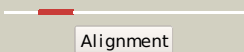

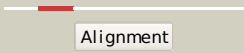







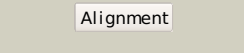

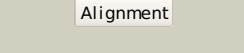

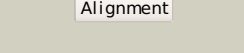



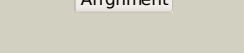
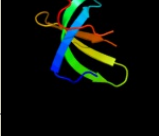
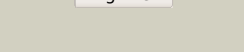

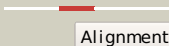

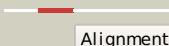


















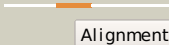
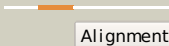
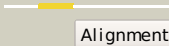
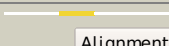



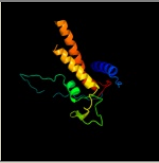
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q01804
Date	Wed Jun 6 09:57:10 BST 2012
Unique Job ID	a723a9e39fe1c18d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c0rC_	 Alignment		100.0	24	PDB header: cell cycle, hydrolase Chain: C: PDB Molecule: ubiquitin thioesterase otu1; PDBTitle: structure of ovarian tumor (otu) domain in complex with ubiquitin
2	c3pfyA_	 Alignment		100.0	32	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 5; PDBTitle: the catalytic domain of human otud5
3	c3pt2A_	 Alignment		99.9	20	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: rna polymerase; PDBTitle: structure of a viral otu domain protease bound to ubiquitin
4	c3phuA_	 Alignment		99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: rna-directed rna polymerase I; PDBTitle: otu domain of crimean congo hemorrhagic fever virus
5	c2zfyA_	 Alignment		99.4	33	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase otub1; PDBTitle: crystal structure of human otubain 1
6	c4dhjL_	 Alignment		99.4	24	PDB header: hydrolase/signaling protein/ligase Chain: L: PDB Molecule: ubiquitin thioesterase otubain-like; PDBTitle: the structure of a ceotub1 ubiquitin aldehyde ubc13~ub complex
7	d1tffa_	 Alignment		99.3	21	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Ubiquitin thioesterase protein OTUB2 (Otubain-2)
8	c4a4fA_	 Alignment		97.2	29	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with 2 symmetrically dimethylated arginine
9	d2d9ta1	 Alignment		97.1	28	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
10	d1mhna_	 Alignment		96.9	26	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
11	c2d9tA_	 Alignment		96.8	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tudor domain-containing protein 3; PDBTitle: solution structure of the tudor domain of tudor domain2 containing protein 3 from mouse

12	c3pnwX_	 Alignment		96.4	27	PDB header: protein binding/immune system Chain: X: PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
13	c3dkbA_	 Alignment		96.4	16	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor, alpha-induced protein 3; PDBTitle: crystal structure of a20, 2.5 angstrom
14	c1g5vA_	 Alignment		96.1	25	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
15	c2vfjA_	 Alignment		95.4	13	PDB header: hydrolase Chain: A: PDB Molecule: tumor necrosis factor; PDBTitle: structure of the a20 ovarian tumour (otu) domain
16	d2diqa1	 Alignment		94.5	21	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
17	c2hqxB_	 Alignment		93.7	13	PDB header: transcription Chain: B: PDB Molecule: p100 co-activator tudor domain; PDBTitle: crystal structure of human p100 tudor domain conserved2 region
18	d2hqxa1	 Alignment		93.7	13	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
19	c2eqkA_	 Alignment		92.1	13	PDB header: transcription Chain: A: PDB Molecule: tudor domain-containing protein 4; PDBTitle: solution structure of the tudor domain of tudor domain-2 containing protein 4
20	c2wacA_	 Alignment		92.0	24	PDB header: splicing Chain: A: PDB Molecule: cg7008-pa; PDBTitle: extended tudor domain of drosophila melanogaster tudor-sn (2 p100)
21	c3qiiA_	 Alignment	not modelled	91.6	19	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
22	c3p8dB_	 Alignment	not modelled	91.4	19	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
23	c2equA_	 Alignment	not modelled	90.0	22	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
24	c3bdlA_	 Alignment	not modelled	85.8	15	PDB header: hydrolase Chain: A: PDB Molecule: staphylococcal nuclease domain-containing PDBTitle: crystal structure of a truncated human tudor-sn
25	c3zrhA_	 Alignment	not modelled	85.5	21	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin thioesterase zranb1; PDBTitle: crystal structure of the lys29, lys33-linkage-specific trabd1 otu2 deubiquitinase domain reveals an ankyrin-repeat ubiquitin binding3 domain (ankubd)
26	d2i8da1	 Alignment	not modelled	74.4	22	Fold: Secretion chaperone-like Superfamily: YdhG-like Family: YdhG-like
27	c1xni_	 Alignment	not modelled	70.0	18	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
28	d1ccda_	 Alignment	not modelled	69.6	20	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like

