



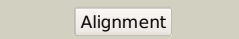

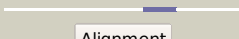
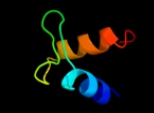
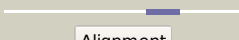

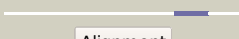
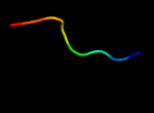





















Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q61070
Date	Tue Jul 30 13:06:05 BST 2013
Unique Job ID	9248d0d2e399ca15

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oe4a_	 Alignment		18.8	46	Fold: Uracil-DNA glycosylase-like Superfamily: Uracil-DNA glycosylase-like Family: Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
2	d3bpya1	 Alignment		15.4	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
3	c1e17A_	 Alignment		15.0	26	PDB header: dna binding domain Chain: A: PDB Molecule: afx; PDBTitle: solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
4	d2c6ya1	 Alignment		14.1	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
5	c3g73A_	 Alignment		11.9	25	PDB header: transcription/dna Chain: A: PDB Molecule: forkhead box protein m1; PDBTitle: structure of the foxm1 dna binding
6	c3ikbB_	 Alignment		11.8	75	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a conserved protein from streptococcus2 mutans ua159.
7	d2a07f1	 Alignment		11.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
8	c2khrA_	 Alignment		11.5	44	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
9	d2gpfa1	 Alignment		11.3	50	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
10	c3co7C_	 Alignment		11.2	21	PDB header: transcription/dna Chain: C: PDB Molecule: forkhead box protein o1; PDBTitle: crystal structure of foxo1 dbd bound to dbe2 dna
11	c3cz3B_	 Alignment		10.7	21	PDB header: viral protein/rna Chain: B: PDB Molecule: protein 2b; PDBTitle: crystal structure of tomato aspermy virus 2b in complex2 with sirna

12	d2pstx1	Alignment		10.3	50	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
13	d1kq8a_	Alignment		9.8	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
14	c1kq8A_	Alignment		9.8	5	PDB header: transcription Chain: A: PDB Molecule: hepatocyte nuclear factor 3 forkhead homolog 1; PDBTitle: solution structure of winged helix protein hfh-1
15	c2zi0B_	Alignment		9.7	21	PDB header: gene regulation/rna Chain: B: PDB Molecule: protein 2b; PDBTitle: crystal structure of tav2b/sirna complex
16	d1dlca3	Alignment		9.1	19	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insectocide), N-terminal domain Family: delta-Endotoxin (insectocide), N-terminal domain
17	d1m5ha1	Alignment		8.8	26	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
18	d1ji6a3	Alignment		8.2	16	Fold: Toxins' membrane translocation domains Superfamily: delta-Endotoxin (insectocide), N-terminal domain Family: delta-Endotoxin (insectocide), N-terminal domain
19	d1d5va_	Alignment		8.1	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
20	c1b9uA_	Alignment		7.9	33	PDB header: hydrolase Chain: A: PDB Molecule: protein (atp synthase); PDBTitle: membrane domain of the subunit b of the e.coli atp synthase
21	d2hfha_	Alignment	not modelled	7.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Forkhead DNA-binding domain
22	c1dfwA_	Alignment	not modelled	7.4	24	PDB header: immune system Chain: A: PDB Molecule: lung surfactant protein b; PDBTitle: conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)
23	d1tfqa_	Alignment	not modelled	7.2	21	Fold: Inhibitor of apoptosis (IAP) repeat Superfamily: Inhibitor of apoptosis (IAP) repeat Family: Inhibitor of apoptosis (IAP) repeat
24	d1ftra1	Alignment	not modelled	7.2	31	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
25	c2lpdA_	Alignment	not modelled	7.1	44	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b
26	c4dmuE_	Alignment	not modelled	7.1	45	PDB header: structural protein/protein binding Chain: E: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide
27	c4dmuA_	Alignment	not modelled	7.1	45	PDB header: structural protein/protein binding Chain: A: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide PDB header: structural protein/protein binding

28	c4dmuC_	Alignment	not modelled	7.1	45	Chain: C: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide
29	c4dmuG_	Alignment	not modelled	7.1	45	PDB header: structural protein/protein binding Chain: G: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide
30	c4dmuL_	Alignment	not modelled	7.1	45	PDB header: structural protein/protein binding Chain: I: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide
31	d1m5sa1	Alignment	not modelled	6.6	26	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
32	c1m5hF_	Alignment	not modelled	6.4	26	PDB header: transferase Chain: F: PDB Molecule: formylmethanofuran--tetrahydromethanopterin PDBTitle: formylmethanofuran:tetrahydromethanopterin2 formyltransferase from archaeoglobus fulgidus
33	c4dmuK_	Alignment	not modelled	6.3	45	PDB header: structural protein/protein binding Chain: K: PDB Molecule: collagen iii derived triple-helical peptide; PDBTitle: crystal structure of the von willebrand factor a3 domain in complex2 with a collagen iii derived triple-helical peptide
34	c2hacB_	Alignment	not modelled	5.7	27	PDB header: membrane protein Chain: B: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
35	c2hacA_	Alignment	not modelled	5.7	27	PDB header: membrane protein Chain: A: PDB Molecule: t-cell surface glycoprotein cd3 zeta chain; PDBTitle: structure of zeta-zeta transmembrane dimer
36	c2fhjD_	Alignment	not modelled	5.3	26	PDB header: transferase Chain: D: PDB Molecule: formylmethanofuran--tetrahydromethanopterin PDBTitle: crystal structure of formylmethanofuran:2 tetrahydromethanopterin formyltransferase in complex with3 its coenzymes
37	c2d3yA_	Alignment	not modelled	5.0	38	PDB header: hydrolase Chain: A: PDB Molecule: uracil-dna glycosylase; PDBTitle: crystal structure of uracil-dna glycosylase from thermus thermophilus2 hb8