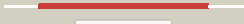



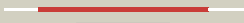











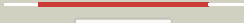

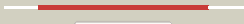







Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	A0PJN4
Date	Wed Jul 10 14:10:37 BST 2013
Unique Job ID	4ba07b4170187a46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1zuoa1	 Alignment		100.0	53	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
2	c1zuoa	 Alignment		100.0	53	PDB header: ligase Chain: A: PDB Molecule: hypothetical protein loc92912; PDBTitle: structure of human ubiquitin-conjugating enzyme (ubci) involved in2 embryo attachment and implantation
3	c4ddiB	 Alignment		100.0	21	PDB header: hydrolase/ligase Chain: B: PDB Molecule: ubiquitin-conjugating enzyme e2 d2, ubiquitin thioesterase PDBTitle: crystal structure of human otub1/ubch5b~ub/ub
4	c3e46A	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2-25 kda; PDBTitle: crystal structure of ubiquitin-conjugating enzyme e2-25kda2 (huntington interacting protein 2) m172a mutant
5	c1ylaB	 Alignment		100.0	22	PDB header: ligase Chain: B: PDB Molecule: ubiquitin-conjugating enzyme e2-25 kda; PDBTitle: ubiquitin-conjugating enzyme e2-25 kda (huntington interacting protein2 2)
6	c1tteA	 Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2-24 kda; PDBTitle: the structure of a class ii ubiquitin-conjugating enzyme,2 ubc1.
7	d2aaka	 Alignment		100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
8	d2uyza1	 Alignment		100.0	16	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
9	c2y9mA	 Alignment		100.0	15	PDB header: ligase/transport protein Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2-21 kda; PDBTitle: pex4p-pex22p structure
10	d1j7db	 Alignment		100.0	23	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
11	d1y6la	 Alignment		100.0	20	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
12	c4gprA	 Alignment		100.0	20	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme family protein; PDBTitle: crystal structure of ehucb5, a ubiquitin conjugating

				enzyme from2 entamoeba histolytica	
13	c3bzhA_	Alignment		100.0	21 PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 e1; PDBTitle: crystal structure of human ubiquitin-conjugating enzyme e2 e1
14	d1ayza_	Alignment		100.0	21 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
15	d1yrva1	Alignment		100.0	15 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
16	d1i7ka_	Alignment		100.0	23 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
17	c3cegA_	Alignment		100.0	16 PDB header: ligase Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 6; PDBTitle: crystal structure of the ubc domain of baculoviral iap repeat-2 containing protein 6
18	d1qcqa_	Alignment		100.0	22 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
19	c2ekeB_	Alignment		100.0	14 PDB header: ligase/protein binding Chain: B: PDB Molecule: sumo-conjugating enzyme ubc9; PDBTitle: structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
20	c1i7kB_	Alignment		100.0	23 PDB header: ligase Chain: B: PDB Molecule: ubiquitin-conjugating enzyme e2 h10; PDBTitle: crystal structure of human mitotic-specific ubiquitin-2 conjugating enzyme, ubch10
21	d1zdna1	Alignment	not modelled	100.0	19 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
22	c2pwqA_	Alignment	not modelled	100.0	23 PDB header: ligase Chain: A: PDB Molecule: ubiquitin conjugating enzyme; PDBTitle: crystal structure of a putative ubiquitin conjugating2 enzyme from plasmodium yoelii
23	c2onuA_	Alignment	not modelled	100.0	17 PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme, putative; PDBTitle: plasmodium falciparum ubiquitin conjugating enzyme pf10_0330, putative2 homologue of human ube2h
24	c2h2yA_	Alignment	not modelled	100.0	18 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquitin-conjugating enzyme; PDBTitle: crystal structure of ubiquitin conjugating enzyme e2 from2 plasmodium falciparum
25	d1pzva_	Alignment	not modelled	100.0	22 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
26	d2e2ca_	Alignment	not modelled	100.0	23 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
27	d2f4za1	Alignment	not modelled	100.0	20 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
28	d2nvuc1	Alignment	not modelled	100.0	11 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
29	d2eska1	Alignment	not modelled	100.0	22 Fold: UBC-like Superfamily: UBC-like Family: UBC-related
30	d1yh2a1	Alignment	not modelled	100.0	17 Fold: UBC-like Superfamily: UBC-like Family: UBC-related

31	d1wzva1	Alignment	not modelled	100.0	16	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
32	d1z3da1	Alignment	not modelled	100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
33	d2ayva1	Alignment	not modelled	100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
34	c3e95A	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: ubiquitin carrier protein; PDBTitle: crystal structure of the plasmodium falciparum ubiquitin2 conjugating enzyme complex, pfubc13-pfuev1a
35	c3fshA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 g2; PDBTitle: crystal structure of the ubiquitin conjugating enzyme2 ube2g2 bound to the g2br domain of ubiquitin ligase gp78
36	d1jata	Alignment	not modelled	100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
37	d1jasa	Alignment	not modelled	100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
38	d2bepa1	Alignment	not modelled	100.0	22	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
39	d1jatb	Alignment	not modelled	100.0	18	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
40	d2ucza	Alignment	not modelled	100.0	23	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
41	d1fzva	Alignment	not modelled	100.0	17	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
42	d1z2ua1	Alignment	not modelled	100.0	22	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
43	c3rczB	Alignment	not modelled	100.0	18	PDB header: protein binding/ligase Chain: B: PDB Molecule: sumo-conjugating enzyme ubc9; PDBTitle: rad60 sld2 ubc9 complex
44	c2f4zB	Alignment	not modelled	100.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: tgtwinscan_2721 - e2 domain; PDBTitle: toxoplasma gondii ubiquitin conjugating enzyme tgtwinscan_2721- e22 domain
45	c2ediA	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: nedd8-conjugating enzyme ube2f; PDBTitle: solution structure of the uq_con domain from human nedd8-2 conjugating enzyme nce2
46	d2fo3a1	Alignment	not modelled	100.0	21	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
47	d1c4zd	Alignment	not modelled	100.0	17	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
48	d2awfa1	Alignment	not modelled	100.0	23	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
49	c2f4wA	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2, j2; PDBTitle: human ubiquitin-conjugating enzyme e2 j2
50	d2f4wa1	Alignment	not modelled	100.0	17	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
51	c3o2uB	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: nedd8-conjugating enzyme ubc12; PDBTitle: s. cerevisiae ubc12
52	d1j74a	Alignment	not modelled	100.0	12	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
53	c2hlwA	Alignment	not modelled	100.0	16	PDB header: ligase, signaling protein Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 variant 1; PDBTitle: solution structure of the human ubiquitin-conjugating2 enzyme variant uev1a
54	c2ob4A	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2-32 kda complementing; PDBTitle: human ubiquitin-conjugating enzyme cdc34
55	c2q0vA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2, putative; PDBTitle: crystal structure of ubiquitin conjugating enzyme e2, putative, from2 plasmodium falciparum
56	d2a4da1	Alignment	not modelled	100.0	13	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
57	c2z5dA	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-conjugating enzyme e2 h; PDBTitle: human ubiquitin-conjugating enzyme e2 h
						Fold: UBC-like

58	d1yf9a1	Alignment	not modelled	100.0	13	Superfamily: UBC-like Family: UBC-related
59	d2a7la1	Alignment	not modelled	100.0	23	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
60	d1y8xa1	Alignment	not modelled	100.0	11	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
61	d1yh6a1	Alignment	not modelled	100.0	12	Fold: UBC-like Superfamily: UBC-like Family: UBC-related
62	c4ds2B_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: ubiquitin-conjugating enzyme e2, putative; PDBTitle: ubiquitin conjugating enzyme (putative) from trypanosoma cruzi
63	d1s1qa_	Alignment	not modelled	99.5	16	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
64	c3kpaB_	Alignment	not modelled	96.8	19	PDB header: ligase Chain: B: PDB Molecule: probable ubiquitin fold modifier conjugating enzyme; PDBTitle: ubiquitin fold modifier conjugating enzyme from leishmania major2 (probable)
65	d2in1a1	Alignment	not modelled	96.4	16	Fold: UBC-like Superfamily: UBC-like Family: UFC1-like
66	d1uzxa_	Alignment	not modelled	96.4	21	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
67	d2daya1	Alignment	not modelled	95.5	19	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
68	c2ebmA_	Alignment	not modelled	94.6	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rwd domain-containing protein 1; PDBTitle: solution structure of the rwd domain of human rwd domain2 containing protein 1
69	c2yz0A_	Alignment	not modelled	91.4	15	PDB header: transferase Chain: A: PDB Molecule: serine/threonine-protein kinase gcn2; PDBTitle: solution structure of rwd/gi domain of saccharomyces2 cerevisiae gcn2
70	c3zqsB_	Alignment	not modelled	91.3	21	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase fanc1; PDBTitle: human fanc1 central domain
71	d2dawa1	Alignment	not modelled	89.6	19	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
72	d1ukxa_	Alignment	not modelled	89.5	13	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
73	d2daxa1	Alignment	not modelled	87.5	27	Fold: UBC-like Superfamily: UBC-like Family: RWD domain
74	c2ebkA_	Alignment	not modelled	79.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: rwd domain-containing protein 3; PDBTitle: solution structure of the rwd domain of human rwd domain2 containing protein 3
75	c4ilvB_	Alignment	not modelled	37.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: intradiol ring-cleavage dioxygenase; PDBTitle: structure of the dioxygenase domain of sacte_2871, a novel dioxygenase2 carbohydrate-binding protein fusion from the cellulolytic bacterium3 streptomyces sp. sirexaa-e
76	c4gzvH_	Alignment	not modelled	33.0	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a hypothetical protein (bacova_00364) from2 bacteroides ovatus atcc 8483 at 1.95 a resolution
77	c3csgA_	Alignment	not modelled	24.3	14	PDB header: de novo protein, sugar binding protein Chain: A: PDB Molecule: maltose-binding protein monobody ys1 fusion; PDBTitle: crystal structure of monobody ys1(mbp-74)/maltose binding2 protein fusion complex
78	c3ca8B_	Alignment	not modelled	22.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydcf; PDBTitle: crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
79	d2pgda1	Alignment	not modelled	12.9	8	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
80	d2ezha_	Alignment	not modelled	11.3	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
81	c2p4qA_	Alignment	not modelled	10.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
82	c3uo9B_	Alignment	not modelled	9.6	13	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
83	d1f53a_	Alignment	not modelled	9.3	30	Fold: gamma-Crystallin-like Superfamily: gamma-Crystallin-like

						Family: Killer toxin-like protein SKLP
84	c2iz1C_	Alignment	not modelled	9.1	12	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
85	c3fwnB_	Alignment	not modelled	8.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
86	c1pgqA_	Alignment	not modelled	8.4	8	PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
87	c4g7xB_	Alignment	not modelled	8.4	3	PDB header: protein binding/protein binding Chain: B: PDB Molecule: tola protein; PDBTitle: crystal structure of a complex between the ctxphi piii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
88	d2ezia_	Alignment	not modelled	7.6	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
89	c1hxvA_	Alignment	not modelled	7.4	29	PDB header: chaperone Chain: A: PDB Molecule: trigger factor; PDBTitle: ppiase domain of the mycoplasma genitalium trigger factor
90	d1hxva_	Alignment	not modelled	7.4	29	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
91	d1z0kb1	Alignment	not modelled	7.3	6	Fold: Long alpha-hairpin Superfamily: Rabenosyn-5 Rab-binding domain-like Family: Rabenosyn-5 Rab-binding domain-like
92	c2jtmA_	Alignment	not modelled	6.6	21	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of sso6901 from sulfolobus solfataricus2 p2
93	c3kxtA_	Alignment	not modelled	6.5	21	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromatin protein cren7; PDBTitle: crystal structure of sulfolobus cren7-dsdna complex
94	c3k1A_	Alignment	not modelled	6.4	11	PDB header: ligase Chain: A: PDB Molecule: fancI; PDBTitle: crystal structure of fancI
95	d1dmha_	Alignment	not modelled	6.4	22	Fold: Prealbumin-like Superfamily: Aromatic compound dioxygenase Family: Aromatic compound dioxygenase
96	c2azqA_	Alignment	not modelled	6.2	9	PDB header: oxidoreductase Chain: A: PDB Molecule: catechol 1,2-dioxygenase; PDBTitle: crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
97	c3n9tA_	Alignment	not modelled	5.7	26	PDB header: oxidoreductase Chain: A: PDB Molecule: pnpC; PDBTitle: cryatal structure of hydroxyquinol 1,2-dioxygenase from pseudomonas2 putida dll-e4
98	c1tmxA_	Alignment	not modelled	5.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyquinol 1,2-dioxygenase; PDBTitle: crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e