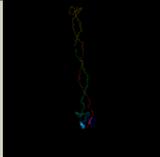
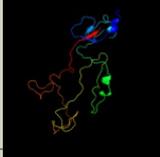
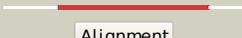
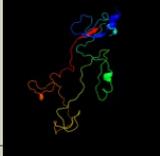
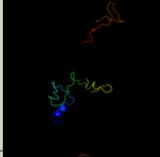
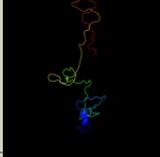
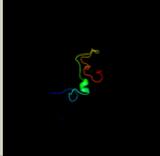
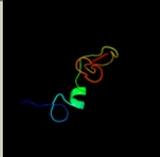
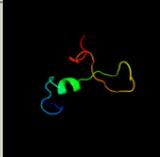
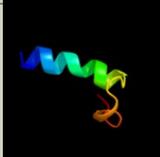


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P77515
Date	Thu Jan 5 12:30:11 GMT 2012
Unique Job ID	c71dfe9d0b877a80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2xgfA_</a>	 Alignment		100.0	70	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> long tail fiber protein p37; <b>PDBTitle:</b> structure of the bacteriophage t4 long tail fibre needle-2 shaped receptor-binding tip
2	<a href="#">c1pdiQ_</a>	 Alignment		100.0	19	<b>PDB header:</b> structural protein <b>Chain:</b> Q; <b>PDB Molecule:</b> short tail fiber protein; <b>PDBTitle:</b> fitting of the c-terminal part of the short tail fibers2 into the cryo-em reconstruction of t4 baseplate
3	<a href="#">d1ocya_</a>	 Alignment		100.0	21	<b>Fold:</b> Receptor-binding domain of short tail fibre protein gp12 <b>Superfamily:</b> Receptor-binding domain of short tail fibre protein gp12 <b>Family:</b> Receptor-binding domain of short tail fibre protein gp12
4	<a href="#">c1h6wA_</a>	 Alignment		99.5	17	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> bacteriophage t4 short tail fibre; <b>PDBTitle:</b> crystal structure of a heat- and protease-stable fragment2 of the bacteriophage t4 short fibre
5	<a href="#">c2fkkA_</a>	 Alignment		88.3	15	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> baseplate structural protein gp10; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the bacteriophage t42 gene product 10
6	<a href="#">c2f18N_</a>	 Alignment		68.1	16	<b>PDB header:</b> virus/viral protein <b>Chain:</b> N; <b>PDB Molecule:</b> baseplate structural protein gp10; <b>PDBTitle:</b> fitting of the gp10 trimer structure into the cryoem map of the2 bacteriophage t4 baseplate in the hexagonal conformation.
7	<a href="#">d1m5ha2</a>	 Alignment		38.2	26	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
8	<a href="#">d1m5sa2</a>	 Alignment		33.9	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
9	<a href="#">c1m5hF_</a>	 Alignment		21.3	25	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> formylmethanofuran--tetrahydromethanopterin <b>PDBTitle:</b> formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus
10	<a href="#">c1m5sC_</a>	 Alignment		17.6	23	<b>PDB header:</b> transferase <b>Chain:</b> C; <b>PDB Molecule:</b> formylmethanofuran--tetrahydromethanopterin <b>PDBTitle:</b> formylmethanofuran:tetrahydromethanopterin2 formyltransferase from methanosarcina barkeri
11	<a href="#">c2pfcA_</a>	 Alignment		9.9	38	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein rv0098/mt0107; <b>PDBTitle:</b> structure of mycobacterium tuberculosis rv0098

12	<a href="#">c2x3lA_</a>	Alignment		7.8	43	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> orn/lys/arg decarboxylase family protein; <b>PDBTitle:</b> crystal structure of the orn_lys_arg decarboxylase family2 protein sar0482 from methicillin-resistant staphylococcus3 aureus
13	<a href="#">d1fmd1_</a>	Alignment		7.4	28	<b>Fold:</b> Nucleoplasmin-like/VP (viral coat and capsid proteins) <b>Superfamily:</b> Positive stranded ssRNA viruses <b>Family:</b> Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
14	<a href="#">d1ftra2</a>	Alignment		7.2	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase <b>Family:</b> Formylmethanofuran:tetrahydromethanopterin formyltransferase
15	<a href="#">d1k25a2</a>	Alignment		7.0	60	<b>Fold:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Superfamily:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Family:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain
16	<a href="#">d1pyya2</a>	Alignment		6.8	55	<b>Fold:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Superfamily:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain <b>Family:</b> Penicillin-binding protein 2x (pbp-2x), c-terminal domain
17	<a href="#">d1c4ka3</a>	Alignment		6.3	36	<b>Fold:</b> Ornithine decarboxylase C-terminal domain <b>Superfamily:</b> Ornithine decarboxylase C-terminal domain <b>Family:</b> Ornithine decarboxylase C-terminal domain
18	<a href="#">c2wzr1_</a>	Alignment		5.8	18	<b>PDB header:</b> virus <b>Chain:</b> 1: <b>PDB Molecule:</b> polyprotein; <b>PDBTitle:</b> the structure of foot and mouth disease virus serotype sat1
19	<a href="#">c3kioB_</a>	Alignment		5.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonuclease h2 subunit b; <b>PDBTitle:</b> mouse rnase h2 complex
20	<a href="#">c3n75E_</a>	Alignment		5.5	45	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> lysine decarboxylase, inducible; <b>PDBTitle:</b> x-ray crystal structure of the escherichia coli inducible lysine2 decarboxylase ldci
21	<a href="#">c2vycA_</a>	Alignment	not modelled	5.4	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biodegradative arginine decarboxylase; <b>PDBTitle:</b> crystal structure of acid induced arginine decarboxylase2 from e. coli
22	<a href="#">d1uptb_</a>	Alignment	not modelled	5.4	22	<b>Fold:</b> GRIP domain <b>Superfamily:</b> GRIP domain <b>Family:</b> GRIP domain