


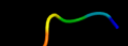





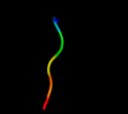



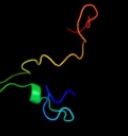







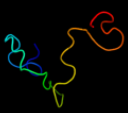







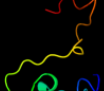



# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P75616
Date	Thu Jan 5 12:12:47 GMT 2012
Unique Job ID	0145006987be40b6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3nc7A_</a>	 Alignment		20.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> cytochrome p450 cypx; <b>PDBTitle:</b> cyp134a1 2-phenylimidazole bound structure
2	<a href="#">d1wj2a_</a>	 Alignment		13.8	67	<b>Fold:</b> WRKY DNA-binding domain <b>Superfamily:</b> WRKY DNA-binding domain <b>Family:</b> WRKY DNA-binding domain
3	<a href="#">c2ve3A_</a>	 Alignment		10.3	13	<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
4	<a href="#">c2rnmC_</a>	 Alignment		10.3	15	<b>PDB header:</b> protein fibril <b>Chain:</b> C; <b>PDB Molecule:</b> small s protein; <b>PDBTitle:</b> structure of the het-s(218-289) prion in its amyloid form2 obtained by solid-state nmr
5	<a href="#">c2aydA_</a>	 Alignment		10.0	67	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> wrky transcription factor 1; <b>PDBTitle:</b> crystal structure of the c-terminal wrky domainof atwrky1,2 an sa-induced and partially npr1-dependent transcription3 factor
6	<a href="#">d1m5ha1</a>	 Alignment		9.7	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
7	<a href="#">d3czha1</a>	 Alignment		9.5	16	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
8	<a href="#">c2de0X_</a>	 Alignment		9.2	39	<b>PDB header:</b> transferase <b>Chain:</b> X; <b>PDB Molecule:</b> alpha-(1,6)-fucosyltransferase; <b>PDBTitle:</b> crystal structure of human alpha 1,6-fucosyltransferase, fut8
9	<a href="#">d1qb5d_</a>	 Alignment		9.1	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Bacterial enterotoxins <b>Family:</b> Bacterial AB5 toxins, B-subunits
10	<a href="#">c3iyuY_</a>	 Alignment		8.8	24	<b>PDB header:</b> virus <b>Chain:</b> Y; <b>PDB Molecule:</b> outer capsid protein vp4; <b>PDBTitle:</b> atomic model of an infectious rotavirus particle
11	<a href="#">c3glqC_</a>	 Alignment		8.4	11	<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)2 from trypanosoma brucei in ligand free state

12	<a href="#">c2fhjD_</a>	Alignment		8.4	13	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> formylmethanofuran--tetrahydromethanopterin <b>PDBTitle:</b> crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
13	<a href="#">d1tqna_</a>	Alignment		8.1	14	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
14	<a href="#">d1po5a_</a>	Alignment		7.1	9	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
15	<a href="#">c3k9vB_</a>	Alignment		6.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1,25-dihydroxyvitamin d(3) 24-hydroxylase, <b>PDBTitle:</b> crystal structure of rat mitochondrial p450 24a1 s57d in2 complex with chaps
16	<a href="#">c3p5nA_</a>	Alignment		6.8	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin uptake protein; <b>PDBTitle:</b> structure and mechanism of the s component of a bacterial ecf2 transporter
17	<a href="#">c2c0zA_</a>	Alignment		6.8	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> novw; <b>PDBTitle:</b> the 1.6 a resolution crystal structure of novw: a 4-keto-6-2 deoxy sugar epimerase from the novobiocin biosynthetic3 gene cluster of streptomyces spheroides
18	<a href="#">c3na0B_</a>	Alignment		6.8	9	<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
19	<a href="#">d1nr6a_</a>	Alignment		6.5	7	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
20	<a href="#">d2nnja1</a>	Alignment		5.9	7	<b>Fold:</b> Cytochrome P450 <b>Superfamily:</b> Cytochrome P450 <b>Family:</b> Cytochrome P450
21	<a href="#">d1bvp12</a>	Alignment	not modelled	5.7	26	<b>Fold:</b> Viral protein domain <b>Superfamily:</b> Viral protein domain <b>Family:</b> Top domain of virus capsid protein
22	<a href="#">c3m3wA_</a>	Alignment	not modelled	5.6	25	<b>PDB header:</b> endocytosis <b>Chain:</b> A: <b>PDB Molecule:</b> protein kinase c and casein kinase ii substrate protein 3; <b>PDBTitle:</b> crystal strcuture of mouse pacsin3 bar domain mutant
23	<a href="#">c1yewF_</a>	Alignment	not modelled	5.4	38	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> particulate methane monooxygenase, a subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
24	<a href="#">d1m5sa1</a>	Alignment	not modelled	5.2	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
25	<a href="#">d1h3ga1</a>	Alignment	not modelled	5.2	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
26	<a href="#">c3e4eA_</a>	Alignment	not modelled	5.1	7	<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
27	<a href="#">c1g92A_</a>	Alignment	not modelled	5.1	35	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> poneratoxin; <b>PDBTitle:</b> solution structure of poneratoxin
28	<a href="#">c3o0rC_</a>	Alignment	not modelled	5.0	15	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment