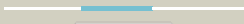
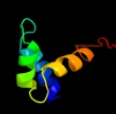
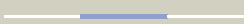
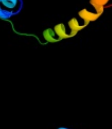
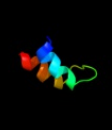
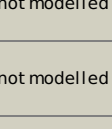


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	D6VPM8
Date	Mon Jul 2 19:10:02 BST 2012
Unique Job ID	dc9f5d08c9cc38c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2cqra1	 Alignment		46.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
2	d2cqqa1	 Alignment		33.7	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
3	c2d9aA_	 Alignment		27.0	15	PDB header: transcription Chain: A: PDB Molecule: myb-related protein b; PDBTitle: solution structure of rsgi ruh-050, a myb dna-binding2 domain in mouse cdna
4	c2dinA_	 Alignment		25.9	21	PDB header: dna binding protein Chain: A: PDB Molecule: cell division cycle 5-like protein; PDBTitle: solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein
5	d1wgxa_	 Alignment		25.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
6	c2yusA_	 Alignment		25.3	19	PDB header: transcription Chain: A: PDB Molecule: swi/snf-related matrix-associated actin- PDBTitle: solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
7	c3fovA_	 Alignment		22.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0102 protein rpa0323; PDBTitle: crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
8	c4eefl_	 Alignment		20.4	8	PDB header: immune system/inhibitor Chain: I: PDB Molecule: f-hb80.4, designed hemagglutinin binding protein; PDBTitle: crystal structure of the designed inhibitor protein f-hb80.4 in2 complex with the 1918 influenza virus hemagglutinin.
9	d1un2a_	 Alignment		19.6	17	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
10	c3l9vE_	 Alignment		16.7	12	PDB header: oxidoreductase Chain: E: PDB Molecule: putative thiol-disulfide isomerase or thioredoxin; PDBTitle: crystal structure of salmonella enterica serovar typhimurium srga
11	d2f76x1	 Alignment		15.6	20	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: Mason-Pfizer monkey virus matrix protein

12	c2ebiA_	Alignment		15.6	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna binding protein gt-1; PDBTitle: arabidopsis gt-1 dna-binding domain with t133d phosphomimetic mutation
13	c3c7mB_	Alignment		15.4	10	PDB header: oxidoreductase Chain: B: PDB Molecule: thiol:disulfide interchange protein dsba-like; PDBTitle: crystal structure of reduced dsbl
14	c2kdtA_	Alignment		14.7	11	PDB header: protein transport Chain: A: PDB Molecule: neuroendocrine convertase 1; PDBTitle: pc1/3 dcsg sorting domain structure in dpc
15	d1q5za_	Alignment		14.6	54	Fold: Invasion protein A (SipA) , C-terminal actin binding domain Superfamily: Invasion protein A (SipA) , C-terminal actin binding domain Family: Invasion protein A (SipA) , C-terminal actin binding domain
16	c1q5za_	Alignment		14.6	54	PDB header: cell invasion Chain: A: PDB Molecule: sipa; PDBTitle: crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa)
17	d1kkxa_	Alignment		13.5	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
18	c3gykC_	Alignment		12.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: 27kda outer membrane protein; PDBTitle: the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
19	c3gn3B_	Alignment		12.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative protein-disulfide isomerase; PDBTitle: crystal structure of a putative protein-disulfide isomerase from2 pseudomonas syringae to 2.5a resolution.
20	d1ig6a_	Alignment		12.2	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
21	c2cjjA_	Alignment	not modelled	11.0	8	PDB header: dna-binding protein Chain: A: PDB Molecule: radialis; PDBTitle: crystal structure of the myb domain of the rad2 transcription factor from antirrhinum majus
22	d2cjjal	Alignment	not modelled	11.0	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
23	d1mwpa_	Alignment	not modelled	10.7	25	Fold: SRCR-like Superfamily: A heparin-binding domain Family: A heparin-binding domain
24	d1c20a_	Alignment	not modelled	10.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
25	c3kzqE_	Alignment	not modelled	10.0	9	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: putative uncharacterized protein vp2116; PDBTitle: the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
26	c3hd5A_	Alignment	not modelled	10.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein dsba; PDBTitle: crystal structure of a thiol:disulfide interchange protein2 dsba from bordetella parapertussis
27	d2g3ra1	Alignment	not modelled	9.8	18	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
28	c2eqyA_	Alignment	not modelled	9.6	18	PDB header: dna binding protein Chain: A: PDB Molecule: jumonji, at rich interactive domain 1b; PDBTitle: solution structure of the arid domain of jarid1b protein
						PDB header: dna binding protein Chain: A: PDB Molecule: lysine-specific demethylase lid;

29	c2lm1A	Alignment	not modelled	9.2	14	PDBTitle: solution nmr structure of lysine-specific demethylase lid from2 drosophila melanogaster, northeast structural genomics consortium3 target fr824d
30	c4ffeX	Alignment	not modelled	9.2	21	PDB header: viral protein Chain: X: PDB Molecule: cpxv018 protein; PDBTitle: the structure of cowpox virus cpxv018 (omcp)
31	c2jxA	Alignment	not modelled	8.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: histone demethylase jarid1a; PDBTitle: nmr structure of the arid domain from the histone h3k42 demethylase rbp2
32	c3mopC	Alignment	not modelled	8.2	14	PDB header: signaling protein, immune system Chain: C: PDB Molecule: myeloid differentiation primary response protein myd88; PDBTitle: the ternary death domain complex of myd88, irak4, and irak2
33	d2eiaa2	Alignment	not modelled	7.6	29	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
34	d2hwna1	Alignment	not modelled	7.6	18	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
35	c2dimA	Alignment	not modelled	7.5	11	PDB header: dna binding protein Chain: A: PDB Molecule: cell division cycle 5-like protein; PDBTitle: solution structure of the myb_dna-binding domain of human2 cell division cycle 5-like protein
36	c2yqeA	Alignment	not modelled	7.4	14	PDB header: dna binding protein Chain: A: PDB Molecule: jumonji/arid domain-containing protein 1d; PDBTitle: solution structure of the arid domain of jarid1d protein
37	d1m9dc	Alignment	not modelled	7.4	29	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
38	c1x41A	Alignment	not modelled	7.1	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional adaptor 2-like, isoform b; PDBTitle: solution structure of the myb-like dna binding domain of 2 human transcriptional adaptor 2-like, isoform b
39	c3n7nE	Alignment	not modelled	7.1	35	PDB header: replication Chain: E: PDB Molecule: monopolin complex subunit lrs4; PDBTitle: structure of csml/lrs4 complex
40	d1h8ac1	Alignment	not modelled	7.1	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
41	d1z6ma1	Alignment	not modelled	7.1	9	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
42	c3bciA	Alignment	not modelled	7.0	9	PDB header: oxidoreductase Chain: A: PDB Molecule: disulfide bond protein a; PDBTitle: crystal structure of staphylococcus aureus dsba
43	d1r2aa	Alignment	not modelled	6.2	18	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
44	c2rh0B	Alignment	not modelled	6.1	21	PDB header: nuclear protein Chain: B: PDB Molecule: nucd domain-containing protein 2; PDBTitle: crystal structure of nucd domain-containing protein 22 (13542905) from mus musculus at 1.95 a resolution
45	d1gvda	Alignment	not modelled	5.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
46	c3ktmB	Alignment	not modelled	5.7	25	PDB header: cell adhesion, signaling protein Chain: B: PDB Molecule: amyloid beta a4 protein; PDBTitle: structure of the heparin-induced e1-dimer of the amyloid precursor2 protein (app)
47	c2l6wB	Alignment	not modelled	5.7	21	PDB header: membrane protein Chain: B: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm
48	c2l6wA	Alignment	not modelled	5.7	21	PDB header: membrane protein Chain: A: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm
49	d1r5la1	Alignment	not modelled	5.6	17	Fold: RuvA C-terminal domain-like Superfamily: CRAL/TRIO N-terminal domain Family: CRAL/TRIO N-terminal domain
50	c2wlvA	Alignment	not modelled	5.5	24	PDB header: virus protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal capsid domain of hiv-2
51	c2xgvA	Alignment	not modelled	5.5	24	PDB header: viral protein Chain: A: PDB Molecule: psiv capsid n-terminal domain; PDBTitle: structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
52	d1beda	Alignment	not modelled	5.4	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
53	d1tuaa2	Alignment	not modelled	5.3	16	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
54	c2rq5A	Alignment	not modelled	5.3	7	PDB header: transcription Chain: A: PDB Molecule: protein jumonji; PDBTitle: solution structure of the at-rich interaction domain

					(arid)2 of jumonji/jarid2
55	d2pxrc1	Alignment	not modelled	5.3	29 Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
56	d1k1fa_	Alignment	not modelled	5.3	46 Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
57	d1wmga_	Alignment	not modelled	5.2	12 Fold: DEATH domain Superfamily: DEATH domain Family: DEATH domain, DD
58	c2xgyA_	Alignment	not modelled	5.1	18 PDB header: viral protein/isomerase Chain: A: PDB Molecule: relik capsid n-terminal domain; PDBTitle: complex of rabbit endogenous lentivirus (relik)capsid with2 cyclophilin a
59	c2pfcA_	Alignment	not modelled	5.1	27 PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein rv0098/mt0107; PDBTitle: structure of mycobacterium tuberculosis rv0098
60	c2ib1A_	Alignment	not modelled	5.1	13 PDB header: apoptosis Chain: A: PDB Molecule: death domain containing membrane protein nradd; PDBTitle: solution structure of p45 death domain