

Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A5Z2X5
Date	Mon Jul 2 19:10:01 BST 2012
Unique Job ID	985783ac6dbbab53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4f43A_	 Alignment		16.4	32	PDB header: recombination/dna Chain: A: PDB Molecule: protelomerase; PDBTitle: protelomerase tela mutant r255a complexed with caag hairpin dna
2	c3d6kB_	 Alignment		13.2	24	PDB header: transferase Chain: B: PDB Molecule: putative aminotransferase; PDBTitle: the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
3	d2pw6a1	 Alignment		9.1	27	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
4	c2l9sA_	 Alignment		8.9	38	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 12; PDBTitle: solution structure of pf1 sid1-msin3a pah2 complex
5	c3a4cA_	 Alignment		6.2	27	PDB header: cell cycle, replication Chain: A: PDB Molecule: dna replication factor cdt1; PDBTitle: crystal structure of cdt1 c terminal domain
6	d1u5sb1	 Alignment		5.5	33	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain

7

[c3pplB_](#)

Alignment



5.4

21

PDB header:transferase
Chain: B: **PDB Molecule:**aspartate aminotransferase;
PDBTitle: crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution