








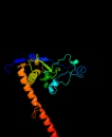













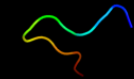

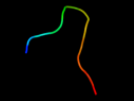

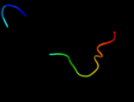
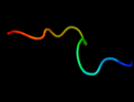

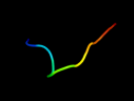



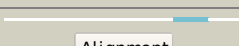

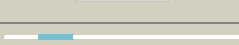
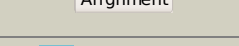
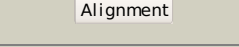
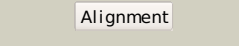
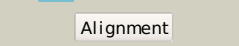
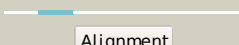

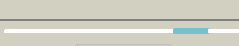
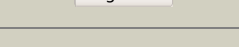
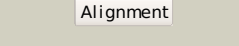
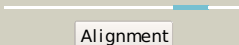
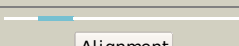
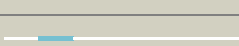
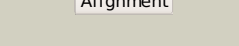

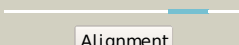

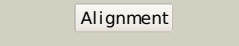
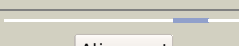
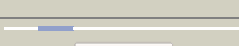
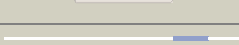
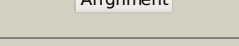
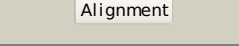
Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P05719
Date	Thu Jan 5 10:58:51 GMT 2012
Unique Job ID	2f2288fafa37e2b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2y7cA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: type-1 restriction enzyme ecoki specificity protein; PDBTitle: atomic model of the ocr-bound methylase complex from the2 type i restriction-modification enzyme ecoki (m2s1). based3 on fitting into em map 1534.
2	c1yf2A_	 Alignment		100.0	15	PDB header: hydrolase regulator Chain: A: PDB Molecule: type i restriction-modification enzyme, s subunit; PDBTitle: three-dimensional structure of dna sequence specificity (s) subunit of2 a type i restriction-modification enzyme and its functional3 implications
3	c3okgB_	 Alignment		100.0	20	PDB header: dna binding protein Chain: B: PDB Molecule: restriction endonuclease s subunits; PDBTitle: crystal structure of hds subunit from thermoanaerobacter2 tengcongensis
4	c1ydxA_	 Alignment		100.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: type i restriction enzyme specificity protein mg438; PDBTitle: crystal structure of type-i restriction-modification system s subunit2 from m. genitalium
5	d1yf2a2	 Alignment		99.9	22	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
6	d1yf2a1	 Alignment		99.9	21	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
7	d1ydx2	 Alignment		99.9	14	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
8	d1ydx1	 Alignment		99.8	18	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: Type I restriction modification DNA specificity domain
9	c1aqjB_	 Alignment		96.8	9	PDB header: methyltransferase Chain: B: PDB Molecule: adenine-n6-dna-methyltransferase taqi; PDBTitle: structure of adenine-n6-dna-methyltransferase taqi
10	c1g38A_	 Alignment		96.5	9	PDB header: transferase/dna Chain: A: PDB Molecule: modification methylase taqi; PDBTitle: adenine-specific methyltransferase m. taq i/dna complex
11	c3s1sA_	 Alignment		91.4	14	PDB header: hydrolase, transferase Chain: A: PDB Molecule: restriction endonuclease bpusi; PDBTitle: characterization and crystal structure of the type iig restriction2 endonuclease bpusi

12	d2ih2a2	Alignment		78.3	10	Fold: DNA methylase specificity domain Superfamily: DNA methylase specificity domain Family: TaqI C-terminal domain-like
13	c1yiuA	Alignment		61.7	38	PDB header: ligase Chain: A: PDB Molecule: itchy e3 ubiquitin protein ligase; PDBTitle: itch e3 ubiquitin ligase ww3 domain
14	c2kykA	Alignment		58.0	38	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: the sandwich region between two Imp2a py motif regulates the2 interaction between aip4ww2domain and py motif
15	c2djyA	Alignment		51.1	46	PDB header: ligase/signaling protein Chain: A: PDB Molecule: smad ubiquitination regulatory factor 2; PDBTitle: solution structure of smurf2 ww3 domain-smad7 py peptide2 complex
16	c2jmfA	Alignment		49.5	46	PDB header: ligase/signaling protein Chain: A: PDB Molecule: e3 ubiquitin-protein ligase suppressor of deltex; PDBTitle: solution structure of the su(dx) ww4- notch py peptide2 complex
17	c2yscA	Alignment		48.8	43	PDB header: protein binding Chain: A: PDB Molecule: amyloid beta a4 precursor protein-binding family PDBTitle: solution structure of the ww domain from the human amyloid2 beta a4 precursor protein-binding family b member 3, apbb3
18	d1tk7a2	Alignment		46.7	46	Fold: WW domain-like Superfamily: WW domain Family: WW domain
19	c2lawA	Alignment		43.4	55	PDB header: signaling protein/transcription Chain: A: PDB Molecule: yorkie homolog; PDBTitle: structure of the second ww domain from human yap in complex with a2 human smad1 derived peptide
20	d2jmfa1	Alignment		42.4	55	Fold: WW domain-like Superfamily: WW domain Family: WW domain
21	d1tk7a1	Alignment	not modelled	39.9	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
22	c2dmvA	Alignment	not modelled	39.3	31	PDB header: ligase Chain: A: PDB Molecule: itchy homolog e3 ubiquitin protein ligase; PDBTitle: solution structure of the second ww domain of itchy homolog2 e3 ubiquitin protein ligase (itch)
23	c2yshA	Alignment	not modelled	39.0	31	PDB header: protein binding Chain: A: PDB Molecule: growth-arrest-specific protein 7; PDBTitle: solution structure of the ww domain from the human growth-2 arrest-specific protein 7, gas-7
24	c2lb0A	Alignment	not modelled	38.2	40	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a di-2 phosphorylated human smad1 derived peptide
25	c2lazA	Alignment	not modelled	38.2	40	PDB header: signaling protein/transcription Chain: A: PDB Molecule: e3 ubiquitin-protein ligase smurf1; PDBTitle: structure of the first ww domain of human smurf1 in complex with a2 mono-phosphorylated human smad1 derived peptide
26	d1seda	Alignment	not modelled	36.0	20	Fold: Hypothetical protein Yhal Superfamily: Hypothetical protein Yhal Family: Hypothetical protein Yhal
27	d1gxha	Alignment	not modelled	35.9	35	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
28	d2vlqa1	Alignment	not modelled	35.3	26	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins

29	c1pqvS_		Alignment	not modelled	35.2	20	PDB header: transferase/transcription Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis complex
30	dlayia_		Alignment	not modelled	34.3	30	Fold: Acyl carrier protein-like Superfamily: Colicin E immunity proteins Family: Colicin E immunity proteins
31	c1wmvA_		Alignment	not modelled	34.1	43	PDB header: oxidoreductase, apoptosis Chain: A: PDB Molecule: ww domain containing oxidoreductase; PDBTitle: solution structure of the second ww domain of wwox
32	c2ysgA_		Alignment	not modelled	33.9	38	PDB header: protein binding Chain: A: PDB Molecule: syntaxin-binding protein 4; PDBTitle: solution structure of the ww domain from the human syntaxin-2 binding protein 4
33	c1wr7A_		Alignment	not modelled	33.7	29	PDB header: ligase Chain: A: PDB Molecule: nedd4-2; PDBTitle: solution structure of the third ww domain of nedd4-2
34	d1pina1		Alignment	not modelled	33.6	56	Fold: WW domain-like Superfamily: WW domain Family: WW domain
35	c2dwvB_		Alignment	not modelled	32.9	29	PDB header: protein binding Chain: B: PDB Molecule: salvador homolog 1 protein; PDBTitle: solution structure of the second ww domain from mouse2 salvador homolog 1 protein (mww45)
36	c3l4hA_		Alignment	not modelled	32.9	38	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw1; PDBTitle: helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
37	c2l4jA_		Alignment	not modelled	32.9	70	PDB header: transcription Chain: A: PDB Molecule: yes-associated protein 2 (yap2); PDBTitle: yap ww2
38	c1y1yS_		Alignment	not modelled	32.5	20	PDB header: transferase/transcription/dna-rna hybrid Chain: S: PDB Molecule: transcription elongation factor s-ii; PDBTitle: rna polymerase ii-tfiis-dna/rna complex
39	c3m9hB_		Alignment	not modelled	32.2	24	PDB header: chaperone Chain: B: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
40	c2no8A_		Alignment	not modelled	32.1	35	PDB header: immune system Chain: A: PDB Molecule: colicin-e2 immunity protein; PDBTitle: nmr structure analysis of the colicin immunity protein im2
41	d1i5hw_		Alignment	not modelled	30.9	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
42	c2ysfA_		Alignment	not modelled	30.7	38	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase itchy homolog; PDBTitle: solution structure of the fourth ww domain from the human2 e3 ubiquitin-protein ligase itchy homolog, itch
43	d2p0ta1		Alignment	not modelled	30.7	16	Fold: PSPTO4464-like Superfamily: PSPTO4464-like Family: PSPTO4464-like
44	c2p0tA_		Alignment	not modelled	30.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0307 protein pspto_4464; PDBTitle: structural genomics, the crystal structure of a conserved putative2 protein from pseudomonas syringae pv. tomato str. dc3000
45	c2ysdA_		Alignment	not modelled	30.0	50	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the first ww domain from the human2 membrane-associated guanylate kinase, ww and pdz domain-3 containing protein 1. magi-1
46	c3bc1F_		Alignment	not modelled	29.9	17	PDB header: signaling protein/transport protein Chain: F: PDB Molecule: synaptotagmin-like protein 2; PDBTitle: crystal structure of the complex rab27a-slp2a
47	d1i8gb_		Alignment	not modelled	29.2	56	Fold: WW domain-like Superfamily: WW domain Family: WW domain
48	c3p8cE_		Alignment	not modelled	28.6	16	PDB header: protein binding Chain: E: PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex
49	d2crua1		Alignment	not modelled	25.9	16	Fold: RuvA C-terminal domain-like Superfamily: Double-stranded DNA-binding domain Family: Double-stranded DNA-binding domain
50	c1yw5A_		Alignment	not modelled	23.9	38	PDB header: isomerase Chain: A: PDB Molecule: peptidyl prolyl cis/trans isomerase; PDBTitle: peptidyl-prolyl isomerase ess1 from candida albicans
51	c2dmeA_		Alignment	not modelled	23.4	23	PDB header: metal binding protein Chain: A: PDB Molecule: phd finger protein 3; PDBTitle: solution structure of the tfiis domain ii of human phd2 finger protein 3
52	c2gl2B_		Alignment	not modelled	22.9	17	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
53	c3le4A_		Alignment	not modelled	22.3	44	PDB header: nuclear protein Chain: A: PDB Molecule: microprocessor complex subunit dgcr8; PDBTitle: crystal structure of the dgcr8 dimerization domain
54	c1k7A_		Alignment	not modelled	21.8	38	PDB header: signaling protein Chain: A: PDB Molecule: cg4244-pb;