29	c1puoA	Alignment	not modelled	67.9	17	PDB header: allergen Chain: A: PDB Molecule: major allergen i polypeptide, fused chain 2, PDBTitle: crystal structure of fel d 1- the major cat allergen
30	c3nthA	Alignment	not modelled	65.2	13	PDB header: transcription Chain: A: PDB Molecule: maternal protein tudor; PDBTitle: crystal structure of tudor and aubergine [r13(me2s)] complex
31	c3db3A	Alignment	not modelled	63.6	14	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase uhfr1; PDBTitle: crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhfr1 in complex with trimethylated histone h3-k93 peptide
32	d1utra	Alignment	not modelled	59.7	20	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
33	d1wn7a2	Alignment		57.7	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
34	c2jvvA	Alignment	not modelled	57.2	23	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of e. coli nusg carboxyterminal domain
35	c2kvqG	Alignment	not modelled	57.2	23	PDB header: transcription Chain: G: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of nuse:nusg-ctd complex
36	d1utga	Alignment	not modelled	55.6	13	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
37	c3q1jA	Alignment	not modelled	54.0	28	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 1 of human phd finger protein 20
38	d1nppa2	Alignment	not modelled	53.5	21	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
39	d2guka1	Alignment	not modelled	53.0	18	Fold: PG1857-like Superfamily: PG1857-like Family: PG1857-like
40	c2o4xA	Alignment	not modelled	52.9	15	PDB header: hydrolase Chain: A: PDB Molecule: staphylococcal nuclease domain-containing PDBTitle: crystal structure of human p100 tudor domain
41	d1nz9a	Alignment	not modelled	51.7	23	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
42	d1poia	Alignment	not modelled	51.1	20	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: CoA transferase alpha subunit-like
43	c2zfuA	Alignment	not modelled	49.9	16	PDB header: nuclear protein Chain: A: PDB Molecule: cerebral protein 1; PDBTitle: structure of the methyltransferase-like domain of nucleomethilin
44	d1vhka1	Alignment	not modelled	49.8	17	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
45	c2xzmL	Alignment	not modelled	47.7	38	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s12; 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
46	c1ssfA	Alignment	not modelled	44.0	16	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
47	c2zmeB	Alignment	not modelled	42.9	23	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 36; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
48	d1nxza1	Alignment	not modelled	42.3	14	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
49	d2oc6a1	Alignment	not modelled	41.7	19	Fold: Secretion chaperone-like Superfamily: YdhG-like Family: YdhG-like
50	c3askC	Alignment	not modelled	41.2	14	PDB header: ligase/dna binding protein Chain: C: PDB Molecule: e3 ubiquitin-protein ligase uhfr1; PDBTitle: structure of uhfr1 in complex with histone tail
51	c2kl4A	Alignment	not modelled	40.8	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2032 protein; PDBTitle: nmr structure of the protein nb7804a
52	d2f5ka1	Alignment	not modelled	40.1	14	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
53	c2egwB	Alignment	not modelled	35.3	17	PDB header: rna methyltransferase Chain: B: PDB Molecule: upf0088 protein aq_165; PDBTitle: crystal structure of rna methyltransferase with sah

						ligand
54	c3nafA	Alignment	not modelled	34.8	12	PDB header: ion transport Chain: A: PDB Molecule: calcium-activated potassium channel subunit alpha-1; PDBTitle: structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
55	d2g7sa2	Alignment	not modelled	34.3	14	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
56	c3kopB	Alignment	not modelled	33.1	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with a cyclophilin-like fold2 (yp_831253.1) from arthrobacter sp. fb24 at 1.90 a resolution
57	c2db0B	Alignment	not modelled	33.0	12	PDB header: protein binding Chain: B: PDB Molecule: 253aa long hypothetical protein; PDBTitle: crystal structure of ph0542
58	d2cp6a1	Alignment	not modelled	33.0	23	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
59	c2ro0A	Alignment	not modelled	32.1	21	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
60	c1zv4X	Alignment	not modelled	31.9	9	PDB header: signaling protein Chain: X: PDB Molecule: regulator of g-protein signaling 17; PDBTitle: structure of the regulator of g-protein signaling 17 (rgsz2)
61	c2zkql	Alignment	not modelled	31.6	41	PDB header: ribosomal protein/rna Chain: L: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
62	d1wgsa	Alignment	not modelled	31.4	21	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
63	c2ec3A	Alignment	not modelled	31.0	20	PDB header: cell adhesion Chain: A: PDB Molecule: fibronectin; PDBTitle: solution structure of the 11th fn1 domain from human2 fibronectin 1
64	c2eqmA	Alignment	not modelled	30.9	28	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
65	d1v38a	Alignment	not modelled	29.4	29	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
66	c2py8B	Alignment	not modelled	28.5	13	PDB header: chaperone Chain: B: PDB Molecule: hypothetical protein rbcx; PDBTitle: rbcx
67	d3bl2a1	Alignment	not modelled	27.9	31	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
68	c3m1rF	Alignment	not modelled	27.6	21	PDB header: hydrolase Chain: F: PDB Molecule: formimidoyl glutamase; PDBTitle: the crystal structure of formimidoyl glutamase from bacillus2 subtilis subsp. subtilis str. 168
69	c3s63B	Alignment	not modelled	27.1	29	PDB header: lipid binding protein Chain: B: PDB Molecule: saposin-like protein; PDBTitle: saposin-like protein na-slp-1
70	c1m1gB	Alignment	not modelled	26.2	20	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of aquifex aeolicus n-utilization2 substance g (nusg), space group p2(1)
71	c1ofsC	Alignment	not modelled	25.7	19	PDB header: lectin Chain: C: PDB Molecule: pea lectin alpha chain; PDBTitle: pea lectin-sucrose complex
72	c2penE	Alignment	not modelled	25.3	21	PDB header: chaperone Chain: E: PDB Molecule: orf134; PDBTitle: crystal structure of rbcx, crystal form i
73	d2ejna1	Alignment	not modelled	25.3	16	Fold: Uteroglobin-like Superfamily: Uteroglobin-like Family: Uteroglobin-like
74	c1w7pD	Alignment	not modelled	25.0	20	PDB header: protein transport Chain: D: PDB Molecule: vps36p, ylr417w; PDBTitle: the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
75	c2ekoA	Alignment	not modelled	25.0	17	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: solution structure of ruh-073, a pseudo chromo domain from2 human cdna
76	c1ngmM	Alignment	not modelled	24.1	28	PDB header: transcription/dna Chain: M: PDB Molecule: transcription initiation factor tfiid; PDBTitle: crystal structure of a yeast brf1-tbp-dna ternary complex
77	c1rm1A	Alignment	not modelled	24.1	28	PDB header: transcription/dna Chain: A: PDB Molecule: tata-box binding protein; PDBTitle: structure of a yeast tfiia/tbp/tata-box dna complex
78	d2pbla1	Alignment	not modelled	23.9	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
79	c3iuwA	Alignment	not modelled	23.9	16	PDB header: rna binding protein Chain: A: PDB Molecule: activating signal cointegrator; PDBTitle: crystal structure of activating signal cointegrator

						(np_814290.1) from2 enterococcus faecalis v583 at 1.58 a resolution
80	d2do3a1	Alignment	not modelled	23.8	8	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
81	c1s1hL_	Alignment	not modelled	23.5	38	PDB header: ribosome Chain: L: PDB Molecule: 40s ribosomal protein s23; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
82	c3fwcN_	Alignment	not modelled	22.0	18	PDB header: cell cycle, transcription Chain: N: PDB Molecule: nuclear mrna export protein sac3; PDBTitle: sac3:sus1:cdc31 complex
83	c2lbaA_	Alignment	not modelled	21.5	9	PDB header: lipid binding protein Chain: A: PDB Molecule: babp protein; PDBTitle: solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
84	d2peqa1	Alignment	not modelled	21.2	21	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
85	d1nh2a2	Alignment	not modelled	20.7	23	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
86	d1w98b1	Alignment	not modelled	20.6	10	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
87	d1i94l_	Alignment	not modelled	20.5	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
88	c3pzlA_	Alignment	not modelled	20.2	18	PDB header: hydrolase Chain: A: PDB Molecule: agmatine ureohydrolase; PDBTitle: the crystal structure of agmatine ureohydrolase of thermoplasma2 volcanium
89	c3labA_	Alignment	not modelled	20.1	18	PDB header: PDB COMPND:
90	c3kw2A_	Alignment	not modelled	19.9	24	PDB header: transferase Chain: A: PDB Molecule: probable r-rna methyltransferase; PDBTitle: crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
91	d1svma_	Alignment	not modelled	19.4	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	d2py8a1	Alignment	not modelled	19.2	11	Fold: RbcX-like Superfamily: RbcX-like Family: RbcX-like
93	d1vg5a_	Alignment	not modelled	18.6	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
94	c3lhIA_	Alignment	not modelled	18.4	24	PDB header: hydrolase Chain: A: PDB Molecule: putative agmatinase; PDBTitle: crystal structure of a putative agmatinase from clostridium difficile
95	c1qu2A_	Alignment	not modelled	18.3	22	PDB header: ligase/rna Chain: A: PDB Molecule: isoleucyl-trna synthetase; PDBTitle: insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
96	c2eamA_	Alignment	not modelled	17.9	33	PDB header: signaling protein Chain: A: PDB Molecule: putative 47 kda protein; PDBTitle: solution structure of the n-terminal sam-domain of a human2 putative 47 kda protein
97	d1tgoa2	Alignment	not modelled	17.7	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: DNA polymerase I
98	c3df0C_	Alignment	not modelled	17.6	24	PDB header: hydrolase Chain: C: PDB Molecule: calpastatin; PDBTitle: calcium-dependent complex between m-calpain and calpastatin
99	d1cdwa2	Alignment	not modelled	17.6	24	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain