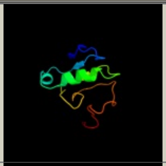
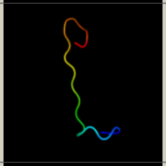
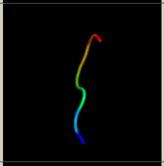
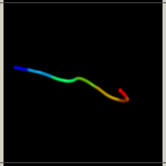
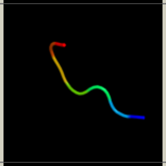
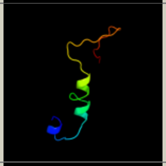
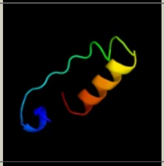
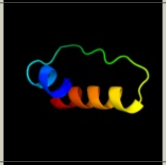
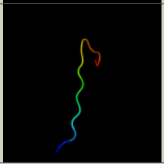
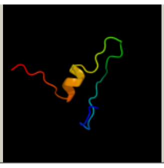
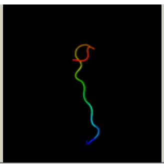
Email	l.a.kelley@imperial.ac.uk
Description	P75675
Date	Thu Jan 5 12:12:52 GMT 2012
Unique Job ID	dc27a9b0c1aaa123

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1uc2a_	Alignment		99.9	26	**Fold:**Hypothetical protein PH1602 **Superfamily:**Hypothetical protein PH1602 **Family:**Hypothetical protein PH1602
2	c2epgB_	Alignment		99.9	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ttha1785; **PDBTitle:** crystal structure of ttha1785
3	d1wkqa_	Alignment		24.4	30	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
4	d1w96a2	Alignment		16.1	29	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
5	d1ulza2	Alignment		15.1	57	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
6	d2j9ga2	Alignment		14.7	57	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
7	d1el6a_	Alignment		11.1	20	**Fold:**Baseplate structural protein gp11 **Superfamily:**Baseplate structural protein gp11 **Family:**Baseplate structural protein gp11
8	d1j8yf2	Alignment		10.1	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
9	d1jqlb_	Alignment		6.4	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	c2zkqm_	Alignment		6.3	8	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
11	d2hxva2	Alignment		6.3	33	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like

12	c2b7fD_	Alignment		5.4	21	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design

13	d1wwra1	 Alignment		5.3	27	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like