54	c1k7A	Alignment	not modelled	21.8	38	PDBTitle: nmr structure of ww domains (ww3-4) from suppressor of2 deltex
55	c1e0mA	Alignment	not modelled	21.7	44	PDB header: de novo protein Chain: A: PDB Molecule: wwprototype; PDBTitle: prototype ww domain
56	c1ymzA	Alignment	not modelled	21.4	40	PDB header: unknown function Chain: A: PDB Molecule: cc45; PDBTitle: cc45, an artificial ww domain designed using statistical2 coupling analysis
57	d2f21a1	Alignment	not modelled	20.6	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
58	d2itka1	Alignment	not modelled	20.5	63	Fold: WW domain-like Superfamily: WW domain Family: WW domain
59	c2ysbA	Alignment	not modelled	20.4	36	PDB header: protein binding Chain: A: PDB Molecule: salvador homolog 1 protein; PDBTitle: solution structure of the first ww domain from the mouse2 salvador homolog 1 protein (sav1)
60	d1k9ra	Alignment	not modelled	20.1	38	Fold: WW domain-like Superfamily: WW domain Family: WW domain
61	c2zajA	Alignment	not modelled	19.6	40	PDB header: protein binding Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz PDBTitle: solution structure of the short-isoform of the second ww2 domain from the human membrane-associated guanylate kinase,3 ww and pdz domain-containing protein 1 (magi-1)
62	c1wr4A	Alignment	not modelled	18.5	44	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-protein ligase nedd4-2; PDBTitle: solution structure of the second ww domain of nedd4-2
63	c2kq0A	Alignment	not modelled	18.4	44	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: human nedd4 3rd ww domain complex with ebola zaire virus matrix2 protein vp40 derived peptide ilptappeyme
64	d3dlqi1	Alignment	not modelled	18.0	27	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
65	c2jv4A	Alignment	not modelled	18.0	38	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis/trans isomerase; PDBTitle: structure characterisation of pina ww domain and comparison2 with other group iv ww domains, pin1 and ess1
66	c2ez5W	Alignment	not modelled	17.6	23	PDB header: signalling protein,ligase Chain: W: PDB Molecule: e3 ubiquitin-protein ligase nedd4; PDBTitle: solution structure of the dnedd4 ww3* domain- comm lpsy2 peptide complex
67	d1ig4a	Alignment	not modelled	17.2	17	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: Methyl-CpG-binding domain, MBD
68	d2ho2a1	Alignment	not modelled	17.0	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain
69	d1f8ab1	Alignment	not modelled	16.8	36	Fold: WW domain-like Superfamily: WW domain Family: WW domain
70	c3olmA	Alignment	not modelled	15.6	63	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase rsp5; PDBTitle: structure and function of a ubiquitin binding site within the2 catalytic domain of a hect ubiquitin ligase
71	d1dd5a	Alignment	not modelled	14.8	17	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
72	c2gleA	Alignment	not modelled	14.0	7	PDB header: protein binding Chain: A: PDB Molecule: neurabin-1; PDBTitle: solution structure of neurabin sam domain
73	c1bm4A	Alignment	not modelled	14.0	41	PDB header: viral protein Chain: A: PDB Molecule: protein (moloney murine leukemia virus capsid); PDBTitle: momlv capsid protein major homology region peptide analog
74	c2fh0A	Alignment	not modelled	14.0	13	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 16.0 kda protein in abf2-chl12 PDBTitle: nmr ensemble of the yeast saccharomyces cerevisiae protein2 ymr074cp core region
75	d1ek8a	Alignment	not modelled	13.3	20	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
76	d2ysca1	Alignment	not modelled	13.1	44	Fold: WW domain-like Superfamily: WW domain Family: WW domain
77	c3uorB	Alignment	not modelled	12.6	18	PDB header: sugar binding protein Chain: B: PDB Molecule: abc transporter sugar binding protein; PDBTitle: the structure of the sugar-binding protein male from the phytopathogen2 xanthomonas citri
78	c3kxEd	Alignment	not modelled	12.1	13	PDB header: protein binding Chain: D: PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
79	d1wqga1	Alignment	not modelled	12.0	19	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
						PDB header: chaperone

80	c3cqxD_	Alignment	not modelled	12.0	30	Chain: D: PDB Molecule: bag family molecular chaperone regulator 2; PDBTitle: chaperone complex
81	d1nmva1	Alignment	not modelled	11.6	46	Fold: WW domain-like Superfamily: WW domain Family: WW domain
82	d1zkea1	Alignment	not modelled	11.4	12	Fold: ROP-like Superfamily: HP1531-like Family: HP1531-like
83	d1ge9a_	Alignment	not modelled	11.3	29	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
84	c2ky8A_	Alignment	not modelled	11.3	19	PDB header: transcription/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 2; PDBTitle: solution structure and dynamic analysis of chicken mbd2 methyl binding2 domain bound to a target methylated dna sequence
85	c2ysiA_	Alignment	not modelled	11.2	23	PDB header: protein binding Chain: A: PDB Molecule: transcription elongation regulator 1; PDBTitle: solution structure of the first ww domain from the mouse2 transcription elongation regulator 1, transcription factor3 ca150
86	c2ejxA_	Alignment	not modelled	10.8	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: st0812; PDBTitle: crystal structure of the hypothetical protein st0812 from2 sulfobus tokodaii
87	d1eh1a_	Alignment	not modelled	10.8	14	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
88	c1f8aB_	Alignment	not modelled	10.6	42	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima- PDBTitle: structural basis for the phosphoserine-proline recognition2 by group iv ww domains
89	d1is1a_	Alignment	not modelled	10.4	17	Fold: RRF/tRNA synthetase additional domain-like Superfamily: Ribosome recycling factor, RRF Family: Ribosome recycling factor, RRF
90	d2gsva1	Alignment	not modelled	10.0	21	Fold: Open three-helical up-and-down bundle Superfamily: YvfG-like Family: YvfG-like
91	c1lypA_	Alignment	not modelled	9.4	17	PDB header: lipopolysaccharide-binding protein Chain: A: PDB Molecule: cap18; PDBTitle: the solution structure of the active domain of cap18: a2 lipopolysaccharide binding protein from rabbit leukocytes
92	d2clyb1	Alignment	not modelled	9.3	12	Fold: ATP synthase D chain-like Superfamily: ATP synthase D chain-like Family: ATP synthase D chain-like
93	c3npfB_	Alignment	not modelled	9.2	13	PDB header: hydrolase Chain: B: PDB Molecule: putative dipeptidyl-peptidase vi; PDBTitle: crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
94	d2evra2	Alignment	not modelled	9.2	13	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: NlpC/P60
95	d2nrka1	Alignment	not modelled	9.2	11	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: GrpB-like
96	c3qufB_	Alignment	not modelled	9.0	17	PDB header: transport protein Chain: B: PDB Molecule: extracellular solute-binding protein, family 1; PDBTitle: the structure of a family 1 extracellular solute-binding protein from2 bifidobacterium longum subsp. infantis
97	c2oarA_	Alignment	not modelled	8.9	16	PDB header: membrane protein Chain: A: PDB Molecule: large-conductance mechanosensitive channel; PDBTitle: mechanosensitive channel of large conductance (mscl)
98	c3pmdA_	Alignment	not modelled	8.9	29	PDB header: lipid binding protein Chain: A: PDB Molecule: conserved domain protein; PDBTitle: crystal structure of the sporulation inhibitor pxo1-118 from bacillus2 anthracis
99	c2xzmW_	Alignment	not modelled	8.7	14	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s4; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1