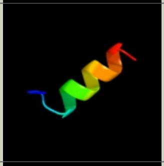
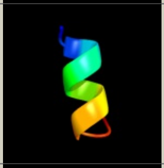
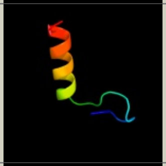
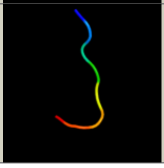
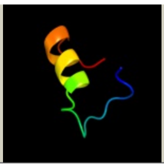
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFW2
Date	Thu Jan 5 11:27:25 GMT 2012
Unique Job ID	f439bb36f356ab43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jrmA_	Alignment		100.0	63	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ribosome modulation factor; **PDBTitle:** solution nmr structure of ribosome modulation factor vp1593 from2 vibrio parahaemolyticus. northeast structural genomics target vpr55
2	c2rusB_	Alignment		13.0	21	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**rubisco (ribulose-1,5-bisphosphate **PDBTitle:** crystal structure of the ternary complex of ribulose-1,5-2 bisphosphate carboxylase, mg(ii), and activator co2 at 2.3-3 angstroms resolution
3	c9rubB_	Alignment		13.0	23	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose-1,5-bisphosphate carboxylase; **PDBTitle:** crystal structure of activated ribulose-1,5-bisphosphate2 carboxylase complexed with its substrate, ribulose-1,5-3 bisphosphate
4	d3buxb3	Alignment		9.9	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
5	c2cazB_	Alignment		8.6	27	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** escrt-i core
6	d2cazb1	Alignment		8.6	27	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
7	d5ruba1	Alignment		8.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
8	c2wybA_	Alignment		7.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
9	d2f6mb1	Alignment		7.7	27	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
10	d1k0ma2	Alignment		7.6	31	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione S-transferase (GST), N-terminal domain
11	d1t1ja_	Alignment		7.0	38	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**Hypothetical protein PA1492

12	c3bitA_	Alignment		6.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of yeast spt16 n-terminal domain

13	c2ae3A_	 Alignment		5.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism