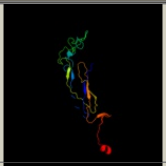
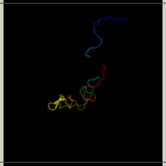
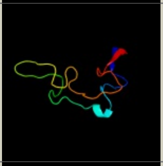
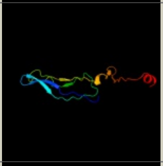
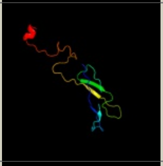
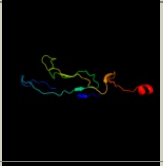
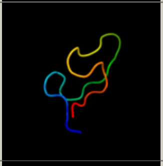
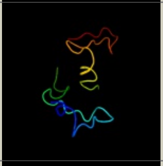
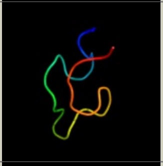
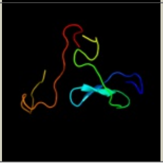
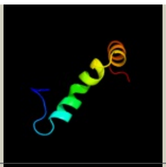
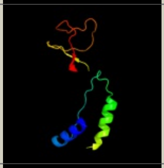
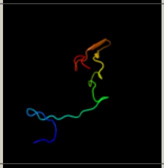
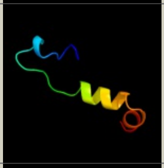
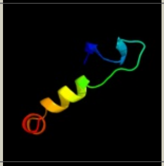
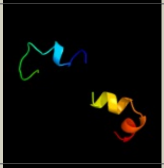
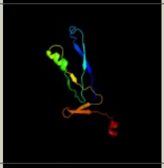
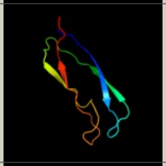
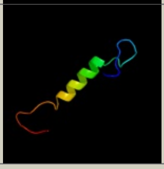
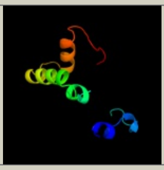
Email	l.a.kelley@imperial.ac.uk
Description	P76161
Date	Thu Jan 5 12:19:56 GMT 2012
Unique Job ID	03908fb7538dd54f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nltA_	Alignment		99.9	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
2	c2cttA_	Alignment		99.7	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of zinc finger domain from human dnaj2 subfamily a menber 3
3	d1exka_	Alignment		99.4	24	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
4	d1nlta3	Alignment		99.3	22	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
5	c2q2gA_	Alignment		98.0	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock 40 kda protein, putative (fragment); **PDBTitle:** crystal structure of dimerization domain of hsp40 from2 cryptosporidium parvum, cgd2_1800
6	c3lz8A_	Alignment		97.7	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone dnaj from klebsiella pneumoniae2 subsp. pneumoniae mgh 78578 at 2.9 a resolution.
7	c2qldA_	Alignment		97.6	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 1; **PDBTitle:** human hsp40 hdj1
8	c3ld0Q_	Alignment		97.1	37	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
9	c2k3vA_	Alignment		96.8	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
10	c2bx9J_	Alignment		94.9	41	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
11	d2fiya1	Alignment		86.7	14	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like

12	c3apqB_	Alignment		86.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
13	c2kdxA_	Alignment		81.0	19	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
14	c3pihA_	Alignment		80.0	37	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
15	c1fpoA_	Alignment		78.0	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
16	c3hhoA_	Alignment		74.4	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
17	c3bvoA_	Alignment		73.4	6	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
18	c2b26A_	Alignment		70.5	20	**PDB header:**chaperone/protein transport **Chain:** A: **PDB Molecule:**sis1 protein; **PDBTitle:** the crystal structure of the protein complex of yeast hsp402 sis1 and hsp70 ssa1
19	d1c3ga1	Alignment		69.6	14	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
20	d1gh6a_	Alignment		69.4	14	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
21	c2cugA_	Alignment	not modelled	64.3	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
22	c2l6lA_	Alignment	not modelled	62.7	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
23	d1hdja_	Alignment	not modelled	62.5	11	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
24	c2ctqA_	Alignment		60.7	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 menber 12
25	c1bq0A_	Alignment	not modelled	57.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj; **PDBTitle:** j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
26	c2o37A_	Alignment	not modelled	54.9	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
27	c2ctrA_	Alignment	not modelled	53.7	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 9; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 menber 9

28	c3a44D_	Alignment	not modelled	52.8	14	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
29	c2ys8A_	Alignment	not modelled	51.9	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**rab-related gtp-binding protein rabj; **PDBTitle:** solution structure of the dnaj-like domain from human ras-2 associated protein rap1
30	d1p9ra_	Alignment	not modelled	49.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
31	c3trzE_	Alignment	not modelled	48.0	24	**PDB header:**rna binding protein/rna **Chain:** E: **PDB Molecule:**protein lin-28 homolog a; **PDBTitle:** mouse lin28a in complex with let-7d microrna pre-element
32	c2dn9A_	Alignment	not modelled	47.0	13	**PDB header:**apoptosis, chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily a member 3; **PDBTitle:** solution structure of j-domain from the dnaj homolog, human2 tid1 protein
33	d1nz6a_	Alignment	not modelled	45.6	6	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
34	c2yuaA_	Alignment	not modelled	44.5	8	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**williams-beuren syndrome chromosome region 18 **PDBTitle:** solution structure of the dnaj domain from human williams-2 beuren syndrome chromosome region 18 protein
35	c2kqxA_	Alignment	not modelled	43.1	21	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
36	d1fpoa1	Alignment	not modelled	40.7	24	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
37	c2qsaA_	Alignment	not modelled	39.5	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog dnj-2; **PDBTitle:** crystal structure of j-domain of dnaj homolog dnj-2 precursor from2 c.elegans.
38	c2ctwA_	Alignment	not modelled	38.1	21	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 5; **PDBTitle:** solution structure of j-domain from mouse dnaj subfamily c2 member 5
39	d1iura_	Alignment	not modelled	37.8	22	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
40	c2k2dA_	Alignment	not modelled	37.8	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
41	c2lgwA_	Alignment	not modelled	36.9	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 2; **PDBTitle:** solution structure of the j domain of hsj1a
42	d1xbla_	Alignment	not modelled	36.8	17	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
43	d1qypa_	Alignment	not modelled	35.4	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
44	d1wjza_	Alignment	not modelled	34.7	11	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
45	c2dmxA_	Alignment	not modelled	33.2	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
46	d1tfia_	Alignment	not modelled	30.1	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
47	c2ctpA_	Alignment	not modelled	29.0	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 12
48	c2jrpA_	Alignment	not modelled	27.7	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
49	c2jneA_	Alignment	not modelled	26.7	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
50	d2jnea1	Alignment	not modelled	26.7	14	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
51	c2opfA_	Alignment	not modelled	23.7	8	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
52	d1aafa_	Alignment	not modelled	23.7	20	**Fold:**Retrovirus zinc finger-like domains **Superfamily:**Retrovirus zinc finger-like domains **Family:**Retrovirus zinc finger-like domains
53	d1zbdb_	Alignment	not modelled	23.6	18	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain

54	c1ee8A_	Alignment	not modelled	23.4	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
55	c2ochA_	Alignment	not modelled	22.1	11	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
56	d1fafa_	Alignment	not modelled	20.4	13	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
57	d1twfi2	Alignment	not modelled	20.0	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
58	d1ee8a3	Alignment	not modelled	18.0	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
59	c2jvnA_	Alignment	not modelled	17.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
60	c3hq7A_	Alignment	not modelled	17.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
61	c2riqA_	Alignment	not modelled	17.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
62	c1yuzB_	Alignment	not modelled	16.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
63	c2qkdA_	Alignment	not modelled	15.0	8	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
64	c2c4rL_	Alignment	not modelled	14.9	16	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**ribonuclease e; **PDBTitle:** catalytic domain of e. coli rnase e
65	d1pfva3	Alignment	not modelled	14.8	21	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
66	c2cqfA_	Alignment	not modelled	14.6	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna-binding protein lin-28; **PDBTitle:** solution structure of the zinc-finger domain in lin-28
67	d2k4xa1	Alignment	not modelled	14.3	12	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
68	c2ihxA_	Alignment	not modelled	14.1	23	**PDB header:**viral protein/rna **Chain:** A: **PDB Molecule:**nucleocapsid (nc) protein; **PDBTitle:** solution structure of the rous sarcoma virus nucleocapsid2 protein:upsi rna packaging signal complex
69	d1jlza_	Alignment	not modelled	13.7	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
70	c1jlzA_	Alignment	not modelled	13.7	38	**PDB header:**toxin **Chain:** A: **PDB Molecule:**tityustoxin alpha-ktx; **PDBTitle:** solution structure of a k+-channel blocker from the2 scorpion toxin of tityus cambridgei
71	d1hk8a_	Alignment	not modelled	13.6	25	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
72	c1hk8A_	Alignment	not modelled	13.6	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
73	d1k3xa3	Alignment	not modelled	13.6	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
74	c3h0gI_	Alignment	not modelled	13.2	17	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
75	c3gn5B_	Alignment	not modelled	13.2	21	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
76	c2gb5B_	Alignment	not modelled	13.0	26	**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
77	c3k7aM_	Alignment	not modelled	12.9	15	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
78	c2c1uB_	Alignment	not modelled	12.5	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
79	c2e2zA_	Alignment	not modelled	12.4	25	**PDB header:**protein transport, chaperone regulator **Chain:** A: **PDB Molecule:**tim15; **PDBTitle:** solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
						Fold: Ribbon-helix-helix

80	d2cpga_	Alignment	not modelled	12.2	19	**Superfamily:**Ribbon-helix-helix **Family:**CopG-like
81	c1i3ql_	Alignment	not modelled	12.1	17	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
82	c3cc4Z_	Alignment	not modelled	11.7	28	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
83	c2pf4E_	Alignment	not modelled	11.5	11	**PDB header:**hydrolase regulator/viral protein **Chain:** E: **PDB Molecule:**small t antigen; **PDBTitle:** crystal structure of the full-length simian virus 40 small t antigen2 complexed with the protein phosphatase 2a aalpha subunit
84	d1wgea1	Alignment	not modelled	11.4	11	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
85	d2ey4e1	Alignment	not modelled	11.4	21	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
86	d1pfta_	Alignment	not modelled	11.2	15	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
87	c1y1yS_	Alignment	not modelled	10.8	25	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
88	c1pqvS_	Alignment	not modelled	10.6	25	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
89	c2li8A_	Alignment	not modelled	10.5	23	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**protein lin-28 homolog a; **PDBTitle:** the solution structure of the lin28-znf domains bound to aggagau of2 pre-let-7 mirna
90	d1nlta2	Alignment	not modelled	10.1	17	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
91	c3nybB_	Alignment	not modelled	10.0	20	**PDB header:**transferase/rna binding protein **Chain:** B: **PDB Molecule:**protein air2; **PDBTitle:** structure and function of the polymerase core of tramp, a rna2 surveillance complex
92	c1nmlA_	Alignment	not modelled	9.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
93	d2zjrz1	Alignment	not modelled	9.5	24	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
94	d1iqca1	Alignment	not modelled	9.1	24	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
95	c3o5cA_	Alignment	not modelled	9.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** cytochrome c peroxidase bccp of shewanella oneidensis
96	d1ibia1	Alignment	not modelled	8.9	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
97	d1nlta1	Alignment	not modelled	8.4	15	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
98	d1nmla1	Alignment	not modelled	8.4	19	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
99	d1dl6a_	Alignment	not modelled	8.3	7	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain