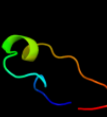


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4D3
Date	Sun Jul 8 11:45:11 BST 2012
Unique Job ID	76c9a5713729c915

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2d8va1	 Alignment		59.2	40	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
2	d1lv3a_	 Alignment		58.0	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Hypothetical zinc finger protein YacG
3	d1libia2	 Alignment		46.8	47	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
4	c3q8dB_	 Alignment		45.1	23	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein reco; PDBTitle: e. coli reco complex with ssb c-terminus
5	c1u5kA_	 Alignment		33.4	18	PDB header: recombination,replication Chain: A: PDB Molecule: hypothetical protein; PDBTitle: recombinational repair protein reco
6	d1u5ka2	 Alignment		26.2	18	Fold: ArfGap/RecO-like zinc finger Superfamily: ArfGap/RecO-like zinc finger Family: RecO C-terminal domain-like
7	c3o37D_	 Alignment		22.9	38	PDB header: transcription/protein binding Chain: D: PDB Molecule: transcription intermediary factor 1-alpha; PDBTitle: crystal structure of trim24 phd-bromo complexed with h3(1-10)k42 peptide
8	c1brvA_	 Alignment		21.7	50	PDB header: glycoprotein Chain: A: PDB Molecule: protein g; PDBTitle: solution nmr structure of the immunodominant region of 2 protein g of bovine respiratory syncytial virus, 483 structures
9	d2jw6a1	 Alignment		21.3	38	Fold: HIT/MYND zinc finger-like Superfamily: HIT/MYND zinc finger-like Family: MYND zinc finger
10	c2danA_	 Alignment		21.0	29	PDB header: metal binding protein Chain: A: PDB Molecule: zinc finger mynd domain containing protein 10; PDBTitle: the solution structure of the mynd domain (Ieu384-cys430)2 of human zinc finger mynd domain containing protein 10
11	c2yqqA_	 Alignment		20.5	30	PDB header: protein binding Chain: A: PDB Molecule: zinc finger hit domain-containing protein 3; PDBTitle: solution structure of the zf-hit domain in zinc finger hit2 domain-containing protein 3 (trip-3)

12	c2oddA	Alignment		18.2	45	PDB header: metal binding protein Chain: A: PDB Molecule: protein cbfa2t1; PDBTitle: solution structure of the mynd domain from aml1-eto2 complexed with smrt, a corepressor
13	c2jw6A	Alignment		18.2	38	PDB header: transcription Chain: A: PDB Molecule: deformed epidermal autoregulatory factor 1 homolog; PDBTitle: solution structure of the deaf1 mynd domain
14	c2dj8A	Alignment		16.6	50	PDB header: metal binding protein Chain: A: PDB Molecule: protein cbfa2t1; PDBTitle: solution structure of zf-mynd domain of protein cbfa2t12 (protein mtg8)
15	d2dana1	Alignment		16.0	40	Fold: HIT/MYND zinc finger-like Superfamily: HIT/MYND zinc finger-like Family: MYND zinc finger
16	c3lqiA	Alignment		14.3	17	PDB header: transferase Chain: A: PDB Molecule: ml11 phd3-bromo; PDBTitle: crystal structure of ml11 phd3-bromo complexed with h3(1-9)k4me22 peptide
17	c3qtlD	Alignment		13.6	50	PDB header: hydrolase/hydrolase inhibitor Chain: D: PDB Molecule: kazal-type serine protease inhibitor spi-1; PDBTitle: structural basis for dual-inhibition mechanism of a non-classical2 kazal-type serine protease inhibitor from horseshoe crab in complex3 with subtilisin
18	c2iybG	Alignment		13.1	45	PDB header: metal-binding Chain: G: PDB Molecule: testin; PDBTitle: structure of complex between the 3rd lim domain of tes and2 the evh1 domain of mena
19	d2dj8a1	Alignment		11.6	45	Fold: HIT/MYND zinc finger-like Superfamily: HIT/MYND zinc finger-like Family: MYND zinc finger
20	d2d8qa1	Alignment		11.6	40	Fold: HIT/MYND zinc finger-like Superfamily: HIT/MYND zinc finger-like Family: MYND zinc finger
21	d1hcqa	Alignment	not modelled	11.4	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
22	c2jxdA	Alignment	not modelled	10.8	56	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: serine protease inhibitor kazal-type 2; PDBTitle: nmr structure of human serine protease inhibitor kazal type2 ii (spink2)
23	c2kcxA	Alignment	not modelled	10.4	56	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: folistatin-related protein 3; PDBTitle: solution nmr structure of kazal-1 domain of human2 follistatin-related protein 3 (fstl-3). northeast3 structural genomics target hr6186a.
24	d2jz6a1	Alignment	not modelled	10.2	42	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
25	d1pcea	Alignment	not modelled	9.8	63	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
26	c1y1cA	Alignment	not modelled	9.5	56	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: elastase inhibitor; PDBTitle: solution structure of anemonia elastase inhibitor analogue
27	d2cona1	Alignment	not modelled	9.5	46	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
28	d1lr7a2	Alignment	not modelled	9.2	63	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like

29	d2nlla_	Alignment	not modelled	8.6	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
30	c1sgdl_	Alignment	not modelled	8.5	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: asp 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b at ph 6.5
31	c2sgdl_	Alignment	not modelled	8.5	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: asp 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b at ph 10.7
32	c3u5pF_	Alignment	not modelled	8.3	38	PDB header: transcription Chain: F: PDB Molecule: e3 ubiquitin-protein ligase trim33; PDBTitle: crystal structure of the complex of trim33 phd-bromo and h3(1-28)2 k9me3k14ack18ack23ac histone peptide
33	c2gb5B_	Alignment	not modelled	8.2	23	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
34	c2jl81_	Alignment	not modelled	7.9	17	PDB header: ribosome Chain: 1: PDB Molecule: 50s ribosomal protein l28; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
35	c3bboY_	Alignment	not modelled	7.9	17	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein l28; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
36	c2ybfB_	Alignment	not modelled	7.8	56	PDB header: ligase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rad18; PDBTitle: complex of rad18 (rad6 binding domain) with rad6b
37	c2k0aA_	Alignment	not modelled	7.8	22	PDB header: metal binding protein Chain: A: PDB Molecule: pre-mrna-splicing factor rds3; PDBTitle: 1h, 15n and 13c chemical shift assignments for rds3 protein
38	c2nu2l_	Alignment	not modelled	7.8	31	PDB header: hydrolase Chain: I: PDB Molecule: ovomucoid; PDBTitle: accommodation of positively-charged residues in a2 hydrophobic specificity pocket: crystal structures of sgpb3 in complex with omtky3 variants lys18i and arg18i
39	c2wg7B_	Alignment	not modelled	7.7	33	PDB header: hydrolase Chain: B: PDB Molecule: putative phospholipase a2; PDBTitle: structure of oryza sativa (rice) pla2
40	d2qamz1	Alignment	not modelled	7.7	33	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L28
41	c1sgpl_	Alignment	not modelled	7.6	31	PDB header: complex (serine protease/inhibitor) Chain: I: PDB Molecule: turkey ovomucoid inhibitor; PDBTitle: ala 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b
42	d1kmaa_	Alignment	not modelled	7.5	56	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
43	c1zr9A_	Alignment	not modelled	7.4	29	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 593; PDBTitle: solution structure of a human c2h2-type zinc finger protein
44	d1zr9a1	Alignment	not modelled	7.4	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
45	d2yt9a2	Alignment	not modelled	7.4	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
46	d1dx5i3	Alignment	not modelled	7.2	57	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
47	c2jmiA_	Alignment	not modelled	7.2	17	PDB header: protein binding Chain: A: PDB Molecule: protein yng1; PDBTitle: nmr solution structure of phd finger fragment of yeast yng12 protein in free state
48	c1m8cA_	Alignment	not modelled	7.2	25	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: ovomucoid; PDBTitle: solution structure of the t state of turkey ovomucoid at ph2 2.5
49	d2hepa1	Alignment	not modelled	7.2	40	Fold: Long alpha-hairpin Superfamily: YnC-like Family: YnC-like
50	c2hepA_	Alignment	not modelled	7.2	40	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0291 protein yncz; PDBTitle: solution nmr structure of the upf0291 protein yncz from2 bacillus subtilis. northeast structural genomics target3 sr384.
51	d2erwa1	Alignment	not modelled	7.1	50	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
52	c1sgnl_	Alignment	not modelled	7.1	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: asn 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b
53	c1imlA_	Alignment	not modelled	6.9	33	PDB header: metal-binding protein Chain: A: PDB Molecule: cysteine rich intestinal protein; PDBTitle: cysteine rich intestinal protein, nmr, 48 structures
54	d1hraa_	Alignment	not modelled	6.9	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain)

						Family: Nuclear receptor
55	d1p91a	Alignment	not modelled	6.9	27	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: rRNA methyltransferase RImA
56	d1b8ta4	Alignment	not modelled	6.9	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
57	c3n71A	Alignment	not modelled	6.7	24	PDB header: transcription Chain: A: PDB Molecule: histone lysine methyltransferase smyd1; PDBTitle: crystal structure of cardiac specific histone methyltransferase smyd1
58	c2sgel	Alignment	not modelled	6.6	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: glu 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b at ph 10.7
59	c1sgel	Alignment	not modelled	6.6	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: glu 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b at ph 6.5
60	c1tbqS	Alignment	not modelled	6.4	44	PDB header: complex (serine protease/inhibitor) Chain: S: PDB Molecule: rhodniin; PDBTitle: crystal structure of insect derived double domain kazal2 inhibitor rhodniin in complex with thrombin
61	d1jjda	Alignment	not modelled	6.4	50	Fold: Metallothionein Superfamily: Metallothionein Family: Metallothionein
62	d2dara1	Alignment	not modelled	6.3	57	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
63	d1dsza	Alignment	not modelled	6.2	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
64	d1y0pa1	Alignment	not modelled	6.2	42	Fold: Multiheme cytochromes Superfamily: Multiheme cytochromes Family: Di-heme elbow motif
65	c2a66A	Alignment	not modelled	6.0	43	PDB header: transcription/dna Chain: A: PDB Molecule: orphan nuclear receptor nr5a2; PDBTitle: human liver receptor homologue dna-binding domain (hlrh-12 dbd) in complex with dsdna from the hcyp7a1 promoter
66	c2kyuA	Alignment	not modelled	6.0	32	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase ml1; PDBTitle: the solution structure of the phd3 finger of ml1
67	d1cita	Alignment	not modelled	6.0	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
68	c3sgql	Alignment	not modelled	5.9	31	PDB header: hydrolase/hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: gln 18 variant of turkey ovomucoid inhibitor third domain2 complexed with streptomyces griseus proteinase b at ph 10.7
69	d1xx6a2	Alignment	not modelled	5.9	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
70	d1tbr1	Alignment	not modelled	5.8	56	Fold: Kazal-type serine protease inhibitors Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
71	d2hana1	Alignment	not modelled	5.8	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
72	d2b3aa1	Alignment	not modelled	5.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
73	c3cbbA	Alignment	not modelled	5.7	38	PDB header: transcription/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 4-alpha, dna binding PDBTitle: crystal structure of hepatocyte nuclear factor 4alpha in2 complex with dna: diabetes gene product
74	d1lo1a	Alignment	not modelled	5.6	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
75	c2gktl	Alignment	not modelled	5.4	31	PDB header: hydrolase inhibitor Chain: I: PDB Molecule: ovomucoid; PDBTitle: crystal structure of the p14'-ala32 variant of the n-2 terminally truncated omtky3-del(1-5)
76	c2gkvB	Alignment	not modelled	5.4	31	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: ovomucoid; PDBTitle: crystal structure of the sgpb:p14'-ala32 omtky3-del(1-5)2 complex
77	c2gkvA	Alignment	not modelled	5.4	31	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: ovomucoid; PDBTitle: crystal structure of the sgpb:p14'-ala32 omtky3-del(1-5)2 complex
78	d1r4ra	Alignment	not modelled	5.4	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
79	d2pnxa1	Alignment	not modelled	5.4	18	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
						Fold: Kazal-type serine protease inhibitors

80	d1nuba3	Alignment	not modelled	5.3	40	Superfamily: Kazal-type serine protease inhibitors Family: Ovomucoid domain III-like
81	d1glua	Alignment	not modelled	5.3	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor
82	d1we9a	Alignment	not modelled	5.3	17	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
83	c2nu4l	Alignment	not modelled	5.2	31	PDB header: hydrolase Chain: I: PDB Molecule: ovomucoid; PDBTitle: accommodation of positively-charged residues in a2 hydrophobic specificity pocket: crystal structures of sgpb3 in complex with omtky3 variants lys18i and arg18i
84	c2nu3l	Alignment	not modelled	5.2	31	PDB header: hydrolase Chain: I: PDB Molecule: ovomucoid; PDBTitle: accommodation of positively-charged residues in a2 hydrophobic specificity pocket: crystal structures of sgpb3 in complex with omtky3 variants lys18i and arg18i
85	c1hjal	Alignment	not modelled	5.2	31	PDB header: complex (hydrolase/inhibitor) Chain: I: PDB Molecule: ovomucoid inhibitor; PDBTitle: lys 18 variant of turkey ovomucoid inhibitor third domain2 complexed with alpha-chymotrypsin
86	d1r0na	Alignment	not modelled	5.1	38	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Nuclear receptor