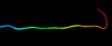
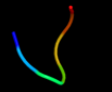


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P77330
Date	Thu Jan 5 12:27:49 GMT 2012
Unique Job ID	36c634875471f6ea

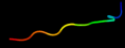
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlzca2	 Alignment		20.2	33	Fold: Cytidine deaminase-like Superfamily: Cytidine deaminase-like Family: AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
2	clzcaA_	 Alignment		12.3	24	PDB header: transferase/hydrolase Chain: A: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
3	c4a1oB_	 Alignment		11.3	29	PDB header: transferase-hydrolase Chain: B: PDB Molecule: bifunctional purine biosynthesis protein purh; PDBTitle: crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
4	dlxrua1	 Alignment		9.2	21	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Kdul-like
5	dlh59b_	 Alignment		9.1	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain

6

dlgqpa_

Alignment



5.9

36

Fold:Galactose-binding domain-like
Superfamily:Galactose-binding domain-like
Family:APC10-like