



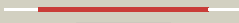




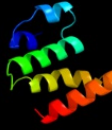












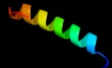


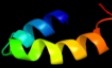

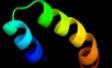





Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P69853
Date	Thu Jan 5 12:12:13 GMT 2012
Unique Job ID	ce1d5ebc75111394

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dls9ua_	 Alignment		100.0	76	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
2	dln1ca_	 Alignment		100.0	17	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
3	c2o9xA_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: reductase, assembly protein; PDBTitle: crystal structure of a putative redox enzyme maturation protein from2 archaeoglobus fulgidus
4	d2o9xa1	 Alignment		100.0	21	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
5	d2idga1	 Alignment		99.7	19	Fold: TorD-like Superfamily: TorD-like Family: TorD-like
6	c1q8hA_	 Alignment		17.2	27	PDB header: metal binding protein Chain: A: PDB Molecule: osteocalcin; PDBTitle: crystal structure of porcine osteocalcin
7	d1q8ha_	 Alignment		17.2	27	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
8	c2r7mA_	 Alignment		15.3	21	PDB header: ligase Chain: A: PDB Molecule: 5-formaminoimidazole-4-carboxamide-1-(beta)-d- PDBTitle: crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
9	d1m3va2	 Alignment		12.2	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
10	d1q3ma_	 Alignment		12.1	29	Fold: GLA-domain Superfamily: GLA-domain Family: GLA-domain
11	d1ysga1	 Alignment		10.8	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death

12	d1yt3a2	Alignment		8.8	15	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
13	d1lcda_	Alignment		8.4	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
14	c2qecA_	Alignment		7.3	13	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase hpa2 and related PDBTitle: crystal structure of histone acetyltransferase hpa2 and related2 acetyltransferase (np_600742.1) from corynebacterium glutamicum atcc3 13032 at 1.90 a resolution
15	c3qbrA_	Alignment		7.2	12	PDB header: apoptosis Chain: A: PDB Molecule: sjchgc06286 protein; PDBTitle: bakbh3 in complex with sja
16	d2ponb1	Alignment		6.9	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
17	d1g5ma_	Alignment		6.5	15	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
18	d1pq1a_	Alignment		6.0	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
19	d1qpza1	Alignment		5.9	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
20	d1f16a_	Alignment		5.7	20	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
21	c2kngA_	Alignment	not modelled	5.4	27	PDB header: dna binding protein Chain: A: PDB Molecule: protein lsr2; PDBTitle: solution structure of c-domain of lsr2