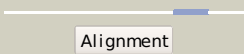

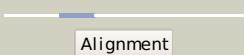

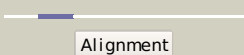



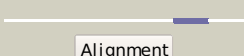
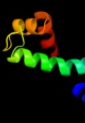











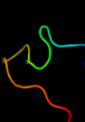





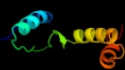

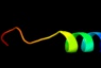



Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q46901
Date	Thu Jan 5 12:35:40 GMT 2012
Unique Job ID	5ae3c8b85df24dbc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fipa_	 Alignment		20.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
2	d2ns0a1	 Alignment		20.5	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
3	c3k6qB_	 Alignment		19.0	12	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
4	d1w36c2	 Alignment		17.7	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
5	d1etxa_	 Alignment		14.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
6	d1nj1a2	 Alignment		14.0	29	Fold: IF3-like Superfamily: C-terminal domain of ProRS Family: C-terminal domain of ProRS
7	d2ak3a2	 Alignment		11.0	26	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
8	d1e4va2	 Alignment		10.4	30	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
9	d1p3ja2	 Alignment		10.3	30	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
10	d1t6sa1	 Alignment		10.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ScpB/YpuH-like
11	d1zina2	 Alignment		10.2	35	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain

12	dls3ga2	Alignment		9.4	35	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
13	dlakya2	Alignment		8.9	22	Fold: Rubredoxin-like Superfamily: Microbial and mitochondrial ADK, insert "zinc finger" domain Family: Microbial and mitochondrial ADK, insert "zinc finger" domain
14	dlpoia_	Alignment		7.6	8	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
15	dlg2ha_	Alignment		7.5	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
16	dlxx6a1	Alignment		7.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
17	c1qhhB_	Alignment		6.9	13	PDB header: hydrolase Chain: B: PDB Molecule: protein (pcra (subunit)); PDBTitle: structure of dna helicase with adpnp
18	c2qfaC_	Alignment		5.9	17	PDB header: cell cycle/cell cycle/cell cycle Chain: C: PDB Molecule: inner centromere protein; PDBTitle: crystal structure of a survivin-borealin-incenp core complex
19	c3ndhA_	Alignment		5.9	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease thai; PDBTitle: restriction endonuclease in complex with substrate dna
20	c2wdtA_	Alignment		5.8	9	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 13; PDBTitle: crystal structure of plasmodium falciparum uch13 in complex2 with the suicide inhibitor ubvme
21	d2f7fa2	Alignment	not modelled	5.7	50	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
22	d1nbwa1	Alignment	not modelled	5.4	22	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Swiveling domain of dehydratase reactivase alpha subunit Family: Swiveling domain of dehydratase reactivase alpha subunit
23	c3e2iA_	Alignment	not modelled	5.3	11	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: crystal structure of thymidine kinase from s. aureus
24	d1etob_	Alignment	not modelled	5.3	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
25	c1nj2A_	Alignment	not modelled	5.2	29	PDB header: ligase Chain: A: PDB Molecule: proline-trna synthetase; PDBTitle: crystal structure of prolyl-trna synthetase from methanothermobacter2 thermotrophicus