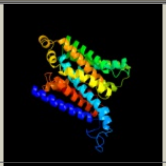
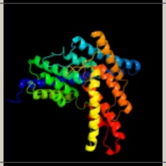
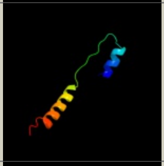
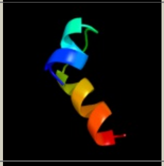
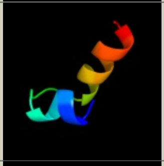
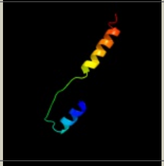
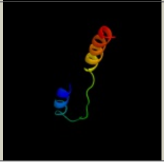
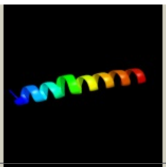
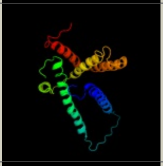
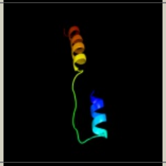
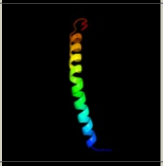
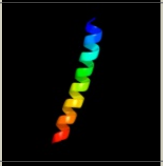
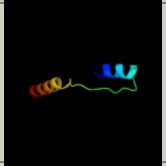
Email	l.a.kelley@imperial.ac.uk
Description	P06972
Date	Thu Jan 5 10:59:37 GMT 2012
Unique Job ID	c10a195fbc2cd4c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l7va_	Alignment		100.0	27	**Fold:**ABC transporter involved in vitamin B12 uptake, BtuC **Superfamily:**ABC transporter involved in vitamin B12 uptake, BtuC **Family:**ABC transporter involved in vitamin B12 uptake, BtuC
2	c2nq2A_	Alignment		100.0	27	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**hypothetical abc transporter permease protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
3	d1otsa_	Alignment		51.2	11	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
4	d1kpla_	Alignment		46.2	14	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
5	c3k3gA_	Alignment		38.0	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**urea transporter; **PDBTitle:** crystal structure of the urea transporter from desulfovibrio vulgaris2 bound to 1,3-dimethylurea
6	c1yceD_	Alignment		27.6	14	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**subunit c; **PDBTitle:** structure of the rotor ring of f-type na+-atpase from ilyobacter2 tartaricus
7	c1q1hA_	Alignment		22.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor e; **PDBTitle:** an extended winged helix domain in general transcription2 factor e/iie alpha
8	d1q1ha_	Alignment		22.2	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcription factor E/IIe-alpha, N-terminal domain
9	c2ht2B_	Alignment		20.9	12	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
10	c2w5jM_	Alignment		18.6	20	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**atp synthase c chain, chloroplastic; **PDBTitle:** structure of the c14-rotor ring of the proton translocating2 chloroplast atp synthase
11	c2xndK_	Alignment		17.5	21	**PDB header:**hydrolase **Chain:** K: **PDB Molecule:**atp synthase lipid-binding protein, mitochondrial; **PDBTitle:** crystal structure of bovine f1-c8 sub-complex of atp2 synthase

12	d2p7tc1	Alignment		16.6	34	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
13	c3lrcC_	Alignment		15.3	7	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**arginine/agmatine antiporter; **PDBTitle:** structure of e. coli adic (p1)
14	c2b2hA_	Alignment		15.3	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter; **PDBTitle:** ammonium transporter amt-1 from a. fulgidus (as)
15	c2wpdP_	Alignment		14.5	23	**PDB header:**hydrolase **Chain:** P: **PDB Molecule:**atp synthase subunit 9, mitochondrial; **PDBTitle:** the mg.adp inhibited state of the yeast f1c10 atp synthase
16	c3qnqD_	Alignment		14.4	7	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
17	d2r5fa1	Alignment		13.5	33	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
18	c2kncA_	Alignment		12.3	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
19	c2x2vG_	Alignment		12.0	18	**PDB header:**membrane protein **Chain:** G: **PDB Molecule:**atp synthase subunit c; **PDBTitle:** structural basis of a novel proton-coordination type in an2 f1fo-atp synthase rotor ring
20	d1y88a1	Alignment		11.6	21	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**Hypothetical protein AF1548, C-terminal domain
21	c2zt9E_	Alignment	not modelled	11.5	34	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
22	c2o012_	Alignment	not modelled	11.2	48	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**type ii chlorophyll a/b binding protein from **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
23	c3a03A_	Alignment	not modelled	11.1	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**t-cell leukemia homeobox protein 2; **PDBTitle:** crystal structure of hox11l1 homeodomain
24	c2jd3B_	Alignment	not modelled	10.8	33	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**stbb protein; **PDBTitle:** parr from plasmid pb171
25	d1du0a_	Alignment	not modelled	10.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	d1x2ma1	Alignment	not modelled	10.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
27	c3mk7F_	Alignment	not modelled	10.5	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
28	c2kfsA_	Alignment	not modelled	10.4	28	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c

29	d1ku2a1	Alignment	not modelled	10.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
30	d1rh5b_	Alignment	not modelled	10.3	33	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
31	c1iijA_	Alignment	not modelled	10.0	35	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**erbb-2 receptor protein-tyrosine kinase; **PDBTitle:** solution structure of the neu/erbb-2 membrane spanning2 segment
32	c2vi6F_	Alignment	not modelled	9.6	11	**PDB header:**transcription **Chain:** F: **PDB Molecule:**homeobox protein nanog; **PDBTitle:** crystal structure of the nanog homeodomain
33	c1l0oC_	Alignment	not modelled	9.6	28	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
34	d1l0oc_	Alignment	not modelled	9.6	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
35	c3cmwA_	Alignment	not modelled	9.5	27	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
36	d2p7vb1	Alignment	not modelled	9.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
37	c2da4A_	Alignment	not modelled	9.4	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
38	c1fftG_	Alignment	not modelled	9.4	5	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
39	c2xglB_	Alignment	not modelled	9.3	18	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m immunity protein; **PDBTitle:** the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
40	c3nd0A_	Alignment	not modelled	9.3	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
41	c2jwaA_	Alignment	not modelled	9.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
42	d1rp3a1	Alignment	not modelled	9.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
43	d1akha_	Alignment	not modelled	9.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
44	d1sana_	Alignment	not modelled	9.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
45	c1yi7C_	Alignment	not modelled	8.9	31	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-xylosidase, family 43 glycosyl hydrolase; **PDBTitle:** beta-d-xylosidase (selenomethionine) xynd from clostridium2 acetobutylicum
46	d1ku3a_	Alignment	not modelled	8.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
47	c3aqpB_	Alignment	not modelled	8.8	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
48	c2kz3A_	Alignment	not modelled	8.8	24	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein rad51l3; **PDBTitle:** backbone 1h, 13c, and 15n chemical shift assignments for human rad51d2 from 1 to 83
49	d2o34a1	Alignment	not modelled	8.7	20	**Fold:**T-fold **Superfamily:**ApbE-like **Family:**DVU1097-like
50	c1wu0A_	Alignment	not modelled	8.5	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase c chain; **PDBTitle:** solution structure of subunit c of f1fo-atp synthase from2 the thermophilic bacillus ps3
51	d1wh5a_	Alignment	not modelled	8.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
52	d1le8a_	Alignment	not modelled	8.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
53	d1ttya_	Alignment	not modelled	8.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
54	d1p7ia_	Alignment	not modelled	8.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like

						Family: Homeodomain
55	d2p81a1	Alignment	not modelled	8.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
56	c3t72o_	Alignment	not modelled	8.3	12	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
57	d2asba2	Alignment	not modelled	8.2	29	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
58	c3k69A_	Alignment	not modelled	8.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
59	c2da7A_	Alignment	not modelled	8.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
60	c2xvtC_	Alignment	not modelled	8.2	42	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**receptor activity-modifying protein 2; **PDBTitle:** structure of the extracellular domain of human ramp2
61	c2k1aA_	Alignment	not modelled	8.2	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** bicelle-embedded integrin alpha(iib) transmembrane segment
62	d1b8ia_	Alignment	not modelled	8.1	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
63	c2jmlA_	Alignment	not modelled	8.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
64	d1rhzb_	Alignment	not modelled	8.0	24	**Fold:**Single transmembrane helix **Superfamily:**Preprotein translocase SecE subunit **Family:**Preprotein translocase SecE subunit
