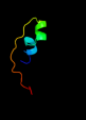
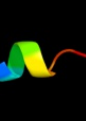
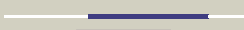
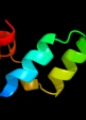
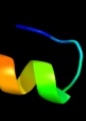
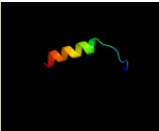
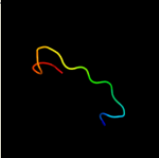
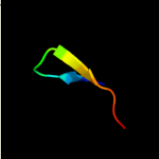
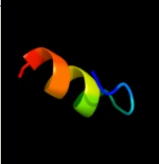


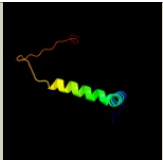
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O43137
Date	Mon Jul 2 19:10:22 BST 2012
Unique Job ID	55229c1cee4c76ea

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2imuA_	 Alignment		12.0	53	PDB header: viral protein Chain: A: PDB Molecule: structural polyprotein (pp) p1; PDBTitle: nmr structure of pep46 from the infectious bursal disease2 virus (ibdv) in dodecylphosphocholin (dpc).
2	c2uzqE_	 Alignment		10.5	35	PDB header: hydrolase Chain: E: PDB Molecule: m-phase inducer phosphatase 2; PDBTitle: protein phosphatase, new crystal form
3	d1qasa3	 Alignment		9.7	42	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
4	d2zkmx4	 Alignment		7.9	33	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
5	d1w0ba_	 Alignment		7.8	56	Fold: Spectrin repeat-like Superfamily: Alpha-hemoglobin stabilizing protein AHSP Family: Alpha-hemoglobin stabilizing protein AHSP
6	c2w0gA_	 Alignment		6.5	23	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: hsp90 co-chaperone cdc37
7	c1nohB_	 Alignment		6.4	32	PDB header: viral protein Chain: B: PDB Molecule: head morphogenesis protein; PDBTitle: the structure of bacteriophage phi29 scaffolding protein2 gp7 after prohead assembly
8	d1us7b_	 Alignment		6.1	23	Fold: Hsp90 co-chaperone CDC37 Superfamily: Hsp90 co-chaperone CDC37 Family: Hsp90 co-chaperone CDC37
9	c1us7B_	 Alignment		6.1	23	PDB header: chaperone Chain: B: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: complex of hsp90 and p50
10	d1r4qa_	 Alignment		6.0	20	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Shiga toxin, A-chain
11	c3iz5W_	 Alignment		5.7	33	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein I22 (I22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

12	c3izcW_	Alignment		5.7	26	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpl22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
13	c4ebgA_	Alignment		5.7	41	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein (sav0303) from2 staphylococcus aureus subsp. aureus mu50 at 1.35 a resolution
14	d3buxb3	Alignment		5.3	46	Fold: SH2-like Superfamily: SH2 domain Family: SH2 domain
15	d1r4pa_	Alignment		5.3	20	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Shiga toxin, A-chain

16 c2xr1A_ Alignment		5.1	24 PDB header:hydrolase Chain: A: PDB Molecule:cleavage and polyadenylation specificity factor 100 kd PDBTitle: dimeric archaeal cleavage and polyadenylation specificity2 factor with n-terminal kh domains (kh-cpsf) from methanosarcina3 mazei
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