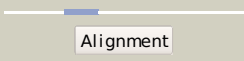
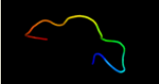
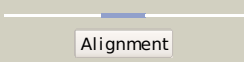
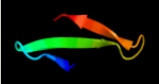
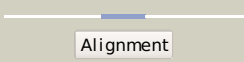
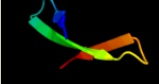
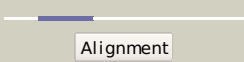
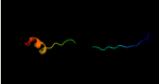
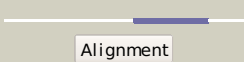

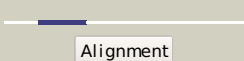

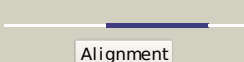

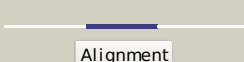
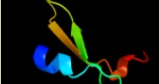
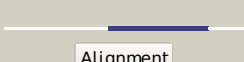

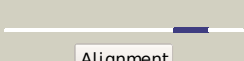

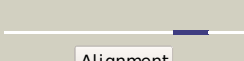
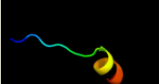
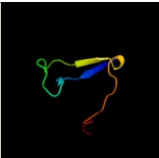



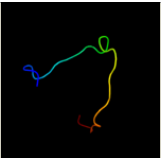
# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P64506
Date	Thu Jan 5 12:09:00 GMT 2012
Unique Job ID	c2502d4eb270a89f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1d8ja_</a>	 Alignment		28.7	29	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> The central core domain of TFIIE beta
2	<a href="#">d1z1ba1</a>	 Alignment		20.7	23	<b>Fold:</b> DNA-binding domain <b>Superfamily:</b> DNA-binding domain <b>Family:</b> lambda integrase N-terminal domain
3	<a href="#">clkjka_</a>	 Alignment		20.7	23	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> integrase; <b>PDBTitle:</b> solution structure of the lambda integrase amino-terminal2 domain
4	<a href="#">d2jnaa1</a>	 Alignment		16.8	56	<b>Fold:</b> Dodecin subunit-like <b>Superfamily:</b> YdgH-like <b>Family:</b> YdgH-like
5	<a href="#">c3ctzA_</a>	 Alignment		15.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> xaa-pro aminopeptidase 1; <b>PDBTitle:</b> structure of human cytosolic x-prolyl aminopeptidase
6	<a href="#">d2axti1</a>	 Alignment		8.9	16	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein I, Psbl <b>Family:</b> Psbl-like
7	<a href="#">d1lm7a_</a>	 Alignment		8.8	16	<b>Fold:</b> beta-hairpin-alpha-hairpin repeat <b>Superfamily:</b> Plakin repeat <b>Family:</b> Plakin repeat
8	<a href="#">d1liccc_</a>	 Alignment		7.9	22	<b>Fold:</b> Cytochrome b5-like heme/steroid binding domain <b>Superfamily:</b> Cytochrome b5-like heme/steroid binding domain <b>Family:</b> Cytochrome b5
9	<a href="#">c1vjqaB_</a>	 Alignment		6.6	19	<b>PDB header:</b> structural genomics, de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> designed protein; <b>PDBTitle:</b> designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
10	<a href="#">d1s21a_</a>	 Alignment		6.3	19	<b>Fold:</b> ADP-ribosylation <b>Superfamily:</b> ADP-ribosylation <b>Family:</b> AvrPphF ORF2, a type III effector
11	<a href="#">c1s21A_</a>	 Alignment		6.3	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> orf2; <b>PDBTitle:</b> crystal structure of avrpvhf orf2, a type iii effector from2 p. syringae

12	<a href="#">c2rm4A_</a>	Alignment		6.0	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> cg6311-pb; <b>PDBTitle:</b> solution structure of the lsm domain of dm edc3 (enhancer2 of decapping 3)
13	<a href="#">dlst6a4</a>	Alignment		5.9	25	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin

14	<a href="#">c2vc8A</a>	Alignment		5.8	15	<b>PDB header:</b> protein-binding <b>Chain:</b> A: <b>PDB Molecule:</b> enhancer of mrna-decapping protein 3; <b>PDBTitle:</b> crystal structure of the lsm domain of human edc3 (enhancer2 of decapping 3)
----	------------------------	-----------	--	-----	----	--