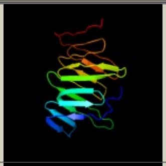
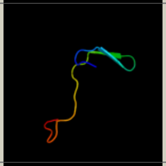
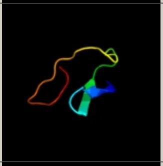
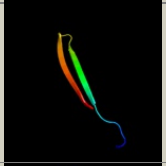
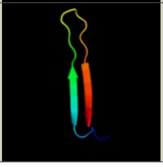
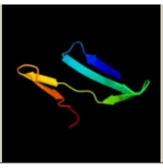
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADV1
Date	Thu Jan 5 11:21:54 GMT 2012
Unique Job ID	7e2b64c05d90dac9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2r1aD_	Alignment		100.0	99	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**protein yhbn; **PDBTitle:** crystal structure of the periplasmic lipopolysaccharide transport2 protein lpta (yhbn), trigonal form
2	c3my2A_	Alignment		98.8	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipopolysaccharide export system protein lptc; **PDBTitle:** crystal structure of lptc
3	d1g7sa1	Alignment		25.0	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
4	d1ueba3	Alignment		8.6	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
5	c1xctL_	Alignment		7.2	14	**PDB header:**immune system **Chain:** L: **PDB Molecule:**protein l; **PDBTitle:** complex hcv core-fab 19d9d6-protein l mutant (d55a, l57h, y64w) in2 space group p21212
6	d2ptla_	Alignment		7.1	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Immunoglobulin-binding domains **Family:**Immunoglobulin-binding domains

7	c2jmbA_	Alignment		6.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu4866; **PDBTitle:** solution structure of the protein atu4866 from agrobacterium2 tumefaciens