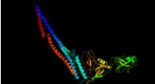
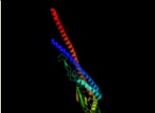
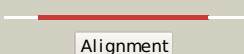
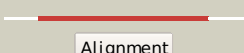
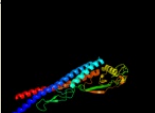
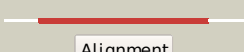
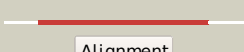
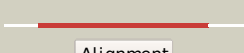
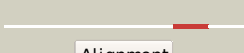
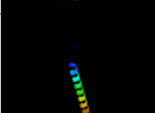
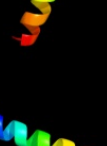
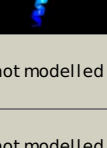


Phyre2

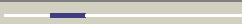
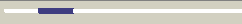
Email	I.a.kelley@imperial.ac.uk
Description	P04949
Date	Thu Jan 5 10:58:25 GMT 2012
Unique Job ID	71527a9564a91be7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlucua_	 Alignment		100.0	45	Fold: Phase 1 flagellin Superfamily: Phase 1 flagellin Family: Phase 1 flagellin
2	c3k8vB_	 Alignment		100.0	39	PDB header: structural protein Chain: B: PDB Molecule: flagellin homolog; PDBTitle: cysatl structure of a bacterial cell-surface flagellin n20c20
3	dllo1a_	 Alignment		100.0	37	Fold: Phase 1 flagellin Superfamily: Phase 1 flagellin Family: Phase 1 flagellin
4	c3k8wA_	 Alignment		100.0	36	PDB header: structural protein Chain: A: PDB Molecule: flagellin homolog; PDBTitle: cysatl structure of a bacterial cell-surface flagellin n20c45
5	c2zbiB_	 Alignment		100.0	33	PDB header: structural protein Chain: B: PDB Molecule: flagellin homolog; PDBTitle: cysatl structure of a bacterial cell-surface flagellin
6	c2d4xA_	 Alignment		100.0	17	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 3; PDBTitle: crystal structure of a 26k fragment of hap3 (flgI)
7	c3pwxB_	 Alignment		100.0	18	PDB header: structural protein Chain: B: PDB Molecule: putative flagellar hook-associated protein; PDBTitle: structure of putative flagellar hook-associated protein from vibrio2 parahaemolyticus
8	cloryB_	 Alignment		99.4	45	PDB header: chaperone Chain: B: PDB Molecule: flagellin; PDBTitle: flagellar export chaperone in complex with its cognate binding partner
9	c3a69A_	 Alignment		90.7	22	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook protein flge; PDBTitle: atomic model of the bacterial flagellar hook based on2 docking an x-ray derived structure and terminal two alpha-3 helices into an 7.1 angstrom resolution cryoem map
10	c3k1hA_	 Alignment		64.5	19	PDB header: chaperone Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of hp1076 from h.pylori
11	c3hfeC_	 Alignment		29.8	30	PDB header: transport protein Chain: C: PDB Molecule: potassium voltage-gated channel subfamily kqt member 1; PDBTitle: a trimeric form of the kv7.1 a domain tail

12	d1dt9a3	Alignment		29.1	16	Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
13	c3bj4B_	Alignment		28.1	24	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt PDBTitle: the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
14	d256ba_	Alignment		21.5	13	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome b562
15	c3c6vB_	Alignment		17.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: probable tautomerase/dehalogenase au4130; PDBTitle: crystal structure of au4130/apc7354, a probable enzyme from the2 thermophilic fungus aspergillus fumigatus
16	d2jdig1	Alignment		16.4	19	Fold: Pyruvate kinase C-terminal domain-like Superfamily: ATP synthase (F1-ATPase), gamma subunit Family: ATP synthase (F1-ATPase), gamma subunit
17	c3r47J_	Alignment		15.1	25	PDB header: de novo protein Chain: J: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
18	c3r47I_	Alignment		15.1	25	PDB header: de novo protein Chain: I: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
19	c3r47B_	Alignment		15.1	25	PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
20	c2w6jG_	Alignment		14.3	19	PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
21	c3r47F_	Alignment	not modelled	14.1	25	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
22	c3r47C_	Alignment	not modelled	14.1	25	PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
23	c3r47L_	Alignment	not modelled	14.1	25	PDB header: de novo protein Chain: L: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
24	c3r47M_	Alignment	not modelled	14.1	25	PDB header: de novo protein Chain: M: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
25	c3r47H_	Alignment	not modelled	13.5	25	PDB header: de novo protein Chain: H: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
26	c3r47K_	Alignment	not modelled	13.5	25	PDB header: de novo protein Chain: K: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
27	c3r48F_	Alignment	not modelled	13.5	25	PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix w22-I24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
28	c3r47A_	Alignment	not modelled	13.4	25	PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix I24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
29	c3r47E_	Alignment	not modelled	13.4	25	PDB header: de novo protein Chain: E: PDB Molecule: coiled coil helix I24h;

					PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
30	c3r47G_	Alignment	not modelled	13.4	25 PDB header: de novo protein Chain: G: PDB Molecule: coiled coil helix l24h; PDBTitle: crystal structure of a 6-helix coiled coil cc-hex-h24
31	c3r46G_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: G: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
32	c3r46B_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: B: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
33	c3r46A_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
34	c3r46E_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: E: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
35	c3r46F_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: F: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
36	c3r46C_	Alignment	not modelled	13.3	25 PDB header: de novo protein Chain: C: PDB Molecule: coiled coil helix l24d; PDBTitle: crystal structure of a parallel 6-helix coiled coil cc-hex-d24
37	c3at7B_	Alignment	not modelled	13.1	17 PDB header: structural protein Chain: B: PDB Molecule: alginate-binding flagellin; PDBTitle: crystal structure of bacterial cell-surface alginate-binding protein2 algp7
38	c2oszA_	Alignment	not modelled	12.8	15 PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
39	c3r48A_	Alignment	not modelled	12.7	25 PDB header: de novo protein Chain: A: PDB Molecule: coiled coil helix w22-l24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
40	c3r48G_	Alignment	not modelled	12.7	25 PDB header: de novo protein Chain: G: PDB Molecule: coiled coil helix w22-l24h; PDBTitle: crystal structure of a hetero-hexamer coiled coil
41	c3r3kC_	Alignment	not modelled	12.7	25 PDB header: de novo protein Chain: C: PDB Molecule: cchex-phi22 helix; PDBTitle: crystal structure of a parallel 6-helix coiled coil
42	c3r3kB_	Alignment	not modelled	12.7	25 PDB header: de novo protein Chain: B: PDB Molecule: cchex-phi22 helix; PDBTitle: crystal structure of a parallel 6-helix coiled coil
43	c3r3kA_	Alignment	not modelled	12.7	25 PDB header: de novo protein Chain: A: PDB Molecule: cchex-phi22 helix; PDBTitle: crystal structure of a parallel 6-helix coiled coil
44	c3fksY_	Alignment	not modelled	11.6	19 PDB header: hydrolase Chain: Y: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: yeast f1 atpase in the absence of bound nucleotides
45	c2xokG_	Alignment	not modelled	10.4	19 PDB header: hydrolase Chain: G: PDB Molecule: atp synthase subunit gamma, mitochondrial; PDBTitle: refined structure of yeast f1c10 atpase complex to 3 a2 resolution
46	c2flzC_	Alignment	not modelled	9.3	8 PDB header: hydrolase Chain: C: PDB Molecule: cis-3-chloroacrylic acid dehalogenase; PDBTitle: the x-ray structure of cis-3-chloroacrylic acid dehalogenase (cis-2 caad) with a sulfate ion bound in the active site
47	c3e20C_	Alignment	not modelled	9.1	16 PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
48	d2g0ua1	Alignment	not modelled	8.4	16 Fold: Long alpha-hairpin Superfamily: MxiH-like Family: MxiH-like
49	c3fyqA_	Alignment	not modelled	8.2	14 PDB header: cell adhesion Chain: A: PDB Molecule: cg6831-pa (talin); PDBTitle: structure of drosophila melanogaster talin ibs2 domain2 (residues 1981-2168)
50	c1junB_	Alignment	not modelled	7.9	19 PDB header: transcription regulation Chain: B: PDB Molecule: c-jun homodimer; PDBTitle: nmr study of c-jun homodimer
51	c3oaaO_	Alignment	not modelled	6.8	17 PDB header: hydrolase/transport protein Chain: O: PDB Molecule: atp synthase gamma chain; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
52	d1vcsa1	Alignment	not modelled	6.6	16 Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
53	d2g3qa1	Alignment	not modelled	6.5	14 Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
54	c3d5cX_	Alignment	not modelled	6.0	10 PDB header: ribosome Chain: X: PDB Molecule: peptide chain release factor 1; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.

55	c2d4yA_	 Alignment	not modelled	6.0	22	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
56	c2k6sB_	 Alignment	not modelled	5.8	21	PDB header: protein transport Chain: B: PDB Molecule: rab11fip2 protein; PDBTitle: structure of rab11-fip2 c-terminal coiled-coil domain
57	c3ls1A_	 Alignment	not modelled	5.7	12	PDB header: photosynthesis Chain: A: PDB Molecule: slt1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
58	dlsgga_	 Alignment	not modelled	5.6	14	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
59	dlhkxa_	 Alignment	not modelled	5.5	16	Fold: Cystatin-like Superfamily: NTF2-like Family: Association domain of calcium/calmodulin-dependent protein kinase type II alpha subunit, CAMK2A
60	c3pzdB_	 Alignment	not modelled	5.4	13	PDB header: motor protein/apoptosis Chain: B: PDB Molecule: netrin receptor dcc; PDBTitle: structure of the myosin x myth4-ferm/dcc complex
61	c2v8sV_	 Alignment	not modelled	5.3	8	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
62	dlb0xa_	 Alignment	not modelled	5.0	8	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain