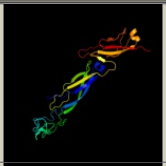
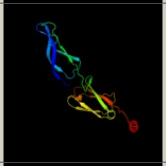
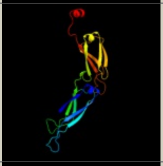
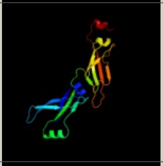
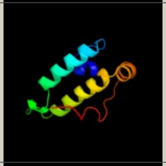
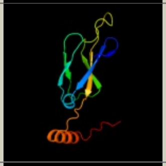
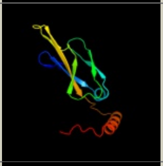
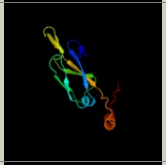
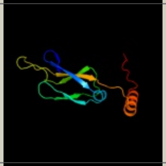
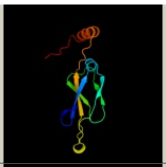
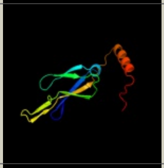
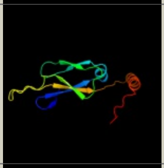
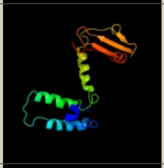
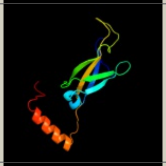
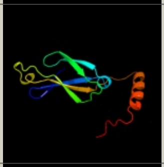
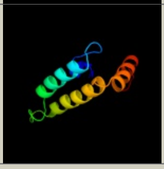
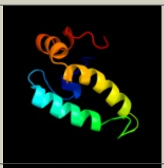
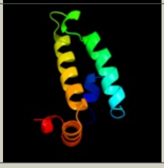
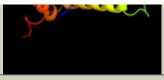
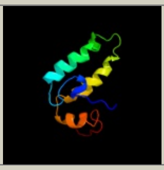
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P08622
Date	Thu Jan 5 11:01:33 GMT 2012
Unique Job ID	40570adf5ff47076

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nltA_	Alignment		100.0	28	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
2	c3lz8A_	Alignment		100.0	36	**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.
3	c2q2gA_	Alignment		100.0	26	**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
4	c2qldA_	Alignment		100.0	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 1; **PDBTitle:** human hsp40 hdj1
5	c2b26A_	Alignment		100.0	25	**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
6	c3apqB_	Alignment		99.9	49	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
7	c3i38D_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
8	c3i38K_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
9	c3i38A_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
10	c3i38G_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** G: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
11	c3i38F_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578

12	c3i38J_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** J: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
13	c3i38B_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
14	c3i38H_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** H: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
15	c3i38C_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
16	c3i38E_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
17	c2l6lA_	Alignment		99.9	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
18	c3i38L_	Alignment		99.9	33	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
19	c3i38I_	Alignment		99.9	32	**PDB header:**chaperone **Chain:** I: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
20	c2ctqA_	Alignment		99.9	28	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 12; **PDBTitle:** solution structure of j-domain from human dnaj subfamily c2 member 12
21	c2yuaA_	Alignment	not modelled	99.9	38	**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
22	d1c3ga2	Alignment	not modelled	99.9	27	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
23	d1hdja_	Alignment		99.9	50	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
24	c2ctwA_	Alignment		99.9	45	**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
25	c1fpoA_	Alignment	not modelled	99.9	20	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein hscb; **PDBTitle:** hsc20 (hscb), a j-type co-chaperone from e. coli
26	d1xbla_	Alignment		99.9	100	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain

						**Family:**Chaperone J-domain
27	c3hhoA_	Alignment	not modelled	99.9	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb homolog; **PDBTitle:** chaperone hscb from vibrio cholerae
28	c2dmxA_	Alignment	not modelled	99.9	48	**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
29	c3bvoA_	Alignment	not modelled	99.9	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
30	c2ctrA_	Alignment	not modelled	99.9	54	**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
31	c1bq0A_	Alignment		99.8	100	**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
32	c2o37A_	Alignment	not modelled	99.8	50	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
33	c1xaoA_	Alignment	not modelled	99.8	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** hsp40-ydj1 dimerization domain
34	c2ctpA_	Alignment	not modelled	99.8	49	**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
35	c2kqxA_	Alignment	not modelled	99.8	53	**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	c2cugA_	Alignment	not modelled	99.8	48	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962
37	c2dn9A_	Alignment	not modelled	99.8	52	**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
38	c2qsaA_	Alignment	not modelled	99.8	36	**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.
39	d1gh6a_	Alignment	not modelled	99.8	26	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
40	d1iura_	Alignment	not modelled	99.8	25	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
41	c2ochA_	Alignment	not modelled	99.8	48	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
42	d1wjza_	Alignment	not modelled	99.8	30	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
43	c2ys8A_	Alignment	not modelled	99.8	34	**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
44	d1nlta2	Alignment	not modelled	99.8	28	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
45	c2pf4E_	Alignment	not modelled	99.7	27	**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
46	d1fpoa1	Alignment	not modelled	99.7	25	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
47	d1fafa_	Alignment	not modelled	99.6	17	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
48	d1n4ca_	Alignment	not modelled	99.6	21	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
49	c2guzO_	Alignment	not modelled	99.6	17	**PDB header:**chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
50	d1nz6a_	Alignment	not modelled	99.5	21	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain

51	c2y4tA_	Alignment	not modelled	99.4	52	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 3; **PDBTitle:** crystal structure of the human co-chaperone p58(ipk)
52	c2cttA_	Alignment	not modelled	99.4	39	**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
53	d1c3ga1	Alignment	not modelled	99.4	20	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
54	c3apoA_	Alignment	not modelled	99.3	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of full-length erdj5
55	c3ag7A_	Alignment	not modelled	99.3	25	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
56	c2guzD_	Alignment	not modelled	99.2	13	**PDB header:**chaperone, protein transport **Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
57	d1nlta1	Alignment	not modelled	99.2	13	**Fold:**HSP40/DnaJ peptide-binding domain **Superfamily:**HSP40/DnaJ peptide-binding domain **Family:**HSP40/DnaJ peptide-binding domain
58	d1exka_	Alignment	not modelled	98.9	100	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
59	c3uo2A_	Alignment	not modelled	98.9	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial; **PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae
60	d1nlta3	Alignment	not modelled	98.2	32	**Fold:**DnaJ/Hsp40 cysteine-rich domain **Superfamily:**DnaJ/Hsp40 cysteine-rich domain **Family:**DnaJ/Hsp40 cysteine-rich domain
61	c3ld0Q_	Alignment	not modelled	85.7	43	**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
62	c2k3vA_	Alignment	not modelled	80.6	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**tetraheme cytochrome c-type; **PDBTitle:** solution structure of a tetrahaem cytochrome from2 shewanella frigidimarina
63	c2bx9J_	Alignment	not modelled	67.1	32	**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
64	d2q37a1	Alignment	not modelled	56.5	20	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
65	c2q37A_	Alignment	not modelled	56.5	20	**PDB header:**plant protein, lyase **Chain:** A: **PDB Molecule:**ohcu decarboxylase; **PDBTitle:** crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
66	d1ug2a_	Alignment	not modelled	52.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
67	d1akha_	Alignment	not modelled	47.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
68	c3epvB_	Alignment	not modelled	46.8	21	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
69	c3dkqB_	Alignment	not modelled	46.1	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pkhd-type hydroxylase sbal_3634; **PDBTitle:** crystal structure of putative oxygenase (yp_001051978.1) from2 shewanella baltica os155 at 2.26 a resolution
70	c1wz6A_	Alignment	not modelled	45.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx; **PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog
71	d2o8ia1	Alignment	not modelled	43.6	23	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
72	d3saka_	Alignment	not modelled	43.3	42	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
73	c2cs1A_	Alignment	not modelled	42.3	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
74	c2da7A_	Alignment	not modelled	39.7	17	**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)
75	c2co9A_	Alignment	not modelled	39.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
76	c2crjA_	Alignment	not modelled	39.6	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg

						domain2 protein hmgx2
77	c3m1gC_	Alignment	not modelled	37.8	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative glutathione s-transferase; **PDBTitle:** the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
78	d2ecca1	Alignment	not modelled	37.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
79	c1mszA_	Alignment	not modelled	37.0	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
80	d1msza_	Alignment	not modelled	37.0	25	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
81	d2o70a1	Alignment	not modelled	35.3	23	**Fold:**UraD-like **Superfamily:**UraD-Like **Family:**UraD-like
82	d1o4xa1	Alignment	not modelled	35.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
83	c3nv4A_	Alignment	not modelled	33.8	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin 9 short isoform variant; **PDBTitle:** crystal structure of human galectin-9 c-terminal crd in complex with2 sialyllactose
84	c2e6oA_	Alignment	not modelled	32.8	11	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1
85	d3c7bb2	Alignment	not modelled	32.2	21	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
86	c3pihA_	Alignment	not modelled	31.3	28	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
87	d1wgfa_	Alignment	not modelled	31.1	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
88	c2jucA_	Alignment	not modelled	29.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor urn1; **PDBTitle:** urn1 ff domain yeast
89	c3u2bC_	Alignment	not modelled	29.3	20	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription factor sox-4; **PDBTitle:** structure of the sox4 hmg domain bound to dna
90	c2j11D_	Alignment	not modelled	29.2	42	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant y327s t329g q331g
91	d1aiea_	Alignment	not modelled	28.8	42	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
92	c2ww9K_	Alignment	not modelled	28.7	47	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l25; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
93	c3c4rC_	Alignment	not modelled	28.5	28	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein encoded by2 cryptic prophage
94	c2j10B_	Alignment	not modelled	28.1	42	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
95	c2j10A_	Alignment	not modelled	28.1	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
96	c2j10D_	Alignment	not modelled	28.1	42	**PDB header:**transcription **Chain:** D: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53 tetramerization domain mutant t329f q331k
97	d1vqos1	Alignment	not modelled	27.8	24	**Fold:**Ribosomal proteins S24e, L23 and L15e **Superfamily:**Ribosomal proteins S24e, L23 and L15e **Family:**L23p
98	d1le8a_	Alignment	not modelled	27.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
99	d1mh3a1	Alignment	not modelled	27.5	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
100	c3narA_	Alignment	not modelled	27.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc fingers and homeoboxes protein 1; **PDBTitle:** crystal structure of zhx1 hd4 (zinc-fingers and homeoboxes protein 1,2 homeodomain 4)
101	d2cqna1	Alignment	not modelled	27.1	16	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
102	c2yroA_	Alignment	not modelled	26.9	9	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-8; **PDBTitle:** solution structure of the c-terminal gal-bind lectin2 protein from human galectin-8
103	c2bl0B_	Alignment	not modelled	26.9	21	**PDB header:**muscle protein **Chain:** B: **PDB Molecule:**myosin regulatory light chain; **PDBTitle:** physarum polycephalum myosin ii regulatory domain

104	d1uzca_	Alignment	not modelled	26.6	23	**Fold:**Another 3-helical bundle **Superfamily:**FF domain **Family:**FF domain
105	c2da2A_	Alignment	not modelled	26.6	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
106	d2j0td1	Alignment	not modelled	26.4	16	**Fold:**OB-fold **Superfamily:**TIMP-like **Family:**Tissue inhibitor of metalloproteinases, TIMP
107	c3fn2A_	Alignment	not modelled	26.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative sensor histidine kinase domain; **PDBTitle:** crystal structure of a putative sensor histidine kinase domain from2 clostridium symbiosum atcc 14940
108	c1x50A_	Alignment	not modelled	25.9	14	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-4; **PDBTitle:** solution structure of the c-terminal gal-bind lectin domain2 from human galectin-4
109	d1e3oc1	Alignment	not modelled	25.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
110	c2go54_	Alignment	not modelled	24.8	29	**PDB header:**translation/rna **Chain:** 4: **PDB Molecule:**ribosomal protein l23; **PDBTitle:** structure of signal recognition particle receptor (sr) in2 complex with signal recognition particle (srp) and3 ribosome nascent chain complex
111	d2fiya1	Alignment	not modelled	24.6	18	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
112	c2da3A_	Alignment	not modelled	24.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the third homeobox domain of at-2 binding transcription factor 1 (atbf1)
113	c2dycA_	Alignment	not modelled	24.1	19	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-4; **PDBTitle:** crystal structure of the n-terminal domain of mouse galectin-4
114	d1h8ba_	Alignment	not modelled	24.1	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
115	d1gefa_	Alignment	not modelled	23.9	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
116	d1cf7a_	Alignment	not modelled	23.9	44	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
117	d1gyxa_	Alignment	not modelled	22.7	24	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
118	c2zkrs_	Alignment	not modelled	22.6	35	**PDB header:**ribosomal protein/rna **Chain:** S: **PDB Molecule:**rna expansion segment es39 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
119	c3c7bE_	Alignment	not modelled	22.5	21	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
120	d1hcza1	Alignment	not modelled	22.3	22	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain