
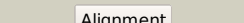

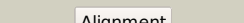





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2268c_cyp128)_2542817_2544286
Date	Mon Aug 5 13:25:40 BST 2019
Unique Job ID	9a7195127a608728

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4l0eA_</a>	 Alignment		100.0	25	<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="#">c6hqgB_</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 phenylobacterium zucineum
3	<a href="#">c6bldA_</a>	 Alignment		100.0	24	<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 with2 pseudoionone
4	<a href="#">c5fyfA_</a>	 Alignment		100.0	23	<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="#">c2wivA_</a>	 Alignment		100.0	24	<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
6	<a href="#">c6giiA_</a>	 Alignment		100.0	26	<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
7	<a href="#">c3buja_</a>	 Alignment		100.0	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calo2; <b>PDBTitle:</b> crystal structure of calo2
8	<a href="#">d1q5da_</a>	 Alignment		100.0	28	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
9	<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 of2 vancomycin-type antibiotics
10	<a href="#">c6hqdB_</a>	 Alignment		100.0	23	<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
11	<a href="#">c2fr7A_</a>	 Alignment		100.0	29	<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

12	<a href="#">d1cpta_</a>	Alignment		100.0	23	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
13	<a href="#">c6hqwb_</a>	Alignment		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 novosphingobium aromaticivorans
14	<a href="#">c3p3oA_</a>	Alignment		100.0	26	<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 aurh (intermii)2 from streptomyces thioluteus
15	<a href="#">c6hqwa_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450-153 from novosphingobium aromaticivorans
16	<a href="#">c2uvnb_</a>	Alignment		100.0	32	<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
17	<a href="#">c5li8A_</a>	Alignment		100.0	32	<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
18	<a href="#">d1re9a_</a>	Alignment		100.0	23	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
19	<a href="#">c5gweB_</a>	Alignment		100.0	27	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> cytochrome p450 crej
20	<a href="#">c5h1za_</a>	Alignment		100.0	25	<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
21	<a href="#">c3tkta_</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> crystal structure of cyp108d1 from novosphingobium aromaticivorans2 dsm12444
22	<a href="#">c2xkra_</a>	Alignment	not modelled	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 novel2 cholesterol oxidase
23	<a href="#">c3nv6A_</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> crystal structure of camphor-bound cyp101d2
24	<a href="#">c3rwiA_</a>	Alignment	not modelled	100.0	24	<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
25	<a href="#">c5hdiA_</a>	Alignment	not modelled	100.0	29	<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
26	<a href="#">c2wm5A_</a>	Alignment	not modelled	100.0	27	<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
27	<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
28	<a href="#">c3lxib_</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> crystal structure of camphor-bound cyp101d1
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c2z3tD</a>	Alignment	not modelled	100.0	29	<b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)
30	<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
31	<a href="#">c3ivyA</a>	Alignment	not modelled	100.0	28	<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
32	<a href="#">c4dxyA</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> crystal structures of cyp101d2 y96a mutant
33	<a href="#">c6g71A</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> structure of cyp1232a24 from arthrobacter sp.
34	<a href="#">c3nc7A</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 cypx; <b>PDBTitle:</b> cyp134a1 2-phenylimidazole bound structure
35	<a href="#">c6gk5A</a>	Alignment	not modelled	100.0	29	<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
36	<a href="#">c5ncbA</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 amycolatopsis cytochrome p450 gooa in complex2 with guaicol.
37	<a href="#">c1t2bA</a>	Alignment	not modelled	100.0	21	<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
38	<a href="#">c4l36B</a>	Alignment	not modelled	100.0	24	<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 txtet
39	<a href="#">c5foiB</a>	Alignment	not modelled	100.0	26	<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 mycc12 from micromonospora griseorubida bound to mycinamicin viii
40	<a href="#">c3a4hA</a>	Alignment	not modelled	100.0	32	<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="#">c6gmfA</a>	Alignment	not modelled	100.0	32	<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
42	<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
43	<a href="#">c3wecA</a>	Alignment	not modelled	100.0	29	<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
44	<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
45	<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
46	<a href="#">c2xbkA</a>	Alignment	not modelled	100.0	24	<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
47	<a href="#">c2z36A</a>	Alignment	not modelled	100.0	26	<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)
48	<a href="#">c6dcdA</a>	Alignment	not modelled	100.0	31	<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
49	<a href="#">c6g5gA</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> the structure of a carbohydrate active p450
50	<a href="#">d1ueda</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
51	<a href="#">c4yzaA</a>	Alignment	not modelled	100.0	25	<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 (pkss) cytochrome2 p450 pkss
52	<a href="#">c3abbA</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <b>PDBTitle:</b> crystal structure of cyp105d6
53	<a href="#">c5hiwA</a>	Alignment	not modelled	100.0	25	<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
54	<a href="#">c6b11B</a>	Alignment	not modelled	100.0	28	<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)

55	<a href="#">d1lfka_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
56	<a href="#">c5hh3C_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxya protein; <b>PDBTitle:</b> oxya from actinoplanes teichomyceticus
57	<a href="#">c4mm0B_</a>	Alignment	not modelled	100.0	31	<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
58	<a href="#">c3ofuE_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure of cytochrome p450 cyp101c1
59	<a href="#">c5z9jA_</a>	Alignment	not modelled	100.0	28	<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
60	<a href="#">c3e5kA_</a>	Alignment	not modelled	100.0	27	<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
61	<a href="#">c5y1iA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> the crystal structure of gfsf
62	<a href="#">c3r9cA_</a>	Alignment	not modelled	100.0	30	<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
63	<a href="#">c3wvsA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of cytochrome p450revi
64	<a href="#">c2c6hB_</a>	Alignment	not modelled	100.0	30	<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 (cyp107/1)
65	<a href="#">c2zbxA_</a>	Alignment	not modelled	100.0	28	<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
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 txc employs substrate conformational switching for2 sequential aliphatic and aromatic thaxtomin hydroxylation
67	<a href="#">c4xe3B_</a>	Alignment	not modelled	100.0	27	<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.
68	<a href="#">d1s1fa_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
69	<a href="#">c4z5pB_</a>	Alignment	not modelled	100.0	31	<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
70	<a href="#">c5j90B_</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> the crystal structure of substrate-free cyp109e1 from bacillus2 megaterium at 2.55 angstrom resolution
71	<a href="#">d1jfbA_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
72	<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
73	<a href="#">c5ofqD_</a>	Alignment	not modelled	100.0	25	<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
74	<a href="#">c3ejdD_</a>	Alignment	not modelled	100.0	25	<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
75	<a href="#">c3o1aA_</a>	Alignment	not modelled	100.0	27	<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
76	<a href="#">c2jjoA_</a>	Alignment	not modelled	100.0	26	<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
77	<a href="#">c5l1sA_</a>	Alignment	not modelled	100.0	25	<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
78	<a href="#">d1n40a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
79	<a href="#">c4oqrA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cyp105a1; <b>PDBTitle:</b> structure of a cyp105a1 mutant in complex with

						compactin
80	<a href="#">c3tywC_</a>	Alignment	not modelled	100.0	25	<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)
81	<a href="#">c4rm4A_</a>	Alignment	not modelled	100.0	28	<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
82	<a href="#">c4ggvA_</a>	Alignment	not modelled	100.0	26	<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
83	<a href="#">c5cjeA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 hydroxylase; <b>PDBTitle:</b> structure of cyp107I2
84	<a href="#">c4ubsA_</a>	Alignment	not modelled	100.0	29	<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
85	<a href="#">c6m7IA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytochrome p450 hydroxylase; <b>PDBTitle:</b> complex of oxa with the x-domain from gpa biosynthesis
86	<a href="#">c2dkkA_</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> structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)
87	<a href="#">d1z8oa1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
88	<a href="#">c4wpzA_</a>	Alignment	not modelled	100.0	29	<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
89	<a href="#">d1gwia_</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
90	<a href="#">c2y46B_</a>	Alignment	not modelled	100.0	30	<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
91	<a href="#">c3oo3A_</a>	Alignment	not modelled	100.0	26	<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
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="#">c5ysmA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450; <b>PDBTitle:</b> crystal structure analysis of rif16
94	<a href="#">c5nwsA_</a>	Alignment	not modelled	100.0	27	<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
95	<a href="#">c4jbtB_</a>	Alignment	not modelled	100.0	23	<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
96	<a href="#">d1odoa_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
97	<a href="#">c5vwsA_</a>	Alignment	not modelled	100.0	28	<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
98	<a href="#">c2rfcB_</a>	Alignment	not modelled	100.0	25	<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 microphilus torridus
99	<a href="#">c4z5gA_</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
100	<a href="#">c4I54A_</a>	Alignment	not modelled	100.0	13	<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
101	<a href="#">c6fyjA_</a>	Alignment	not modelled	100.0	14	<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="#">c3awmA_</a>	Alignment	not modelled	100.0	14	<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
103	<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
104	<a href="#">c2x2nB_</a>	Alignment	not modelled	100.0	15	<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
105	<a href="#">c5yhjB_</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 p450ex alpha (cyp152n1) wild-type with

					myristic acid
106	<a href="#">d1n97a_</a>	Alignment	not modelled	100.0	22 <b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
107	<a href="#">c2iagA_</a>	Alignment	not modelled	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
108	<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
109	<a href="#">c6a18A_</a>	Alignment	not modelled	100.0	16 <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
110	<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
111	<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)
112	<a href="#">c3el3A_</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> distinct monooxygenase and farnesene synthase active sites2 in cytochrome p450 170a1
113	<a href="#">c3na0B_</a>	Alignment	not modelled	100.0	18 <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
114	<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
115	<a href="#">c3g1qC_</a>	Alignment	not modelled	100.0	15 <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
116	<a href="#">c3hf2A_</a>	Alignment	not modelled	100.0	17 <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
117	<a href="#">c2q9fA_</a>	Alignment	not modelled	100.0	17 <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
118	<a href="#">c4lxjA_</a>	Alignment	not modelled	100.0	18 <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
119	<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
120	<a href="#">c2ve3A_</a>	Alignment	not modelled	100.0	21 <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