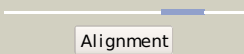

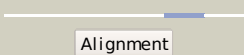

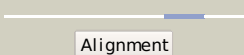


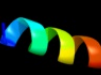
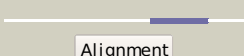

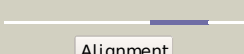
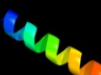
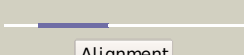
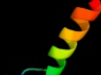
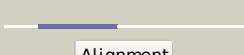

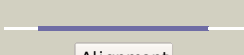

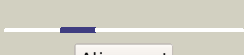


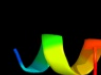
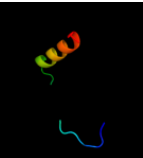

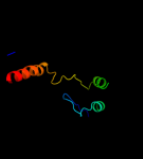




Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P64519
Date	Wed Jan 25 15:20:59 GMT 2012
Unique Job ID	9b94c579b1c4c17d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3saka_	 Alignment		24.7	40	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
2	c2j10B_	 Alignment		23.0	43	PDB header: transcription Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
3	c2j10D_	 Alignment		23.0	43	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
4	c2j10A_	 Alignment		23.0	43	PDB header: transcription Chain: A: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant t329f q331k
5	d1aiea_	 Alignment		17.1	30	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
6	c2j11D_	 Alignment		15.5	30	PDB header: transcription Chain: D: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53 tetramerization domain mutant y327s t329g q331g
7	c2k53A_	 Alignment		11.0	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: a3dk08 protein; PDBTitle: nmr solution structure of a3dk08 protein from clostridium2 thermocellum: northeast structural genomics consortium3 target cmr9
8	c2k5eA_	 Alignment		10.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of putative uncharacterized protein2 gsu1278 from methanocaldococcus jannaschii, northeast3 structural genomics consortium (nesg) target gsr195
9	c1qp8A_	 Alignment		10.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
10	c2vzdD_	 Alignment		8.3	60	PDB header: cell adhesion Chain: D: PDB Molecule: paxillin; PDBTitle: crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif
11	c2vzdC_	 Alignment		8.2	60	PDB header: cell adhesion Chain: C: PDB Molecule: paxillin; PDBTitle: crystal structure of the c-terminal calponin homology2 domain of alpha parvin in complex with paxillin ld1 motif

12	d2o8ra3	Alignment		7.1	40	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
13	d1a1ua_	Alignment		6.9	36	Fold: p53 tetramerization domain Superfamily: p53 tetramerization domain Family: p53 tetramerization domain
14	c1dxyA_	Alignment		6.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyisocaproate dehydrogenase; PDBTitle: structure of d-2-hydroxyisocaproate dehydrogenase
15	d1a6da3	Alignment		6.3	31	Fold: GroEL-intermediate domain like Superfamily: GroEL-intermediate domain like Family: Group II chaperonin (CCT, TRIC), intermediate domain
16	c2o8rA_	Alignment		6.2	22	PDB header: transferase Chain: A: PDB Molecule: polyphosphate kinase; PDBTitle: crystal structure of polyphosphate kinase from2 porphyromonas gingivalis

17 [d2gnoa1](#)

Alignment



5.5

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Fold: post-AAA+ oligomerization domain-like
Superfamily: post-AAA+ oligomerization domain-like
Family: DNA polymerase III clamp loader subunits, C-terminal domain