

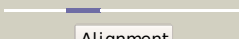

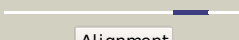















# Phyre2

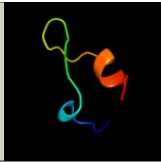
Email	l.a.kelley@imperial.ac.uk
Description	Q5BN46
Date	Thu Apr 26 09:38:59 BST 2012
Unique Job ID	c1094156034a8ea2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1v0da_</a>	 Alignment		10.5	38	<b>Fold:</b> His-Me finger endonucleases <b>Superfamily:</b> His-Me finger endonucleases <b>Family:</b> Caspase-activated DNase, CAD (DffB, DFF40)
2	<a href="#">c1v0dA_</a>	 Alignment		10.5	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna fragmentation factor 40 kda subunit; <b>PDBTitle:</b> crystal structure of caspase-activated dnase (cad)
3	<a href="#">c2dt7A_</a>	 Alignment		8.7	28	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor 3a subunit 3; <b>PDBTitle:</b> solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragmp of3 human splicing factor sf3a60
4	<a href="#">c4a4yA_</a>	 Alignment		6.5	43	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein mxig; <b>PDBTitle:</b> structure of the cytosolic domain of the shigella t3ss2 component mxig
5	<a href="#">c3dv0L_</a>	 Alignment		6.2	20	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
6	<a href="#">c3kz5E_</a>	 Alignment		5.8	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of cdomain
7	<a href="#">d1gwma_</a>	 Alignment		5.8	17	<b>Fold:</b> Galactose-binding domain-like <b>Superfamily:</b> Galactose-binding domain-like <b>Family:</b> Family 29 carbohydrate binding module, CBM29
8	<a href="#">d1w4ha1</a>	 Alignment		5.7	20	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
9	<a href="#">c1wcuA_</a>	 Alignment		5.7	24	<b>PDB header:</b> carbohydrate binding <b>Chain:</b> A: <b>PDB Molecule:</b> non-catalytic protein 1; <b>PDBTitle:</b> cbm29_1, a family 29 carbohydrate binding module from2 piromyces equi

10 [d1bala\\_](#)

Alignment



5.6

20

**Fold:** Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex  
**Superfamily:** Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex  
**Family:** Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex