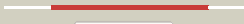
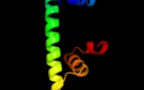
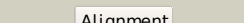
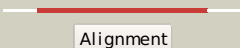
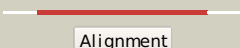
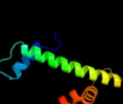
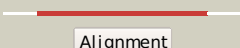
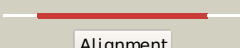
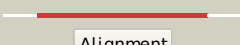
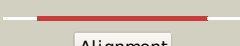
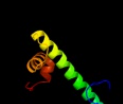
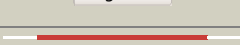
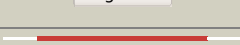
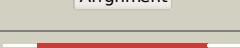
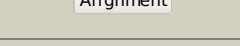


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	C6Y4D0
Date	Sun Jul 8 11:45:10 BST 2012
Unique Job ID	715da638b24e05b9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1nljb_	 Alignment		99.9	35	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
2	d1hioa_	 Alignment		99.8	17	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
3	c2bykA_	 Alignment		99.8	31	PDB header: dna-binding protein Chain: A: PDB Molecule: chrac-16; PDBTitle: histone fold heterodimer of the chromatin accessibility2 complex
4	d2byka1	 Alignment		99.8	31	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
5	d2bykb1	 Alignment		99.7	23	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
6	c2bykB_	 Alignment		99.7	23	PDB header: dna-binding protein Chain: B: PDB Molecule: chrac-14; PDBTitle: histone fold heterodimer of the chromatin accessibility2 complex
7	c1jfiB_	 Alignment		99.7	15	PDB header: transcription/dna Chain: B: PDB Molecule: transcription regulator nc2 beta chain; PDBTitle: crystal structure of the nc2-tbp-dna ternary complex
8	d1jfib_	 Alignment		99.7	15	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
9	d1jfiA_	 Alignment		99.7	27	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
10	c1jfiA_	 Alignment		99.7	27	PDB header: transcription/dna Chain: A: PDB Molecule: transcription regulator nc2 alpha chain; PDBTitle: crystal structure of the nc2-tbp-dna ternary complex
11	d1nlja_	 Alignment		99.7	19	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs

12	dltzya_	 Alignment		99.7	17	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
13	dlkx3c_	 Alignment		99.7	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
14	dlf66c_	 Alignment		99.7	19	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
15	c1f66C_	 Alignment		99.7	19	PDB header: structural protein/dna Chain: C: PDB Molecule: histone h2a.z; PDBTitle: 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
16	dlaaic_	 Alignment		99.7	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
17	dlu35c1	 Alignment		99.7	17	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
18	c2f8nK_	 Alignment		99.7	17	PDB header: structural protein/dna Chain: K: PDB Molecule: histone h2a type 1; PDBTitle: 2.9 angstrom x-ray structure of hybrid macroh2a nucleosomes
19	d2byma1	 Alignment		99.7	30	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
20	d2jssa1	 Alignment		99.6	23	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
21	d1eqza_	 Alignment	not modelled	99.6	17	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
22	dlkx5c_	 Alignment	not modelled	99.6	19	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
23	d1a7wa_	 Alignment	not modelled	99.6	31	Fold: Histone-fold Superfamily: Histone-fold Family: Archaeal histone
24	c2jssA_	 Alignment	not modelled	99.6	22	PDB header: chaperone/nuclear protein Chain: A: PDB Molecule: chimera of histone h2b.1 and histone h2a.z; PDBTitle: nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
25	d1htaa_	 Alignment	not modelled	99.5	30	Fold: Histone-fold Superfamily: Histone-fold Family: Archaeal histone
26	d1ku5a_	 Alignment	not modelled	99.5	22	Fold: Histone-fold Superfamily: Histone-fold Family: Archaeal histone
27	d1id3c_	 Alignment	not modelled	99.5	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
28	c3b0dB_	 Alignment	not modelled	99.4	16	PDB header: dna binding protein Chain: B: PDB Molecule: centromere protein t; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w complex,2 crystal form ii
		 Alignment				Fold: Histone-fold

29	d2huec1	Alignment	not modelled	99.0	17	Superfamily: Histone-fold Family: Nucleosome core histones
30	d1hiod	Alignment	not modelled	98.9	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
31	d1id3b	Alignment	not modelled	98.8	15	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
32	d1kx5b	Alignment	not modelled	98.6	17	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
33	d1p3mh	Alignment	not modelled	98.4	28	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
34	d1hiob	Alignment	not modelled	98.4	26	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
35	d1q9ca	Alignment	not modelled	98.2	13	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
36	c3nquA	Alignment	not modelled	98.2	19	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of partially trypsinized (cenp-a/h4)2 heterotetramer
37	d1id3d	Alignment	not modelled	98.2	28	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
38	d1id3a	Alignment	not modelled	98.2	18	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
39	c3nqiA	Alignment	not modelled	98.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: histone h3-like centromeric protein a; PDBTitle: crystal structure of (cenp-a/h4)2 heterotetramer
40	d1tzyC	Alignment	not modelled	98.1	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
41	d1p3ie	Alignment	not modelled	98.1	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
42	d1tzyb	Alignment	not modelled	98.0	28	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
43	c2l5aA	Alignment	not modelled	98.0	23	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
44	c2hueB	Alignment	not modelled	98.0	22	PDB header: dna binding protein Chain: B: PDB Molecule: histone h3; PDBTitle: structure of the h3-h4 chaperone asf1 bound to histones h3 and h4
45	d1kx5a	Alignment	not modelled	97.9	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
46	d1eqzg	Alignment	not modelled	97.9	22	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
47	c2yfwC	Alignment	not modelled	97.8	19	PDB header: cell cycle Chain: C: PDB Molecule: histone h3-like centromeric protein cse4; PDBTitle: heterotetramer structure of kluyveromyces lactis cse4,h4
48	d1tafb	Alignment	not modelled	97.3	15	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
49	d1flea	Alignment	not modelled	97.2	23	Fold: Histone-fold Superfamily: Histone-fold Family: Archaeal histone
50	c3b0dC	Alignment	not modelled	97.1	26	PDB header: dna binding protein Chain: C: PDB Molecule: centromere protein w; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp- w complex,2 crystal form ii
51	c3b0bA	Alignment	not modelled	97.0	20	PDB header: dna binding protein Chain: A: PDB Molecule: centromere protein s; PDBTitle: crystal structure of the chicken cenp-s/cenp-x complex
52	c3vh5D	Alignment	not modelled	96.9	19	PDB header: dna binding protein Chain: D: PDB Molecule: cenp-x; PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp- w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
53	d1bh9b	Alignment	not modelled	96.7	18	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
54	c3v9rC	Alignment	not modelled	96.6	12	PDB header: dna binding protein Chain: C: PDB Molecule: uncharacterized protein yol086w-a; PDBTitle: crystal structure of saccharomyces cerevisiae mhf complex
55	d1s32d	Alignment	not modelled	96.5	27	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
56	c3vh5A	Alignment	not modelled	96.5	20	PDB header: dna binding protein Chain: A: PDB Molecule: cenp-s;

56	c3v19A_	Alignment	not modelled	96.3	20	PDBTitle: crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
57	d1eqzb_	Alignment	not modelled	96.5	27	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
58	d1kx5d_	Alignment	not modelled	96.4	27	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
59	d1h3ob_	Alignment	not modelled	95.6	17	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
60	c3v9rD_	Alignment	not modelled	94.0	15	PDB header: dna binding protein Chain: D: PDB Molecule: uncharacterized protein ydl160c-a; PDBTitle: crystal structure of saccharomyces cerevisiae mhf complex
61	d1w5sa2	Alignment	not modelled	84.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
62	d1tafa_	Alignment	not modelled	83.1	19	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
63	c3v1fB_	Alignment	not modelled	72.1	29	PDB header: chaperone/protein binding Chain: B: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: crystal structure of yeast proteasome interacting protein
64	c2dzoD_	Alignment	not modelled	71.0	22	PDB header: protein binding Chain: D: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: crystal structure analysis of yeast nas6p complexed with2 the proteasome subunit, rpt3
65	c2krkA_	Alignment	not modelled	68.0	32	PDB header: protein binding Chain: A: PDB Molecule: 26s protease regulatory subunit 8; PDBTitle: solution nmr structure of 26s protease regulatory subunit 82 from h.sapiens, northeast structural genomics consortium3 target target hr3102a
66	c2dvwb_	Alignment	not modelled	68.0	19	PDB header: cell cycle/protein-binding Chain: B: PDB Molecule: 26s protease regulatory subunit 6b; PDBTitle: structure of the oncoprotein gankyrin in complex with s62 atpase of the 26s proteasome
67	d1fnna2	Alignment	not modelled	64.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
68	d1wwia1	Alignment	not modelled	63.8	18	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
69	d1lv7a_	Alignment	not modelled	59.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
70	d1r4va_	Alignment	not modelled	53.8	18	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
71	c2ce7B_	Alignment	not modelled	51.9	23	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
72	d1ixza_	Alignment	not modelled	45.3	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
73	c1h3oA_	Alignment	not modelled	41.7	19	PDB header: transcription/tbp-associated factors Chain: A: PDB Molecule: transcription initiation factor tfiid 135 kda PDBTitle: crystal structure of the human taf4-taf122 (tafi1135-tafii20) complex
74	d1h3oa_	Alignment	not modelled	41.7	19	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
75	d2ce7a2	Alignment	not modelled	32.3	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
76	c2x8aA_	Alignment	not modelled	30.6	23	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
77	c3h4mC_	Alignment	not modelled	29.6	26	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
78	c2c9oC_	Alignment	not modelled	28.4	20	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1
79	d1k6ka_	Alignment	not modelled	28.3	9	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
80	c2r65A_	Alignment	not modelled	26.5	23	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
81	c2dhrC_	Alignment	not modelled	24.8	32	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l) PDB header: hydrolase

82	c1iy2A_	Alignment	not modelled	24.7	33	Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
83	d1r6bx2	Alignment	not modelled	24.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
84	d1khya_	Alignment	not modelled	21.7	10	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
85	d1sxjc2	Alignment	not modelled	18.8	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
86	c3fh2A_	Alignment	not modelled	18.4	8	PDB header: hydrolase Chain: A: PDB Molecule: probable atp-dependent protease (heat shock protein); PDBTitle: the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
87	d1g8pa_	Alignment	not modelled	18.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
88	c3kl1A_	Alignment	not modelled	18.1	19	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
89	c2k77A_	Alignment	not modelled	16.6	10	PDB header: chaperone, protein binding Chain: A: PDB Molecule: negative regulator of genetic competence PDBTitle: nmr solution structure of the bacillus subtilis clpc n-2 domain
90	c1u5tA_	Alignment	not modelled	14.1	8	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
91	d1njfa_	Alignment	not modelled	14.1	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
92	d1jr3d2	Alignment	not modelled	12.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
93	d1y1oa_	Alignment	not modelled	12.9	15	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: RecU-like
94	c1rznB_	Alignment	not modelled	12.5	18	PDB header: dna binding protein Chain: B: PDB Molecule: recombination protein u; PDBTitle: crystal structure of penicillin-binding protein-related2 factor a from bacillus subtilis.
95	c3fesB_	Alignment	not modelled	12.5	10	PDB header: atp binding protein Chain: B: PDB Molecule: atp-dependent clp endopeptidase; PDBTitle: crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
96	d1ixsb2	Alignment	not modelled	11.4	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
97	c3f8tA_	Alignment	not modelled	10.8	17	PDB header: hydrolase Chain: A: PDB Molecule: predicted atpase involved in replication control, PDBTitle: crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
98	d1qvra1	Alignment	not modelled	10.4	21	Fold: Double Clp-N motif Superfamily: Double Clp-N motif Family: Double Clp-N motif
99	c3mhvA_	Alignment	not modelled	9.7	14	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein vta1; PDBTitle: crystal structure of vps4 and vta1