<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
34	<a href="#">c5kyoD</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> cyp101j2; <b>PDBTitle:</b> crystal structure of cyp101j2
35	<a href="#">c3e5kA</a>	Alignment	not modelled	100.0	28	<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
36	<a href="#">c4z5pB</a>	Alignment	not modelled	100.0	30	<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
37	<a href="#">c2jjoA</a>	Alignment	not modelled	100.0	29	<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
38	<a href="#">c3tywC</a>	Alignment	not modelled	100.0	23	<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 coelicolor a3(2)
39	<a href="#">c4mm0B</a>	Alignment	not modelled	100.0	26	<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
40	<a href="#">c2xbkA</a>	Alignment	not modelled	100.0	23	<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 pimarinic epoxidase
41	<a href="#">c6hqqB</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from phenylobacterium zucineum
42	<a href="#">c5gweB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450 crej
43	<a href="#">c2z3tD</a>	Alignment	not modelled	100.0	29	<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)
44	<a href="#">c3abbA</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> crystal structure of cyp105d6
45	<a href="#">c4xe3B</a>	Alignment	not modelled	100.0	26	<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.
46	<a href="#">c4e2pA</a>	Alignment	not modelled	100.0	27	<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
47	<a href="#">c5hh3C</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxya protein; <b>PDBTitle:</b> oxa from actinoplanes telchomyceticus
48	<a href="#">c3r9cA</a>	Alignment	not modelled	100.0	25	<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
49	<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
50	<a href="#">c6gmfA</a>	Alignment	not modelled	100.0	28	<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
51	<a href="#">c6g5qA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the structure of a carbohydrate active p450
52	<a href="#">d1s1fa</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
53	<a href="#">c5y1iA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of gfsf
54	<a href="#">d1ueda</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide biosynthesis cytochrome p450

55	<a href="#">c4yzaA</a>	Alignment	not modelled	100.0	30	pkss; <b>PDBTitle:</b> bacillus subtilis 168 bacillaene polyketide synthase (pks) cytochrome2 p450 pkss
56	<a href="#">c2dkkA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)
57	<a href="#">c4yt3B</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450(meg); <b>PDBTitle:</b> cyp106a2
58	<a href="#">c6b11B</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 20-oxo-5-o-mycaminosyltylactone 23-monoxygenase; <b>PDBTitle:</b> tylhi in complex with native substrate 23-deoxy-5-o-mycaminosyl-2 tylonolide (23-dmtl)
59	<a href="#">c2y46B</a>	Alignment	not modelled	100.0	27	<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
60	<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 guaiacol.
61	<a href="#">c5l1sA</a>	Alignment	not modelled	100.0	22	<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 pntr with2 pentalenolactone f
62	<a href="#">c4ubsA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pentalenic acid synthase; <b>PDBTitle:</b> the crystal structure of cytochrome p450 105d7 from streptomyces2 avermitilis in complex with diclofenac
63	<a href="#">c5ofqD</a>	Alignment	not modelled	100.0	32	<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
64	<a href="#">c3ofuE</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp101c1
65	<a href="#">c4l36B</a>	Alignment	not modelled	100.0	23	<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
66	<a href="#">c6f0bA</a>	Alignment	not modelled	100.0	25	<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 for2 sequential aliphatic and aromatic thaxtomin hydroxylation
67	<a href="#">c5l90B</a>	Alignment	not modelled	100.0	30	<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
68	<a href="#">d1lfka</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
69	<a href="#">c6dcdA</a>	Alignment	not modelled	100.0	25	<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-free2 form
70	<a href="#">c6g71A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> structure of cyp1232a24 from arthrobacter sp.
71	<a href="#">c3nc7A</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cypx; <b>PDBTitle:</b> cyp134a1 2-phenylimidazole bound structure
72	<a href="#">d1jfa</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
73	<a href="#">c3ejdD</a>	Alignment	not modelled	100.0	26	<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
74	<a href="#">d1z8oa1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
75	<a href="#">d1io7a</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
76	<a href="#">c5z9jA</a>	Alignment	not modelled	100.0	26	<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-like2 monooxygenases involved in microbial secondary metabolism
77	<a href="#">c4wpzA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp107w1 from streptomyces2 avermitilis
78	<a href="#">c2c6hB</a>	Alignment	not modelled	100.0	29	<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)
79	<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
80	<a href="#">c4ggvA</a>	Alignment	not modelled	100.0	27	<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
81	<a href="#">c4tvfA</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxyb; <b>PDBTitle:</b> oxyb from actinoplanes teichomyceticus
82	<a href="#">c3o1aA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxy protein; <b>PDBTitle:</b> structure of oxye (cyp165d3), a cytochrome p450 involved in2 teicoplanin biosynthesis
83	<a href="#">c5hiwA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cyp260b1; <b>PDBTitle:</b> sorangium cellulosum so ce56 cytochrome p450 260b1
84	<a href="#">c6m7IA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 hydroxylase; <b>PDBTitle:</b> complex of oxya with the x-domain from gpa biosynthesis
85	<a href="#">c3wecA</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> structure of p450 raua (cyp1050a1) complexed with a biosynthetic2 intermediate of aurachin re
86	<a href="#">c4oqrA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cyp105as1; <b>PDBTitle:</b> structure of a cyp105as1 mutant in complex with compactin
87	<a href="#">c4jbtB</a>	Alignment	not modelled	100.0	26	<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
88	<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
89	<a href="#">c4rm4A</a>	Alignment	not modelled	100.0	32	<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
90	<a href="#">d1n40a</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
91	<a href="#">c5cjeA</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <b>PDBTitle:</b> structure of cyp10712
92	<a href="#">d1ue8a</a>	Alignment	not modelled	100.0	28	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
93	<a href="#">c5vvsA</a>	Alignment	not modelled	100.0	27	<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
94	<a href="#">c3oo3A</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxy protein; <b>PDBTitle:</b> crystal structure of the orf6* (cyp165d3) monooxygenase involved in2 teicoplanin biosynthesis
95	<a href="#">c5nwsA</a>	Alignment	not modelled	100.0	29	<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
96	<a href="#">c5ysmA</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure analysis of rif16
97	<a href="#">c6hqwb</a>	Alignment	not modelled	100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans
98	<a href="#">c4z5qA</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <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
99	<a href="#">c4l54A</a>	Alignment	not modelled	100.0	12	<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
100	<a href="#">c2x2nB</a>	Alignment	not modelled	100.0	16	<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
101	<a href="#">c6fyjA</a>	Alignment	not modelled	100.0	11	<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
102	<a href="#">d1izoa</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
103	<a href="#">c6a18A</a>	Alignment	not modelled	100.0	14	<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
104	<a href="#">c3awmA</a>	Alignment	not modelled	100.0	13	<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
105	<a href="#">c3juvA</a>	Alignment	not modelled	100.0	16	<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)
106	<a href="#">c2iagA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> prostacyclin synthase; <b>PDBTitle:</b> crystal structure of human prostacyclin synthase

107	<a href="#">c2rfcB_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> ligand bound (4-phenylimidazole) crystal structure of a2 cytochrome p450 from the thermoacidophilic archaeon3 picophilus torridus
108	<a href="#">c4lxjA_</a>	Alignment	not modelled	100.0	16	<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
109	<a href="#">c2ve3A_</a>	Alignment	not modelled	100.0	18	<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
110	<a href="#">c3e4eA_</a>	Alignment	not modelled	100.0	20	<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
111	<a href="#">c5yhjB_</a>	Alignment	not modelled	100.0	11	<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
112	<a href="#">c2rchA_</a>	Alignment	not modelled	100.0	11	<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
113	<a href="#">c3danA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 74a2; <b>PDBTitle:</b> crystal structure of allene oxide synthase
114	<a href="#">d1r9oa_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
115	<a href="#">c5fsaA_</a>	Alignment	not modelled	100.0	14	<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
116	<a href="#">c6mcwA_</a>	Alignment	not modelled	100.0	17	<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
117	<a href="#">c3b99B_</a>	Alignment	not modelled	100.0	14	<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
118	<a href="#">c3g1qC_</a>	Alignment	not modelled	100.0	17	<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
119	<a href="#">c3el3A_</a>	Alignment	not modelled	100.0	18	<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
120	<a href="#">c3hf2A_</a>	Alignment	not modelled	100.0	15	<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