65	d1mylb_	Alignment	not modelled	8.0	38	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
66	d1o4xa1	Alignment	not modelled	7.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
67	d1ku7a_	Alignment	not modelled	7.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
68	d1rc2a_	Alignment	not modelled	7.9	26	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
69	c2djnA_	Alignment	not modelled	7.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**homeobox protein dlx-5; **PDBTitle:** the solution structure of the homeobox domain of human2 homeobox protein dlx-5
70	d1bw5a_	Alignment	not modelled	7.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	d1f43a_	Alignment	not modelled	7.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
72	c2rn7A_	Alignment	not modelled	7.7	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**is629 orfa; **PDBTitle:** nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
73	c2l2tA_	Alignment	not modelled	7.7	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-4; **PDBTitle:** solution nmr structure of the erbb4 dimeric membrane domain
74	c2o8xA_	Alignment	not modelled	7.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
75	c2k40A_	Alignment	not modelled	7.6	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox expressed in es cells 1; **PDBTitle:** nmr structure of hesx-1 homeodomain double mutant r31l/e42l
76	c3cmuA_	Alignment	not modelled	7.6	24	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
77	d1f6ga_	Alignment	not modelled	7.6	28	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
78	d1pufa_	Alignment	not modelled	7.6	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	d1s7ea1	Alignment	not modelled	7.6	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
80	d1b72a_	Alignment	not modelled	7.6	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain

81	c2kv5A_	Alignment	not modelled	7.6	20	**PDB header:**toxin **Chain:** A: **PDB Molecule:**putative uncharacterized protein rnai; **PDBTitle:** solution structure of the par toxin fst in dpc micelles
82	d2craa1	Alignment	not modelled	7.5	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
83	d1zq3p1	Alignment	not modelled	7.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
84	c2x48B_	Alignment	not modelled	7.5	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**cag38821; **PDBTitle:** orf 55 from sulfolobus islandicus rudivirus 1
85	d2hi3a1	Alignment	not modelled	7.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
86	c3u5eL_	Alignment	not modelled	7.4	26	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**60s ribosomal protein l13-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 resolution
87	c2wwbB_	Alignment	not modelled	7.4	28	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sec61 subunit gamma; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
88	c3a01A_	Alignment	not modelled	7.3	17	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeodomain-containing protein; **PDBTitle:** crystal structure of aristaless and clawless homeodomains bound to dna
89	d1s9ca1	Alignment	not modelled	7.3	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
90	d1l8qa1	Alignment	not modelled	7.3	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
91	d1js2a_	Alignment	not modelled	7.3	25	**Fold:**HIPIP (high potential iron protein) **Superfamily:**HIPIP (high potential iron protein) **Family:**HIPIP (high potential iron protein)
92	c2yx8A_	Alignment	not modelled	7.3	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**receptor activity-modifying protein 1; **PDBTitle:** crystal structure of the extracellular domain of human ramp1
93	d1ocpa_	Alignment	not modelled	7.3	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
94	d1myka_	Alignment	not modelled	7.3	38	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
95	d1smyf2	Alignment	not modelled	7.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
96	c4a18U_	Alignment	not modelled	7.2	21	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**rpl13; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of molecule 1
97	d1yz8p1	Alignment	not modelled	7.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
98	d2dt5a1	Alignment	not modelled	7.1	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
99	c2dmsA_	Alignment	not modelled	7.1	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**homeobox protein otx2; **PDBTitle:** solution structure of the homeobox domain of homeobox2 protein otx2