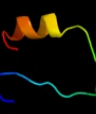
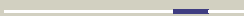


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P75704
Date	Thu Jan 5 12:13:17 GMT 2012
Unique Job ID	67ac1951983b79a7

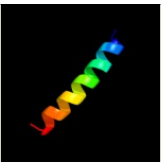
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1sg5a1	 Alignment		24.5	18	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: Rof-like
2	d1h3ga1	 Alignment		12.3	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
3	c3af5a_	 Alignment		9.1	37	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
4	c2a93a_	 Alignment		6.8	50	PDB header: leucine zippers Chain: A: PDB Molecule: c-myc-max heterodimeric leucine zipper; PDBTitle: nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
5	c1a93a_	 Alignment		6.8	50	PDB header: leucine zipper Chain: A: PDB Molecule: myc proto-oncogene protein; PDBTitle: nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, nmr, minimized average structure
6	d2h80a1	 Alignment		6.0	25	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: Variant SAM domain

7

[d2oa5a1](#)

Alignment



5.9

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Fold:BLRF2-like
Superfamily:BLRF2-like
Family:BLRF2-like