Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q79CP2
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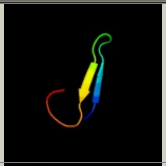
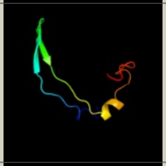
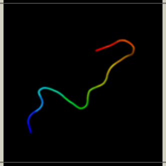
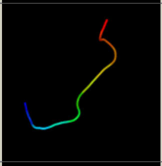
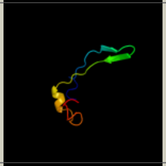
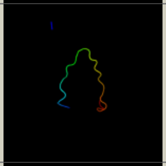
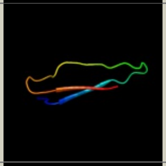
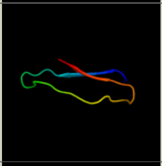
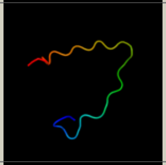
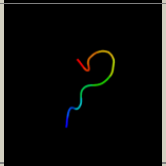
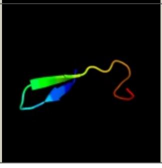
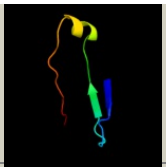
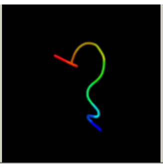
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2knqA_	Alignment		79.5	40	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**general secretion pathway protein h; **PDBTitle:** solution structure of e.coli gsph
2	c1qb3B_	Alignment		20.8	20	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cyclin-dependent kinases regulatory subunit; **PDBTitle:** crystal structure of the cell cycle regulatory protein cks1
3	d2vzsa2	Alignment		17.3	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain **Family:**beta-Galactosidase/glucuronidase domain
4	d1drsa_	Alignment		16.2	50	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Dendroaspin
5	d1qb3a_	Alignment		15.0	20	**Fold:**Cell cycle regulatory proteins **Superfamily:**Cell cycle regulatory proteins **Family:**Cell cycle regulatory proteins
6	c3pfnB_	Alignment		11.9	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
7	d1nm8a2	Alignment		7.3	9	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
8	c2h4tB_	Alignment		6.6	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carnitine o-palmitoyltransferase ii, **PDBTitle:** crystal structure of rat carnitine palmitoyltransferase ii
9	c3afoB_	Alignment		6.6	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
10	d1u1za_	Alignment		6.3	70	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**FabZ-like
11	c3da7G_	Alignment		5.7	39	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**barnase circular permutant; **PDBTitle:** a conformationally strained, circular permutant of barnase

12	c3bjrA_	Alignment		5.7	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxylesterase; **PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
13	d1t1ua2	Alignment		5.5	9	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase

14	c2glvA_	Alignment			5.2	50	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori