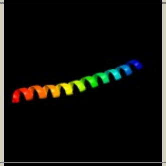
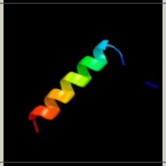
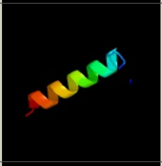
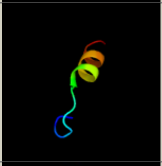
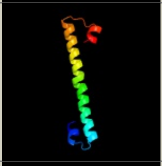
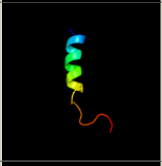
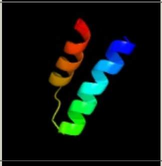
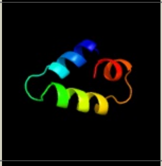
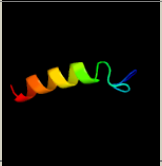
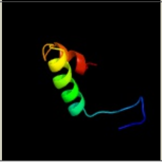
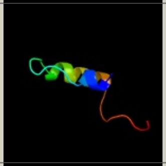
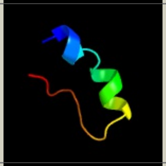
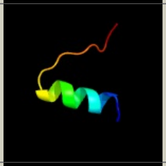
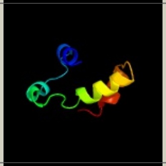
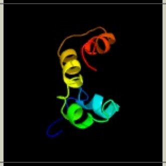
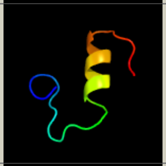
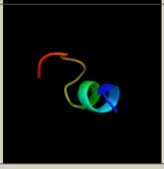
Email	l.a.kelley@imperial.ac.uk
Description	bad_result
Date	Sun Sep 7 16:40:49 BST 2014
Unique Job ID	d4c0b42a3223e636

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dmwA_	Alignment		41.2	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**synaptobrevin-like 1 variant; **PDBTitle:** solution structure of the longin domain of synaptobrevin-2 like protein 1
2	c3htkB_	Alignment		38.7	18	**PDB header:**recombination/replication/ligase **Chain:** B: **PDB Molecule:**structural maintenance of chromosomes protein 5; **PDBTitle:** crystal structure of mms21 and smc5 complex
3	c4bh6L_	Alignment		35.3	41	**PDB header:**cell cycle **Chain:** L: **PDB Molecule:**apc/c-cdh1 modulator 1; **PDBTitle:** insights into degron recognition by apc coactivators from2 the structure of an acm1-cdh1 complex
4	c4bh6I_	Alignment		33.2	41	**PDB header:**cell cycle **Chain:** I: **PDB Molecule:**apc/c-cdh1 modulator 1; **PDBTitle:** insights into degron recognition by apc coactivators from2 the structure of an acm1-cdh1 complex
5	c2laiA_	Alignment		31.0	39	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**avirulence protein atr13; **PDBTitle:** hyaloperonospora arabidopsidis effector protein atr13
6	c2qr4B_	Alignment		28.5	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium
7	c2rrfA_	Alignment		27.3	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 21; **PDBTitle:** the solution structure of the c-terminal region of zinc finger fyve2 domain-containing protein 21
8	c3aqpB_	Alignment		26.7	14	**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
9	d1j2za_	Alignment		25.5	14	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**UDP N-acetylglucosamine acyltransferase
10	c1yx5A_	Alignment		18.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**26s proteasome non-atpase regulatory subunit 4; **PDBTitle:** solution structure of s5a uim-1/ubiquitin complex
11	c4g4sO_	Alignment		17.7	10	**PDB header:**hydrolase/chaperone **Chain:** O: **PDB Molecule:**proteasome chaperone 1; **PDBTitle:** structure of proteasome-pba1-pba2 complex

12	d1oaia_	Alignment		17.6	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
13	d1hh4e_	Alignment		17.5	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
14	d2i4ra1	Alignment		16.8	35	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
15	c4ljoA_	Alignment		16.3	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rnf31; **PDBTitle:** structure of an active ligase (hoip)/ubiquitin transfer complex
16	d1t3qa1	Alignment		16.3	20	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
17	d2ebfx1	Alignment		15.8	20	**Fold:**PMT central region-like **Superfamily:**PMT central region-like **Family:**PMT central region-like
18	d1v97a1	Alignment		15.3	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
19	d1su3a1	Alignment		15.1	22	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
20	d1go5a_	Alignment		14.8	13	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**TAP-C domain-like
21	c4b19A_	Alignment	not modelled	14.8	26	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pepa1; **PDBTitle:** s. aureus pepa1 nmr structure
22	d1ds6b_	Alignment	not modelled	14.5	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
23	d1rm6c1	Alignment	not modelled	13.7	17	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
24	c4pasA_	Alignment	not modelled	13.7	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**gamma-aminobutyric acid type b receptor subunit 1; **PDBTitle:** heterodimeric coiled-coil structure of human gaba(b) receptor
25	c2hjmB_	Alignment	not modelled	13.4	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein pf1176; **PDBTitle:** crystal structure of a singleton protein pf1176 from p. furiosus
26	d2g7la1	Alignment	not modelled	13.0	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
27	c2j0fC_	Alignment	not modelled	12.4	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
28	c4mlcA_	Alignment	not modelled	12.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor; **PDBTitle:** abc transporter substrate-binding protein fromdesulfitobacterium2 hafniense

