

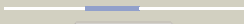


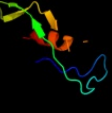



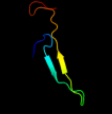
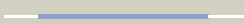




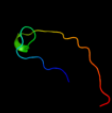





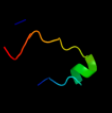
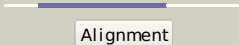
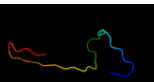

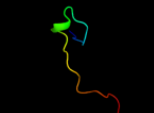
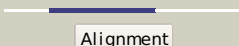

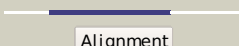
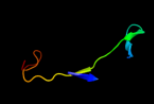
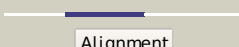
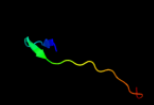
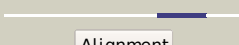

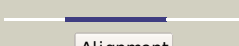



Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0AAN5
Date	Thu Jan 5 11:13:22 GMT 2012
Unique Job ID	4f221efd534908ef

Detailed template information

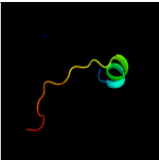
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1	c2kvtA_	 Alignment		100.0	100	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yaia; PDBTitle: solution nmr structure of yaia from escherichia eoli. northeast2 structural genomics target er244
2	c2krxA_	 Alignment		27.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asl3597 protein; PDBTitle: solution nmr structure of asl3597 from nostoc sp. pcc7120.2 northeast structural genomics consortium target id nsr244.
3	d2gskb1	 Alignment		27.0	22	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
4	d1j6wa_	 Alignment		25.9	32	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
5	d1j98a_	 Alignment		25.8	18	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
6	c2grxC_	 Alignment		22.6	22	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
7	c2qqdG_	 Alignment		15.3	31	PDB header: lyase Chain: G: PDB Molecule: pyruvoyl-dependent arginine decarboxylase (ec PDBTitle: n47a mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
8	d1u07a_	 Alignment		14.9	26	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
9	c3t6oA_	 Alignment		12.1	38	PDB header: transport protein Chain: A: PDB Molecule: sulfate transporter/antisigma-factor antagonist stas; PDBTitle: the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
10	c1xx3A_	 Alignment		11.9	22	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
11	d1jj2h_	 Alignment		11.5	43	Fold: alpha/beta-Hammerhead Superfamily: Ribosomal protein L16p/L10e Family: Ribosomal protein L10e

12	c1n13J_	 Alignment		11.2	31	PDB header: lyase Chain: J: PDB Molecule: pyruvoyl-dependent arginine decarboxylase alpha PDBTitle: the crystal structure of pyruvoyl-dependent arginine2 decarboxylase from methanococcus jannashii
13	c4a1aH_	 Alignment		9.1	30	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l10; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
14	d1j6xa_	 Alignment		6.7	28	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
15	d2zkda1	 Alignment		6.2	36	Fold: PUA domain-like Superfamily: PUA domain-like Family: SRA domain-like
16	c2pb7A_	 Alignment		6.0	50	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhrf1; PDBTitle: crystal structure of the sra domain of the human uhrf12 protein
17	c3k6qB_	 Alignment		5.5	21	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
18	d3bi7a1	 Alignment		5.3	43	Fold: PUA domain-like Superfamily: PUA domain-like Family: SRA domain-like

19

[d1ffkf_](#)

Alignment



5.0

43

Fold:alpha/beta-Hammerhead
Superfamily:Ribosomal protein L16p/L10e
Family:Ribosomal protein L10e