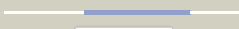
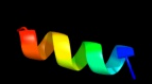


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0A8E5
Date	Thu Jan 5 11:07:38 GMT 2012
Unique Job ID	9755b2a3d4d15b43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ex3b1	 Alignment		41.8	22	Fold: DNA terminal protein Superfamily: DNA terminal protein Family: DNA terminal protein
2	c2kbiA_	 Alignment		34.7	24	PDB header: metal binding protein Chain: A: PDB Molecule: sodium channel protein type 5 subunit alpha; PDBTitle: solution nmr structure of the c-terminal ef-hand domain of2 human cardiac sodium channel nav1.5
3	d1wi0a_	 Alignment		22.9	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
4	d2npta1	 Alignment		14.9	40	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
5	c1m98A_	 Alignment		13.3	42	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
6	c2e1nA_	 Alignment		13.0	0	PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex
7	c3m6jD_	 Alignment		12.7	42	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of unknown function protein from leptospirillum2 rubarum
8	c1nwdB_	 Alignment		11.1	36	PDB header: binding protein/hydrolase Chain: B: PDB Molecule: glutamate decarboxylase; PDBTitle: solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
9	c1nwdC_	 Alignment		11.1	36	PDB header: binding protein/hydrolase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
10	c2kbcB_	 Alignment		10.6	47	PDB header: hormone Chain: B: PDB Molecule: insI5_b-chain; PDBTitle: solution structure of human insulin-like peptide 5 (insI5)
11	d2cy5a1	 Alignment		9.5	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Phosphotyrosine-binding domain (PTB)

12	c3obkH_	Alignment		9.1	8	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
13	c2dqlA_	Alignment		8.6	6	PDB header: circadian clock protein Chain: A: PDB Molecule: pex protein; PDBTitle: crytal structure of the circadian clock associated protein2 pex from anabaena
14	d1k9ua_	Alignment		8.1	13	Fold: EF Hand-like Superfamily: EF-hand Family: Polcalcin
15	c1rijA_	Alignment		6.6	30	PDB header: de novo protein Chain: A: PDB Molecule: e6apn1 peptide; PDBTitle: e6-bind trp-cage (e6apn1)
16	c3c4rC_	Alignment		5.6	8	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein encoded by2 cryptic prophage
17	c2qv6D_	Alignment		5.5	15	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions

18	d1tp6a_	Alignment		5.5	23	Fold: Cystatin-like Superfamily: NTF2-like Family: PA1314-like
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