



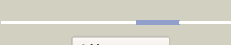






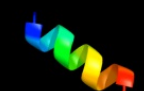
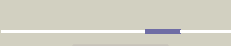


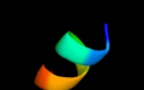










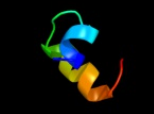






# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	Q9VWX9
Date	Tue Jan 22 11:53:03 GMT 2013
Unique Job ID	04ec191dfa45c549

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1eboE_</a>	 Alignment		40.9	23	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> ebola virus envelope protein chimera consisting <b>PDBTitle:</b> crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
2	<a href="#">c3cm8A_</a>	 Alignment		30.5	11	<b>PDB header:</b> rna binding protein/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polymerase acidic protein; <b>PDBTitle:</b> a rna polymerase subunit structure from virus
3	<a href="#">c4g2kB_</a>	 Alignment		28.9	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4, envelope glycoprotein gp2 <b>PDBTitle:</b> crystal structure of the marburg virus gp2 ectodomain in its post-2 fusion conformation
4	<a href="#">d1rhya1</a>	 Alignment		19.3	21	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
5	<a href="#">d1tw9a1</a>	 Alignment		16.6	10	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
6	<a href="#">d2f1da1</a>	 Alignment		14.1	7	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
7	<a href="#">c213nA_</a>	 Alignment		13.8	40	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rap1, telomere length regulator taz1; <b>PDBTitle:</b> solution structure of rap1-taz1 fusion protein
8	<a href="#">c3csyl_</a>	 Alignment		13.7	63	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> J: <b>PDB Molecule:</b> envelope glycoprotein gp2; <b>PDBTitle:</b> crystal structure of the trimeric prefusion ebola virus glycoprotein2 in complex with a neutralizing antibody from a human survivor
9	<a href="#">d2ae8a1</a>	 Alignment		13.4	0	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Imidazole glycerol phosphate dehydratase
10	<a href="#">c1wr1B_</a>	 Alignment		12.3	35	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-like protein dsk2; <b>PDBTitle:</b> the complex sturcture of dsk2p uba with ubiquitin
11	<a href="#">c3s88J_</a>	 Alignment		12.3	63	<b>PDB header:</b> immune system/viral protein <b>Chain:</b> J: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> crystal structure of sudan ebolavirus glycoprotein (strain gulu) bound2 to 16f6

12	<a href="#">d2bwba1</a>	Alignment		11.8	38	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
13	<a href="#">c2xsuA</a>	Alignment		10.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2 dioxygenase; <b>PDBTitle:</b> crystal structure of the a72g mutant of acinetobacter2 radioresistens catechol 1,2 dioxygenase
14	<a href="#">d2daha1</a>	Alignment		10.3	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
15	<a href="#">c2dbhA</a>	Alignment		10.3	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily <b>PDBTitle:</b> solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
16	<a href="#">c2cwbA</a>	Alignment		10.1	29	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of immunoglobulin g binding protein g <b>PDBTitle:</b> solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
17	<a href="#">c1wazA</a>	Alignment		9.8	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> nmr structure determination of the bacterial mercury2 transporter, merf, in micelles
18	<a href="#">d1k3ya1</a>	Alignment		9.6	13	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
19	<a href="#">c2h3oA</a>	Alignment		9.6	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> structure of merft, a membrane protein with two trans-2 membrane helices
20	<a href="#">d1z96a1</a>	Alignment		9.5	42	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
21	<a href="#">d1glqa1</a>	Alignment	not modelled	9.5	26	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
22	<a href="#">c3fybA</a>	Alignment	not modelled	9.3	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function (duf1244); <b>PDBTitle:</b> crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
23	<a href="#">d1lifa</a>	Alignment	not modelled	8.7	27	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
24	<a href="#">c2lj2A</a>	Alignment	not modelled	8.3	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> integral membrane core domain of the mercury transporter merf in lipid2 bilayer membranes
25	<a href="#">c2jy5A</a>	Alignment	not modelled	8.2	27	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquilin-1; <b>PDBTitle:</b> nmr structure of ubiquilin 1 uba domain
26	<a href="#">c2lifA</a>	Alignment	not modelled	7.9	60	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> core protein p21; <b>PDBTitle:</b> solution structure of kkgf
27	<a href="#">c3q5xA</a>	Alignment	not modelled	7.7	14	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein cut8; <b>PDBTitle:</b> structure of proteasome tether
28	<a href="#">d1s9aa</a>	Alignment	not modelled	7.6	13	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
29	<a href="#">d2o35a1</a>	Alignment	not modelled	7.5	33	<b>Fold:</b> SMc04008-like <b>Superfamily:</b> SMc04008-like

						<b>Family:</b> SMc04008-like
30	<a href="#">c2o35A</a>	Alignment	not modelled	7.5	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf1244; <b>PDBTitle:</b> protein of unknown function (duf1244) from sinorhizobium meliloti
31	<a href="#">c3th1C</a>	Alignment	not modelled	7.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> chlorocatechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of chlorocatechol 1,2-dioxygenase from pseudomonas2 putida
32	<a href="#">c2f5uA</a>	Alignment	not modelled	7.3	50	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> virion protein ul25; <b>PDBTitle:</b> structural characterization of the ul25 dna packaging2 protein from herpes simplex virus type 1
33	<a href="#">c3n9tA</a>	Alignment	not modelled	7.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pnpcc; <b>PDBTitle:</b> cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
34	<a href="#">c2boyC</a>	Alignment	not modelled	6.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-chlorocatechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
35	<a href="#">d2dnaa1</a>	Alignment	not modelled	6.7	26	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
36	<a href="#">d1d2ta</a>	Alignment	not modelled	6.6	14	<b>Fold:</b> Acid phosphatase/Vanadium-dependent haloperoxidase <b>Superfamily:</b> Acid phosphatase/Vanadium-dependent haloperoxidase <b>Family:</b> Type 2 phosphatidic acid phosphatase, PAP2
37	<a href="#">d1p94a</a>	Alignment	not modelled	6.5	27	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
38	<a href="#">d1mlwa</a>	Alignment	not modelled	6.5	18	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
39	<a href="#">d1fqva1</a>	Alignment	not modelled	6.5	35	<b>Fold:</b> F-box domain <b>Superfamily:</b> F-box domain <b>Family:</b> F-box domain
40	<a href="#">c3hj8A</a>	Alignment	not modelled	6.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
41	<a href="#">d1em8a</a>	Alignment	not modelled	6.4	22	<b>Fold:</b> DNA polymerase III chi subunit <b>Superfamily:</b> DNA polymerase III chi subunit <b>Family:</b> DNA polymerase III chi subunit
42	<a href="#">d1toha</a>	Alignment	not modelled	6.3	24	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
43	<a href="#">d1ltza</a>	Alignment	not modelled	6.3	29	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
44	<a href="#">d1phza2</a>	Alignment	not modelled	6.2	18	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
45	<a href="#">d1j8ua</a>	Alignment	not modelled	6.1	18	<b>Fold:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Superfamily:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains <b>Family:</b> Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
46	<a href="#">c3e2tA</a>	Alignment	not modelled	6.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 5-hydroxylase 1; <b>PDBTitle:</b> the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
47	<a href="#">d1dmha</a>	Alignment	not modelled	5.9	22	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Aromatic compound dioxygenase <b>Family:</b> Aromatic compound dioxygenase
48	<a href="#">c2azqA</a>	Alignment	not modelled	5.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> catechol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
49	<a href="#">d2cvda1</a>	Alignment	not modelled	5.7	21	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
50	<a href="#">c2kdrX</a>	Alignment	not modelled	5.7	19	<b>PDB header:</b> viral protein, membrane protein <b>Chain:</b> X: <b>PDB Molecule:</b> non-structural protein 4b; <b>PDBTitle:</b> solution structure of hcv ns4b(227-254)
51	<a href="#">c1rhyB</a>	Alignment	not modelled	5.7	23	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> imidazole glycerol phosphate dehydratase; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate dehydratase
52	<a href="#">d1veja1</a>	Alignment	not modelled	5.6	32	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain

53	<a href="#">d2gsra1</a>	Alignment	not modelled	5.5	16	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain
54	<a href="#">c2x6vB_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> t-box transcription factor tbx5; <b>PDBTitle:</b> crystal structure of human tbx5 in the dna-bound and dna-2 free form
55	<a href="#">d1txna_</a>	Alignment	not modelled	5.5	33	<b>Fold:</b> Coproporphyrinogen III oxidase <b>Superfamily:</b> Coproporphyrinogen III oxidase <b>Family:</b> Coproporphyrinogen III oxidase
56	<a href="#">c1tmxA_</a>	Alignment	not modelled	5.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyquinol 1,2-dioxygenase; <b>PDBTitle:</b> crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardiooides simplex 3e
57	<a href="#">c2v27A_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine hydroxylase; <b>PDBTitle:</b> structure of the cold active phenylalanine hydroxylase from2 colwellia psychrerythraea 34h
58	<a href="#">c3tcyA_</a>	Alignment	not modelled	5.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylalanine-4-hydroxylase; <b>PDBTitle:</b> crystallographic structure of phenylalanine hydroxylase from2 chromobacterium violaceum (cpah) bound to phenylalanine in a site3 distal to the active site
59	<a href="#">d1z0xa2</a>	Alignment	not modelled	5.2	27	<b>Fold:</b> Tetracyclin repressor-like, C-terminal domain <b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain <b>Family:</b> Tetracyclin repressor-like, C-terminal domain
60	<a href="#">d1b4pa1</a>	Alignment	not modelled	5.1	5	<b>Fold:</b> GST C-terminal domain-like <b>Superfamily:</b> GST C-terminal domain-like <b>Family:</b> Glutathione S-transferase (GST), C-terminal domain