

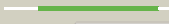


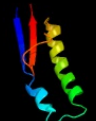



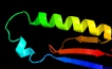
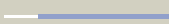


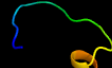

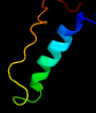







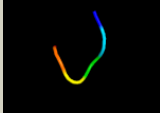


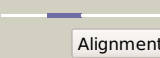

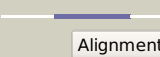



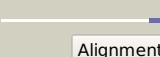

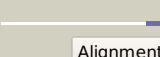

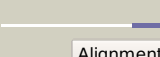
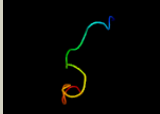
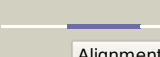

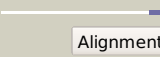

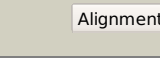
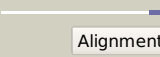
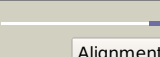
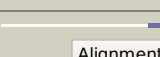
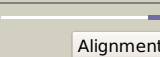



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2561 (-) _2881419_2881712
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	b5d91ea7bab717ad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fx2a_	 Alignment		85.6	21	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
2	d1fx4a_	 Alignment		53.7	22	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
3	c4cIIA_	 Alignment		33.8	23	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase type 10; PDBTitle: crystal structure of human soluble adenylyl cyclase in complex with2 bicarbonate
4	c4wrpB_	 Alignment		27.3	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the c-terminal domain of gene product lpg0944 from legionella2 pneumophila subsp. pneumophila str. philadelphia 1
5	c1cjkA_	 Alignment		26.1	17	PDB header: lyase/lyase/signaling protein Chain: A: PDB Molecule: adenylate cyclase, type v; PDBTitle: complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
6	d1azsa_	 Alignment		25.4	16	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
7	c2mzvA_	 Alignment		19.2	43	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cystatin; PDBTitle: resonance assignments and secondary structure of a phytocystatin from2 sesamum indicum
8	d1t64a_	 Alignment		17.4	24	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
9	c4z5qA_	 Alignment		16.8	40	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of the lnmz cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.8 a resolution
10	c5aj3c_	 Alignment		16.1	58	PDB header: ribosome Chain: C: PDB Molecule: mitoribosomal protein us3m, mrps24; PDBTitle: structure of the small subunit of the mammalian mitoribosome
11	c2d11H_	 Alignment		13.7	83	PDB header: cell adhesion Chain: H: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide

12	c2d11G	 Alignment		13.7	83	PDB header: cell adhesion Chain: G: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
13	c2d11E	 Alignment		13.5	83	PDB header: cell adhesion Chain: E: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
14	c2d11F	 Alignment		13.5	83	PDB header: cell adhesion Chain: F: PDB Molecule: na(+)/h(+) exchange regulatory cofactor nhe-rf2; PDBTitle: crystal structure of the radixin ferm domain complexed with2 the nherf-2 c-terminal tail peptide
15	c5j1hB	 Alignment		12.8	19	PDB header: structural protein Chain: B: PDB Molecule: plectin,plectin; PDBTitle: structure of the spectrin repeats 5 and 6 of the plakin domain of2 plectin
16	c5y1iA	 Alignment		12.6	56	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of gfsf
17	c3danA	 Alignment		11.8	30	PDB header: lyase Chain: A: PDB Molecule: cytochrome p450 74a2; PDBTitle: crystal structure of allene oxide synthase
18	c3ivyA	 Alignment		11.7	38	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 cyp125; PDBTitle: crystal structure of mycobacterium tuberculosis cytochrome p4502 cyp125, p212121 crystal form
19	c4r21B	 Alignment		11.6	29	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 family 17 polypeptide 2; PDBTitle: zebra fish cytochrome p450 17a2 with progesterone
20	c3cwzB	 Alignment		11.0	29	PDB header: transport protein Chain: B: PDB Molecule: rab6-interacting protein 1; PDBTitle: structure of rab6(gtp)-r6ip1 complex
21	c2z3tD	 Alignment	not modelled	10.9	40	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome p450; PDBTitle: crystal structure of substrate free cytochrome p450 stap2 (cyp245a1)
22	c5cjeA	 Alignment	not modelled	10.8	40	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: structure of cyp10712
23	c3et6A	 Alignment	not modelled	10.6	19	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
24	c6f0bA	 Alignment	not modelled	10.5	50	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: cytochrome p450 txtc employs substrate conformational switching for2 sequential aliphatic and aromatic thaxtomin hydroxylation
25	c4z5pB	 Alignment	not modelled	10.4	40	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 hydroxylase; PDBTitle: crystal structure of the lnma cytochrome p450 hydroxylase from the2 leinamycin biosynthetic pathway of streptomyces atroolivaceus s-1403 at 1.9 a resolution
26	c3o1aA	 Alignment	not modelled	10.3	44	PDB header: oxidoreductase Chain: A: PDB Molecule: oxy protein; PDBTitle: structure of oxye (cyp165d3), a cytochrome p450 involved in2 teicoplanin biosynthesis
27	c1t2bA	 Alignment	not modelled	10.3	44	PDB header: unknown function Chain: A: PDB Molecule: p450cin; PDBTitle: crystal structure of cytochrome p450cin complexed with its2 substrate 1,8-cineole
28	d1z8oa1	 Alignment	not modelled	9.8	44	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450

29	c2x2nB_	Alignment	not modelled	9.6	40	PDB header: oxidoreductase Chain: B: PDB Molecule: lanosterol 14-alpha-demethylase; PDBTitle: x-ray structure of cyp51 from trypanosoma brucei in complex2 with posaconazole in two different conformations
30	c5i90B_	Alignment	not modelled	9.6	40	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of substrate-free cyp109e1 from bacillus2 megaterium at 2.55 angstrom resolution
31	c5nbyA_	Alignment	not modelled	9.6	15	PDB header: lyase Chain: A: PDB Molecule: beta subunit of photoactivated adenyllyl cyclase; PDBTitle: structure of a bacterial light-regulated adenyllyl cylcase
32	c4xe3B_	Alignment	not modelled	9.6	50	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p-450; PDBTitle: olep, the cytochrome p450 epoxidase from streptomyces antibioticus2 involved in oleandomycin biosynthesis: functional analysis and3 crystallographic structure in complex with clotrimazole.
33	d1jfa_	Alignment	not modelled	9.5	33	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
34	c3oo3A_	Alignment	not modelled	9.5	44	PDB header: oxidoreductase Chain: A: PDB Molecule: oxy protein; PDBTitle: crystal structure of the orf6* (cyp165d3) monooxygenase involved in2 teicoplanin biosynthesis
35	d1gwia_	Alignment	not modelled	9.5	56	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
36	c5nwsA_	Alignment	not modelled	9.4	40	PDB header: biosynthetic protein Chain: A: PDB Molecule: saacmm; PDBTitle: crystal structure of saacmm involved in actinomycin biosynthesis
37	c6g5qA_	Alignment	not modelled	9.4	38	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the structure of a carbohydrate active p450
38	c3mgxB_	Alignment	not modelled	9.3	40	PDB header: oxidoreductase Chain: B: PDB Molecule: putative p450 monooxygenase; PDBTitle: crystal structure of p450 oxyd that is involved in the biosynthesis of2 vancomycin-type antibiotics
39	c4ggvA_	Alignment	not modelled	9.3	40	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 superfamily protein; PDBTitle: crystal structure of hmtt involved in himastatin biosynthesis
40	c6bldA_	Alignment	not modelled	8.8	56	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 268a2 cyp268a2; PDBTitle: mycobacterium marinum cytochrome p450 cyp268a2 in complex with2 pseudoionone
41	c6dcdA_	Alignment	not modelled	8.7	63	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 150a6 cyp150a6; PDBTitle: mycobacterium marinum cytochrome p450 cyp150a6 in the substrate-free2 form
42	d1ue8a_	Alignment	not modelled	8.6	50	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
43	c5hdiA_	Alignment	not modelled	8.6	44	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 144; PDBTitle: structural characterization of cyp144a1, a mycobacterium tuberculosis2 cytochrome p450
44	c5h1zA_	Alignment	not modelled	8.5	50	PDB header: hydrolase Chain: A: PDB Molecule: putative cyp alkane hydroxylase cyp153d17; PDBTitle: cyp153d17 from sphingomonas sp. pamc 26605
45	c3ejdD_	Alignment	not modelled	8.4	44	PDB header: oxidoreductase/lipid transport Chain: D: PDB Molecule: biotin biosynthesis cytochrome p450-like enzyme; PDBTitle: crystal structure of p450bioi in complex with hexadec-9z-enoic acid2 ligated acyl carrier protein
46	c5li8A_	Alignment	not modelled	8.1	44	PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 126; PDBTitle: crystal structure of mycobacterium tuberculosis cyp126a1 in complex2 with ketoconazole
47	c6m7IA_	Alignment	not modelled	8.1	44	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative cytochrome p450 hydroxylase; PDBTitle: complex of oxa with the x-domain from gpa biosynthesis
48	c5foiB_	Alignment	not modelled	8.0	50	PDB header: oxidoreductase Chain: B: PDB Molecule: mycinamicin viii c21 methyl hydroxylase; PDBTitle: crystal structure of mycinamicin viii c21 methyl hydroxylase mycci2 from micromonospora griseorubida bound to mycinamicin viii
49	c3b99B_	Alignment	not modelled	7.9	33	PDB header: isomerase Chain: B: PDB Molecule: prostaglandin i2 synthase; PDBTitle: crystal structure of zebrafish prostacyclin synthase (cytochrome p4502 8a1) in complex with substrate analog u51605
50	c4tvfA_	Alignment	not modelled	7.8	40	PDB header: oxidoreductase Chain: A: PDB Molecule: oxyb; PDBTitle: oxyb from actinoplanes teichomyceticus
51	c2q9fA_	Alignment	not modelled	7.8	30	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 46a1; PDBTitle: crystal structure of human cytochrome p450 46a1 in complex with2 cholesterol-3-sulphate
52	d1n40a_	Alignment	not modelled	7.7	67	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
53	c3juvA_	Alignment	not modelled	7.7	40	PDB header: oxidoreductase Chain: A: PDB Molecule: lanosterol 14-alpha demethylase; PDBTitle: crystal structure of human lanosterol 14alpha-demethylase (cyp51)
						PDB header: oxidoreductase

54	c3a4hA	Alignment	not modelled	7.7	44	Chain: A; PDB Molecule: vitamin d hydroxylase; PDBTitle: structure of cytochrome p450 vdh from pseudonocardia autotrophica2 (orthorhombic crystal form)
55	d1r9oa	Alignment	not modelled	7.6	30	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
56	c3tkta	Alignment	not modelled	7.4	50	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450; PDBTitle: crystal structure of cyp108d1 from novosphingobium aromaticivorans2 dsm12444
57	c2rchA	Alignment	not modelled	7.4	40	PDB header: lyase Chain: A; PDB Molecule: cytochrome p450 74a; PDBTitle: crystal structure of arabidopsis thaliana allene oxide synthase (aos.2 cytochrome p450 74a, cyp74a) complexed with 13(s)-hod at 1.85 a3 resolution
58	c3dbgA	Alignment	not modelled	7.4	30	PDB header: oxidoreductase Chain: A; PDB Molecule: putative cytochrome p450; PDBTitle: crystal structure of cytochrome p450 170a1 (cyp170a1) from streptomyces coelicolor
59	d1odoa	Alignment	not modelled	7.1	50	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
60	c6gk5A	Alignment	not modelled	7.1	50	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 cyp267b1 protein; PDBTitle: crystal structure of cytochrome p450 cyp267b1 from sorangium2 cellulosum so ce56
61	c4fdhA	Alignment	not modelled	7.0	50	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A; PDB Molecule: cytochrome p450 11b2, mitochondrial; PDBTitle: structure of human aldosterone synthase, cyp11b2, in complex with2 fadrozole
62	c6g71A	Alignment	not modelled	6.9	50	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450; PDBTitle: structure of cyp1232a24 from arthrobacter sp.
63	c6mcwA	Alignment	not modelled	6.8	50	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 51; PDBTitle: crystal structure of the p450 domain of the cyp51-ferredoxin fusion2 protein from methylococcus capsulatus, complex with the detergent3 anapoe-x-114
64	d1lfka	Alignment	not modelled	6.7	44	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
65	c6giiA	Alignment	not modelled	6.7	56	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of tepidiphilus thermophilus p450 heme domain
66	c4ubsA	Alignment	not modelled	6.7	50	PDB header: oxidoreductase Chain: A; PDB Molecule: pentalenic acid synthase; PDBTitle: the crystal structure of cytochrome p450 105d7 from streptomyces2 avermitilis in complex with diclofenac
67	c6hqwb	Alignment	not modelled	6.5	44	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome p450; PDBTitle: cytochrome p450-153 from novosphingobium aromaticivorans
68	c3uvjC	Alignment	not modelled	6.5	12	PDB header: lyase Chain: C; PDB Molecule: guanylate cyclase soluble subunit alpha-3; PDBTitle: crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
69	c3el3A	Alignment	not modelled	6.4	30	PDB header: oxidoreductase Chain: A; PDB Molecule: putative cytochrome p450; PDBTitle: distinct monooxygenase and farnesene synthase active sites2 in cytochrome p450 170a1
70	c3daxB	Alignment	not modelled	6.4	40	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome p450 7a1; PDBTitle: crystal structure of human cyp7a1
71	c3g1qC	Alignment	not modelled	6.4	40	PDB header: oxidoreductase Chain: C; PDB Molecule: sterol 14-alpha-demethylase; PDBTitle: crystal structure of sterol 14-alpha demethylase (cyp51) from2 trypanosoma brucei in ligand free state
72	c4l0eA	Alignment	not modelled	6.3	44	PDB header: oxidoreductase Chain: A; PDB Molecule: p450 monooxygenase; PDBTitle: structure of p450osky (cyp163b3), a cytochrome p450 from skylamycin2 biosynthesis (heme-coordinated expression tag)
73	c4jbtB	Alignment	not modelled	6.2	50	PDB header: oxidoreductase/substrate Chain: B; PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: the 2.2 a crystal structure of cyp154c5 from nocardia farcinica in2 complex with androstenedione
74	c3ebsA	Alignment	not modelled	6.2	30	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 2a6; PDBTitle: human cytochrome p450 2a6 i208s/i300f/g301a/s369g in complex2 with phenacetin
75	c3lxiB	Alignment	not modelled	6.1	50	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome p450; PDBTitle: crystal structure of camphor-bound cyp101d1
76	c6gmfA	Alignment	not modelled	6.1	33	PDB header: oxidoreductase Chain: A; PDB Molecule: putative cytochrome p450 hydroxylase; PDBTitle: structure of cytochrome p450 cyp109q5 from chondromyces apiculatus
77	c4pchE	Alignment	not modelled	6.1	53	PDB header: viral protein Chain: E; PDB Molecule: vp1; PDBTitle: structure of human polyomavirus 7 (hpyv7) vp1 pentamer
78	c4lxjA	Alignment	not modelled	6.1	50	PDB header: oxidoreductase Chain: A; PDB Molecule: lanosterol 14-alpha demethylase; PDBTitle: saccharomyces cerevisiae lanosterol 14-alpha demethylase with2 lanosterol bound
79	c3e4eA	Alignment	not modelled	6.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: cytochrome p450 2e1; PDBTitle: human cytochrome p450 2e1 in complex with the inhibitor 4-2 methylpyrazole

80	c2c6hB_	Alignment	not modelled	6.0	50	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450 monooxygenase; PDBTitle: crystal structure of yc-17-bound cytochrome p450 picc2 (cyp1071l)
81	c2xbkA_	Alignment	not modelled	6.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: pimd protein; PDBTitle: x-ray structure of the substrate-bound cytochrome p450 pimd - a2 polyene macrolide antibiotic pimaricin epoxidase
82	c6fhtB_	Alignment	not modelled	6.0	19	PDB header: lyase Chain: B: PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
83	c3pm0A_	Alignment	not modelled	5.9	30	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450 1b1; PDBTitle: structural characterization of the complex between alpha-2 naphthoflavone and human cytochrome p450 1b1 (cyp1b1)
84	c2dkkA_	Alignment	not modelled	5.9	40	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome p450; PDBTitle: structure/function studies of cytochrome p450 158a1 from streptomyces2 coelicolor a3(2)
85	c4rm4A_	Alignment	not modelled	5.9	40	PDB header: electron transport Chain: A: PDB Molecule: cytochrome p450; PDBTitle: the crystal structure of the versatile cytochrome p450 enzyme cyp109b12 from bacillus subtilis
86	d1s1fa_	Alignment	not modelled	5.9	56	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
87	d2nnja1	Alignment	not modelled	5.9	30	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
88	d1ueda_	Alignment	not modelled	5.8	44	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
89	c4oqrA_	Alignment	not modelled	5.8	67	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: cyp105as1; PDBTitle: structure of a cyp105as1 mutant in complex with compactin
90	c5livC_	Alignment	not modelled	5.7	56	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome p450 cyp260a1,cytochrome p450 cyp260a1; PDBTitle: crystal structure of myxobacterial cyp260a1
91	c3qz1D_	Alignment	not modelled	5.7	30	PDB header: oxidoreductase Chain: D: PDB Molecule: steroid 21-hydroxylase; PDBTitle: crystal structure of bovine steroid of 21-hydroxylase (p450c21)
92	c5tl8A_	Alignment	not modelled	5.7	40	PDB header: oxidoreductase Chain: A: PDB Molecule: protein cyp51; PDBTitle: naegleria fowleri cyp51-posaconazole complex
93	d1io7a_	Alignment	not modelled	5.7	44	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
94	d2evea1	Alignment	not modelled	5.6	30	Fold: PUA domain-like Superfamily: PUA domain-like Family: Atu2648/PH1033-like
95	c4yt3B_	Alignment	not modelled	5.6	44	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome p450(meg); PDBTitle: cyp106a2
96	d1q5da_	Alignment	not modelled	5.5	63	Fold: Cytochrome P450 Superfamily: Cytochrome P450 Family: Cytochrome P450
97	c5kyoD_	Alignment	not modelled	5.5	56	PDB header: oxidoreductase Chain: D: PDB Molecule: cyp101j2; PDBTitle: crystal structure of cyp101j2
98	c2ve3A_	Alignment	not modelled	5.5	40	PDB header: oxidoreductase Chain: A: PDB Molecule: putative cytochrome p450 120; PDBTitle: retinoic acid bound cyanobacterial cyp120a1
99	c5fsaA_	Alignment	not modelled	5.5	50	PDB header: oxidoreductase Chain: A: PDB Molecule: cyp51 variant1; PDBTitle: crystal structure of sterol 14-alpha demethylase (cyp51) from a2 pathogenic yeast candida albicans in complex with the antifungal drug3 posaconazole