29	c2jp7A_	Alignment	not modelled	12.1	32	**PDB header:**translation **Chain:** A: **PDB Molecule:**mrna export factor mex67; **PDBTitle:** nmr structure of the mex67 uba domain
30	d1mwca_	Alignment	not modelled	12.1	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
31	d1ha7a_	Alignment	not modelled	11.8	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
32	d1cpca_	Alignment	not modelled	11.6	5	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
33	d1slma1	Alignment	not modelled	11.5	11	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**MMP N-terminal domain
34	d1jboa_	Alignment	not modelled	11.5	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
35	d1cb8a1	Alignment	not modelled	11.5	11	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
36	d1ug3a2	Alignment	not modelled	11.0	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
37	d1doab_	Alignment	not modelled	10.8	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**RhoGDI-like
38	c1zroB_	Alignment	not modelled	10.4	17	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**erythrocyte binding antigen region ii; **PDBTitle:** crystal structure of eba-175 region ii (rii) crystallized2 in the presence of (alpha)2,3-sialyllactose
39	d2q07a2	Alignment	not modelled	10.4	21	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**AF0587 domain-like
40	c2kdtA_	Alignment	not modelled	10.3	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain structure in dpc
41	d1f1sa1	Alignment	not modelled	10.3	18	**Fold:**alpha/alpha toroid **Superfamily:**Chondroitin AC/alginate lyase **Family:**Hyaluronate lyase-like catalytic, N-terminal domain
42	c2ke3A_	Alignment	not modelled	10.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**neuroendocrine convertase 1; **PDBTitle:** pc1/3 dcsg sorting domain in chaps
43	d1s29a_	Alignment	not modelled	10.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
44	d2cqka1	Alignment	not modelled	10.1	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
45	c3ctvA_	Alignment	not modelled	10.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of central domain of 3-hydroxyacyl-coa2 dehydrogenase from archaeoglobus fulgidus
46	d1outb_	Alignment	not modelled	9.5	12	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
47	d1i3da_	Alignment	not modelled	9.5	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
48	c2m5wA_	Alignment	not modelled	9.4	20	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**lupus la protein; **PDBTitle:** nmr solution structure of the la motif (n-terminal domain, ntd) of2 dictyostelium discoideum la protein
49	c2dnnA_	Alignment	not modelled	9.1	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein 12; **PDBTitle:** solution structure of rna binding domain in rna-binding2 protein 12
50	c1bm4A_	Alignment	not modelled	8.9	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (moloney murine leukemia virus capsid); **PDBTitle:** momlv capsid protein major homology region peptide analog
51	c4j5tA_	Alignment	not modelled	8.8	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannosyl-oligosaccharide glucosidase; **PDBTitle:** crystal structure of processing alpha-glucosidase i
52	d1jroa1	Alignment	not modelled	8.7	16	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
53	c4lrvL_	Alignment	not modelled	8.6	32	**PDB header:**dna binding protein **Chain:** L: **PDB Molecule:**dna sulfur modification protein dnde; **PDBTitle:** crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
54	d1dq3a2	Alignment	not modelled	8.3	24	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**PI-Pfui intein middle domain
55	c2j96B_	Alignment	not modelled	8.3	11	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycoerythrocyanin alpha chain; **PDBTitle:** the e-configuration of alfa-phycoerythrocyanin
						PDB header:hydrolase

56	c1l2aD_	Alignment	not modelled	8.2	16	**Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
57	d1l1ya_	Alignment	not modelled	8.2	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
58	d1zh5a1	Alignment	not modelled	8.1	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
59	d1k3pa_	Alignment	not modelled	8.1	21	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
60	c3tweA_	Alignment	not modelled	8.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
61	c1t3qD_	Alignment	not modelled	7.8	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
62	d1r2za1	Alignment	not modelled	7.8	43	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
63	c1rm6F_	Alignment	not modelled	7.8	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
64	c3tweB_	Alignment	not modelled	7.7	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
65	d2vkea1	Alignment	not modelled	7.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
66	c2l9vA_	Alignment	not modelled	7.7	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** nmr structure of the ff domain l24a mutant's folding transition state
67	c1x1jA_	Alignment	not modelled	7.6	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xanthan lyase; **PDBTitle:** crystal structure of xanthan lyase (n194a) with a substrate.
68	d1csha_	Alignment	not modelled	7.5	15	**Fold:**Citrate synthase **Superfamily:**Citrate synthase **Family:**Citrate synthase
69	d1t56a1	Alignment	not modelled	7.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
70	c2xv9A_	Alignment	not modelled	7.4	8	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**aba-1a1 repeat unit; **PDBTitle:** the solution structure of aba-1a saturated with oleic acid
71	c2lz4B_	Alignment	not modelled	7.4	44	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**amyloid beta a4 protein; **PDBTitle:** solution nmr structure of transmembrane domain of amyloid precursor2 protein v44m
72	c2lz4A_	Alignment	not modelled	7.4	44	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**amyloid beta a4 protein; **PDBTitle:** solution nmr structure of transmembrane domain of amyloid precursor2 protein v44m
73	c2ec5B_	Alignment	not modelled	7.4	20	**PDB header:**toxin **Chain:** B: **PDB Molecule:**dermonecrotic toxin; **PDBTitle:** crystal structures reveal a thiol-protease like catalytic triad in the2 c-terminal region of pasteurella multocida toxin
74	d1xeqa1	Alignment	not modelled	7.2	42	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
75	d1ee8a1	Alignment	not modelled	7.1	36	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
76	d1ffva1	Alignment	not modelled	7.0	7	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
77	c4j15A_	Alignment	not modelled	7.0	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartate--trna ligase, cytoplasmic; **PDBTitle:** crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
78	d1k3ra2	Alignment	not modelled	7.0	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
79	c4il3B_	Alignment	not modelled	6.9	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ste24p; **PDBTitle:** crystal structure of s. mikatae ste24p
80	d1utga_	Alignment	not modelled	6.8	21	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
81	d1fhjb_	Alignment	not modelled	6.8	16	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
82	c2ks1A_	Alignment	not modelled	6.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** heterodimeric association of transmembrane domains of

						erbb1 and erbb22 receptors enabling kinase activation
83	c2jwaA_	Alignment	not modelled	6.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** erbb2 transmembrane segment dimer spatial structure
84	c2h12C_	Alignment	not modelled	6.7	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**citrate synthase; **PDBTitle:** structure of acetobacter aceti citrate synthase complexed2 with oxaloacetate and carboxymethyldethia coenzyme a (cmx)
85	c3zvrA_	Alignment	not modelled	6.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of dynamin
86	c3hrdH_	Alignment	not modelled	6.7	20	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
87	c2cazB_	Alignment	not modelled	6.7	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein **PDBTitle:** escrt-i core
88	d2cazb1	Alignment	not modelled	6.7	15	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS28 N-terminal domain
89	c2db1A_	Alignment	not modelled	6.6	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein f; **PDBTitle:** solution structure of the rna binding domain in2 heterogeneous nuclear ribonucleoprotein f homolog
90	c4afiB_	Alignment	not modelled	6.4	10	**PDB header:**endocytosis **Chain:** B: **PDB Molecule:**ap-3 complex subunit delta-1, vesicle-associated membrane **PDBTitle:** complex between vamp7 longin domain and fragment of delta-2 adaptin from ap3
91	c2hglA_	Alignment	not modelled	6.4	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**heterogeneous nuclear ribonucleoprotein f; **PDBTitle:** nmr structure of the first qrrm domain of human hnrnp f
92	d1hdsb_	Alignment	not modelled	6.4	8	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
93	d1n9wa2	Alignment	not modelled	6.4	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
94	d2o7ta1	Alignment	not modelled	6.3	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
95	d1vi0a2	Alignment	not modelled	6.3	19	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
96	c2mfrA_	Alignment	not modelled	6.3	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**insulin receptor; **PDBTitle:** solution structure of the transmembrane domain of the insulin receptor2 in micelles
97	d3cx5d2	Alignment	not modelled	6.2	14	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
98	c2dgwA_	Alignment	not modelled	6.2	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**probable rna-binding protein 19; **PDBTitle:** solution structure of the second rna recognition motif in2 rna-binding protein 19
99	c4bh6P_	Alignment	not modelled	6.2	41	**PDB header:**cell cycle **Chain:** P: **PDB Molecule:**apc/c-cdh1 modulator 1; **PDBTitle:** insights into degron recognition by apc coactivators from2 the structure of an acm1-cdh1 complex