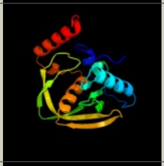
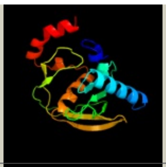
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6K3
Date	Thu Jan 5 11:03:20 GMT 2012
Unique Job ID	7083b07b6dc5bc13

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w3tA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** chloro complex of the ni-form of e.coli deformylase
2	d1ix1a_	Alignment		100.0	56	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
3	d1xeoa1	Alignment		100.0	100	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
4	c3qu1B_	Alignment		100.0	51	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**peptide deformylase 2; **PDBTitle:** peptide deformylase from vibrio cholerae
5	c3ocaB_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of peptide deformylase from ehrlichia chaffeensis
6	c2ew7A_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of helicobacter pylori peptide deformylase
7	c3cpmA_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase, chloroplast; **PDBTitle:** plant peptide deformylase pdf1b crystal structure
8	d1y6ha_	Alignment		100.0	35	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
9	d1jyma_	Alignment		100.0	33	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
10	c1ws1A_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase 1; **PDBTitle:** structure analysis of peptide deformylase from bacillus2 cereus
11	c3e3uA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor

12	d1rl4a_	Alignment		100.0	37	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
13	c3g5pB_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase, mitochondrial; **PDBTitle:** structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
14	d2defa_	Alignment		100.0	100	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
15	d1lmea_	Alignment		100.0	39	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
16	d1v3ya_	Alignment		100.0	33	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
17	c3dldA_	Alignment		100.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of peptide deformylase, xoo1075, from2 xanthomonas oryzae pv. oryzae kacc10331
18	d1lqya_	Alignment		100.0	30	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
19	c3g6nA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** crystal structure of an efpdf complex with met-ala-ser
20	c1zy1B_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptide deformylase, mitochondrial; **PDBTitle:** x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser
21	d1lm4a_	Alignment	not modelled	100.0	29	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
22	d1lm6a_	Alignment	not modelled	100.0	28	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
23	c3l87A_	Alignment	not modelled	100.0	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** the crystal structure of smu.143c from streptococcus mutans ua159
24	d1wmha_	Alignment	not modelled	38.5	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
25	c2kvzA_	Alignment	not modelled	37.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ispe; **PDBTitle:** structure of residues 161-235 of putative peptidoglycan binding2 protein lmo0835 from listeria monocytogenes: target lmr64b of the3 northeast structural genomics consortium
26	d1pqsa_	Alignment	not modelled	34.5	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
27	d1q1oa_	Alignment	not modelled	31.8	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
28	d1quaa_	Alignment	not modelled	30.7	38	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
						Fold:beta-Grasp (ubiquitin-like)

29	d1ip9a_	Alignment	not modelled	26.9	26	**Superfamily:**CAD & PB1 domains **Family:**PB1 domain
30	d1nd1a_	Alignment	not modelled	25.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
31	d1wnia_	Alignment	not modelled	25.8	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
32	d2bkfa1	Alignment	not modelled	25.2	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
33	c1yp1A_	Alignment	not modelled	25.1	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fii; **PDBTitle:** crystal structure of a non-hemorrhagic fibrin(ogen)olytic2 metalloproteinase from venom of agkistrodon acutus
34	d1bswa_	Alignment	not modelled	25.0	50	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
35	d1r55a_	Alignment	not modelled	24.1	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
36	d4aiga_	Alignment	not modelled	23.7	40	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
37	c3c37B_	Alignment	not modelled	21.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase, m48 family; **PDBTitle:** x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
38	d1atla_	Alignment	not modelled	21.4	31	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
39	c3k7nA_	Alignment	not modelled	21.2	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**k-like; **PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
40	c2kt7A_	Alignment	not modelled	20.5	28	**PDB header:**cell adhesion, membrane protein **Chain:** A: **PDB Molecule:**putative peptidoglycan bound protein (lpxtg **PDBTitle:** solution nmr structure of mucin-binding domain of protein2 lmo0835 from listeria monocytogenes, northeast structural3 genomics consortium target lmr64a
41	d1kufa_	Alignment	not modelled	20.5	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Reprolysin-like
42	c3k7lA_	Alignment	not modelled	19.5	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atragin; **PDBTitle:** structures of two elapid snake venom metalloproteases with2 distinct activities highlight the disulfide patterns in the3 d domain of adamalysin family proteins
43	c2dw1B_	Alignment	not modelled	14.3	40	**PDB header:**apoptosis, toxin **Chain:** B: **PDB Molecule:**catrocollastatin; **PDBTitle:** crystal structure of vap2 from crotalus atrox venom (form 2-2 crystal)
44	c3bmbB_	Alignment	not modelled	14.2	15	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
45	c2erpA_	Alignment	not modelled	13.8	53	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vascular apoptosis-inducing protein 1; **PDBTitle:** crystal structure of vascular apoptosis-inducing protein-1(inhibitor-2 bound form)
46	d1c7ka_	Alignment	not modelled	12.9	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Zinc protease
47	c2e3xA_	Alignment	not modelled	12.7	33	**PDB header:**hydrolase, blood clotting, toxin **Chain:** A: **PDB Molecule:**coagulation factor x-activating enzyme heavy chain; **PDBTitle:** crystal structure of russell's viper venom metalloproteinase
48	c3b8zB_	Alignment	not modelled	12.7	46	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein adamts-5; **PDBTitle:** high resolution crystal structure of the catalytic domain2 of adamts-5 (aggrecanase-2)
49	c1z5sD_	Alignment	not modelled	12.6	33	**PDB header:**ligase **Chain:** D: **PDB Molecule:**ran-binding protein 2; **PDBTitle:** crystal structure of a complex between ubc9, sumo-1,2 rangap1 and nup358/ranbp2
50	d1ydla1	Alignment	not modelled	12.4	24	**Fold:**TFB5-like **Superfamily:**TFB5-like **Family:**TFB5-like
51	d1wj6a_	Alignment	not modelled	12.1	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
52	d1ytqa1	Alignment	not modelled	12.0	24	**Fold:**gamma-Crystallin-like **Superfamily:**gamma-Crystallin-like **Family:**Crystallins/Ca-binding development proteins
53	d1cxva_	Alignment	not modelled	11.9	43	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain

54	d1a8ya3	Alignment	not modelled	11.3	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
55	c2jz7A_	Alignment	not modelled	11.1	22	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
56	c2rjpC_	Alignment	not modelled	10.5	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adamts-4; **PDBTitle:** crystal structure of adamts4 with inhibitor bound
57	c3g5cA_	Alignment	not modelled	10.0	25	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**adam 22; **PDBTitle:** structural and biochemical studies on the ectodomain of human adam22
58	d1xuca1	Alignment	not modelled	9.6	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
59	d1v8ca2	Alignment	not modelled	9.3	54	**Fold:**TBP-like **Superfamily:**MoaD-related protein, C-terminal domain **Family:**MoaD-related protein, C-terminal domain
60	d1qiba_	Alignment	not modelled	9.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
61	c1zv8B_	Alignment	not modelled	9.0	56	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**e2 glycoprotein; **PDBTitle:** a structure-based mechanism of sars virus membrane fusion
62	d1hv5a_	Alignment	not modelled	9.0	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
63	d1i76a_	Alignment	not modelled	8.9	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
64	d1rr8c1	Alignment	not modelled	8.7	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
65	d1hova_	Alignment	not modelled	8.5	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
66	d1hy7a_	Alignment	not modelled	8.4	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
67	c2i47A_	Alignment	not modelled	8.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adam 17; **PDBTitle:** crystal structure of catalytic domain of tace with inhibitor
68	c2xs4A_	Alignment	not modelled	8.1	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
69	c2h7fX_	Alignment	not modelled	8.0	17	**PDB header:**isomerase/dna **Chain:** X: **PDB Molecule:**dna topoisomerase 1; **PDBTitle:** structure of variola topoisomerase covalently bound to dna
70	c3nppA_	Alignment	not modelled	7.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pfam duf1093 family protein; **PDBTitle:** crystal structure of a pfam duf1093 family protein (bsu39620) from2 bacillus subtilis at 2.15 a resolution
71	d2k5wa1	Alignment	not modelled	7.9	22	**Fold:**OB-fold **Superfamily:**BC4932-like **Family:**BC4932-like
72	d1cb8a2	Alignment	not modelled	7.6	17	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
73	c2wd6B_	Alignment	not modelled	7.4	29	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**agglutinin receptor; **PDBTitle:** crystal structure of the variable domain of the2 streptococcus gordonii surface protein sspb
74	d1fbla2	Alignment	not modelled	7.4	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
75	d1rm8a_	Alignment	not modelled	7.3	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
76	c2ktrA_	Alignment	not modelled	7.2	13	**PDB header:**signaling protein, transport protein **Chain:** A: **PDB Molecule:**sequestosome-1; **PDBTitle:** nmr structure of p62 pb1 dimer determined based on pcs
77	d2i47a1	Alignment	not modelled	7.1	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**TNF-alpha converting enzyme, TACE, catalytic domain
78	d1y6kr2	Alignment	not modelled	6.9	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
79	d1k4ta2	Alignment	not modelled	6.8	17	**Fold:**DNA breaking-rejoining enzymes **Superfamily:**DNA breaking-rejoining enzymes **Family:**Eukaryotic DNA topoisomerase I, catalytic core
80	d2fkia1	Alignment	not modelled	6.7	25	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like
						PDB header:hydrolase

81	c2x7mA_	Alignment	not modelled	6.4	29	**Chain:** A: **PDB Molecule:**archaemetzincin; **PDBTitle:** crystal structure of archaemetzincin (amza) from methanopyrus2 kandleri at 1.5 a resolution
82	d1jmma_	Alignment	not modelled	6.3	38	**Fold:**Supersandwich **Superfamily:**V-region of surface antigen I/II (SA I/II, PAC) **Family:**V-region of surface antigen I/II (SA I/II, PAC)
83	c3uinD_	Alignment	not modelled	6.1	33	**PDB header:**ligase/isomerase/protein binding **Chain:** D: **PDB Molecule:**e3 sumo-protein ligase ranbp2; **PDBTitle:** complex between human rangap1-sumo2, ubc9 and the ir1 domain from2 ranbp2
84	d2axoa1	Alignment	not modelled	5.8	57	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
85	d2k5qa1	Alignment	not modelled	5.8	44	**Fold:**OB-fold **Superfamily:**BC4932-like **Family:**BC4932-like
86	d1bqqm_	Alignment	not modelled	5.7	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
87	d1y93a1	Alignment	not modelled	5.6	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
88	c2axoA_	Alignment	not modelled	5.5	57	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu2684; **PDBTitle:** x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
89	c1ytqA_	Alignment	not modelled	5.5	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**beta crystallin b2; **PDBTitle:** structure of native human beta b2 crystallin
90	d2ovxa1	Alignment	not modelled	5.4	27	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
91	d1mmqa_	Alignment	not modelled	5.4	36	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain