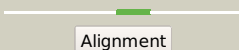

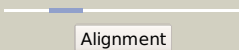

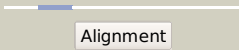

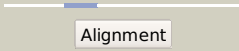

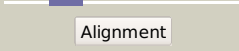



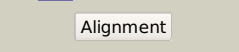

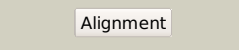

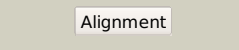



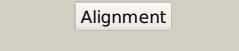
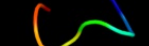


Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A2A559
Date	Wed Jul 10 14:28:33 BST 2013
Unique Job ID	fbeaf2f952f8c7db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2voyG_	 Alignment		55.3	24	PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
2	d1dx5i1	 Alignment		29.5	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
3	c2l2rA_	 Alignment		21.7	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide ecamp1; PDBTitle: helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (echinochloa crus-galli)
4	d1nyra1	 Alignment		21.2	22	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
5	d1ulka1	 Alignment		18.8	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
6	d1ulka2	 Alignment		16.7	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
7	d1m4ua_	 Alignment		14.9	18	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Noggin
8	d1uhaa1	 Alignment		12.9	40	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
9	c2qrxA_	 Alignment		12.4	17	PDB header: dna binding protein Chain: A: PDB Molecule: gm27569p; PDBTitle: crystal structure of drosophila melanogaster translin2 protein
10	d1z1za1	 Alignment		11.3	9	Fold: Phage tail protein-like Superfamily: Phage tail protein-like Family: Lambda phage gpU-like
11	c1rqrA_	 Alignment		10.5	22	PDB header: transferase Chain: A: PDB Molecule: 5'-fluoro-5'-deoxyadenosine synthase; PDBTitle: crystal structure and mechanism of a bacterial fluorinating enzyme,2 product complex

12	c1wu8B_	Alignment		10.4	56	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ph0463; PDBTitle: crystal structure of project ph0463 from pyrococcus horikoshii ot3
13	c2zbcC_	Alignment		10.4	56	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from thermotoga2 maritima
14	d1rqpa2	Alignment		10.1	22	Fold: Bacterial fluorinating enzyme, N-terminal domain Superfamily: Bacterial fluorinating enzyme, N-terminal domain Family: Bacterial fluorinating enzyme, N-terminal domain
15	c2q6oB_	Alignment		10.1	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: hypothetical protein; PDBTitle: sall-y70t with sam and cl
16	c3pjaK_	Alignment		9.2	35	PDB header: hydrolase Chain: K: PDB Molecule: translin-associated protein x; PDBTitle: crystal structure of human c3po complex
17	c3cjhK_	Alignment		8.8	15	PDB header: protein transport Chain: K: PDB Molecule: mitochondrial import inner membrane translocase subunit PDBTitle: tim8-tim13 complex
18	c4dg7D_	Alignment		8.8	17	PDB header: dna binding protein Chain: D: PDB Molecule: gm27569p; PDBTitle: low resolution structure of drosophila translin
19	c3nctC_	Alignment		8.6	45	PDB header: dna binding protein, chaperone Chain: C: PDB Molecule: protein psib; PDBTitle: x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
20	c2wewA_	Alignment		8.5	33	PDB header: lipid transport Chain: A: PDB Molecule: apolipoprotein m; PDBTitle: crystal structure of human apom in complex with myristic2 acid
21	d2axtz1	Alignment	not modelled	8.2	17	Fold: Transmembrane helix hairpin Superfamily: PsbZ-like Family: PsbZ-like
22	d1wila_	Alignment	not modelled	8.2	44	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: variant PHD-like domain
23	d1myla_	Alignment	not modelled	8.0	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
24	d1x5wa1	Alignment	not modelled	7.2	43	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
25	c4j4vD_	Alignment	not modelled	7.1	25	PDB header: viral protein Chain: D: PDB Molecule: nucleocapsid protein; PDBTitle: pentameric sftsvn with su
26	d1xb4a1	Alignment	not modelled	7.1	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
27	c2l4uA_	Alignment	not modelled	7.0	40	PDB header: signaling protein Chain: A: PDB Molecule: 24mer peptide from protein ste5; PDBTitle: solution structure of ste5pm24 in the presence of sds micelle
28	d1en2a2	Alignment	not modelled	6.9	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Plant lectins/antimicrobial peptides Family: Hevein-like agglutinin (lectin) domain
29	c4k7cA_	Alignment	not modelled	6.8	12	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase c;

29	c3k7cA	Alignment	not modelled	6.8	42	PDBTitle: crystal structure of pepw from lactobacillus rhamnosis hn001 (dr20)2 determined as the selenomet derivative PDB header: signaling protein Chain: A; PDB Molecule: protein ste5; PDBTitle: solution structure of ste5pm24 in the zwitterionic dpc2 micelle
30	c2kgnA	Alignment	not modelled	6.7	38	PDB header: signaling protein Chain: A; PDB Molecule: protein ste5; PDBTitle: solution structure of ste5pm24 in the zwitterionic dpc2 micelle
31	c2kgmA	Alignment	not modelled	6.5	38	PDB header: signaling protein Chain: A; PDB Molecule: protein ste5; PDBTitle: solution structure of ste5pm24 in sds micelle
32	d1bdta	Alignment	not modelled	6.5	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
33	d1b28a	Alignment	not modelled	6.5	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
34	d1mylb	Alignment	not modelled	6.4	56	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
35	c1yo4A	Alignment	not modelled	6.3	18	PDB header: viral protein Chain: A; PDB Molecule: hypothetical protein x4; PDBTitle: solution structure of the sars coronavirus orf 7a coded x42 protein
36	c2cw5B	Alignment	not modelled	5.9	22	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: bacterial fluorinating enzyme homolog; PDBTitle: crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8
37	c1mp6A	Alignment	not modelled	5.7	33	PDB header: membrane protein Chain: A; PDB Molecule: matrix protein m2; PDBTitle: structure of the transmembrane region of the m2 protein h+2 channel by solid state nmr spectroscopy
38	c2kqtD	Alignment	not modelled	5.7	33	PDB header: transport protein Chain: D; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
39	c1nyjD	Alignment	not modelled	5.7	33	PDB header: viral protein Chain: D; PDB Molecule: matrix protein m2; PDBTitle: the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
40	c2kqtA	Alignment	not modelled	5.7	33	PDB header: transport protein Chain: A; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
41	c2kqtB	Alignment	not modelled	5.7	33	PDB header: transport protein Chain: B; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
42	c1nyjA	Alignment	not modelled	5.7	33	PDB header: viral protein Chain: A; PDB Molecule: matrix protein m2; PDBTitle: the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
43	c1nyjB	Alignment	not modelled	5.7	33	PDB header: viral protein Chain: B; PDB Molecule: matrix protein m2; PDBTitle: the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
44	c1nyjC	Alignment	not modelled	5.7	33	PDB header: viral protein Chain: C; PDB Molecule: matrix protein m2; PDBTitle: the closed state structure of m2 protein h+ channel by2 solid state nmr spectroscopy
45	c2kqtC	Alignment	not modelled	5.7	33	PDB header: transport protein Chain: C; PDB Molecule: m2 protein; PDBTitle: solid-state nmr structure of the m2 transmembrane peptide of the2 influenza a virus in dmpc lipid bilayers bound to deuterated3 amantadine
46	d1m2vb2	Alignment	not modelled	5.6	30	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: beta-sandwich domain of Sec23/24 Family: beta-sandwich domain of Sec23/24
47	c3axjB	Alignment	not modelled	5.5	30	PDB header: dna binding protein Chain: B; PDB Molecule: translin associated factor x, isoform b; PDBTitle: high resolution crystal structure of c3po
48	c2plxB	Alignment	not modelled	5.4	44	PDB header: hydrolase Chain: B; PDB Molecule: peptide inhibitor; PDBTitle: trypsin complexed to a synthetic peptide from veronica hederifolia
49	d1crba	Alignment	not modelled	5.4	22	Fold: Lipocalins Superfamily: Lipocalins Family: Fatty acid binding protein-like
50	d1j1ja	Alignment	not modelled	5.4	26	Fold: alpha-alpha superhelix Superfamily: Translin Family: Translin
51	d1v54b2	Alignment	not modelled	5.4	17	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
52	c3c9jD	Alignment	not modelled	5.3	25	PDB header: membrane protein Chain: D; PDB Molecule: proton channel protein m2, transmembrane segment; PDBTitle: the crystal structure of transmembrane domain of m2 protein and2 amantadine complex
53	d2q49a2	Alignment	not modelled	5.3	15	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
54	d1djta	Alignment	not modelled	5.3	44	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like

						Family: Long-chain scorpion toxins
55	c2rnnA_	Alignment	not modelled	5.2	15	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase siz1; PDBTitle: solution structure of the n-terminal sap domain of sumo e3 ligases2 from saccharomyces cerevisiae
56	d1ahoa_	Alignment	not modelled	5.2	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Long-chain scorpion toxins
57	c2i5oA_	Alignment	not modelled	5.2	50	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta