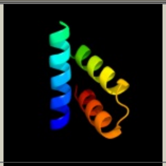
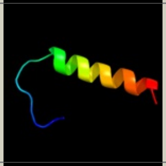
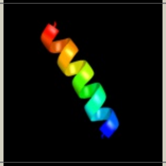
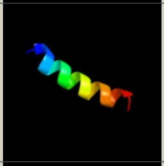
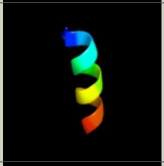
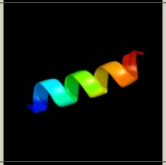
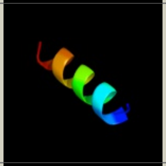
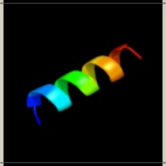
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AD07
Date	Thu Jan 5 11:19:36 GMT 2012
Unique Job ID	4cf5ea5bb7b75f03

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oxlA_	Alignment		58.9	20	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**hypothetical protein ymgb; **PDBTitle:** structure and function of the e. coli protein ymgb: a protein critical2 for biofilm formation and acid resistance
2	c2dt7A_	Alignment		39.7	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
3	c3cl3D_	Alignment		32.2	39	**PDB header:**viral protein/signaling protein **Chain:** D: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** crystal structure of a vflip-ikkgamma complex: insights2 into viral activation of the ikk signalosome
4	c2k6oA_	Alignment		16.8	32	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cathelicidin antimicrobial peptide; **PDBTitle:** human ll-37 structure
5	c2fcgF_	Alignment		15.2	38	**PDB header:**antimicrobial protein **Chain:** F: **PDB Molecule:**antibacterial protein fall-39, core peptide; **PDBTitle:** solution structure of the c-terminal fragment of human ll-37
6	c1ij2C_	Alignment		13.4	40	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
7	c1ztaA_	Alignment		13.3	47	**PDB header:**dna-binding motif **Chain:** A: **PDB Molecule:**leucine zipper monomer; **PDBTitle:** the solution structure of a leucine-zipper motif peptide
8	c1ij2B_	Alignment		12.5	40	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
9	c1ij3B_	Alignment		12.1	40	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
10	c1ij3C_	Alignment		12.1	40	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
11	c1rb6C_	Alignment		12.0	40	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form

12	c3k7zB_	Alignment		12.0	40	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
13	c3k7zA_	Alignment		12.0	40	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
14	c1rb1A_	Alignment		12.0	40	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
15	c1rb1B_	Alignment		12.0	40	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
16	c1swiA_	Alignment		11.4	40	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
17	c2l5gA_	Alignment		11.4	31	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**g protein pathway suppressor 2; **PDBTitle:** co-ordinates and 1h, 13c and 15n chemical shift assignments for the2 complex of gps2 53-90 and smrt 167-207
18	d1gh6a_	Alignment		9.7	20	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
19	c2l6lA_	Alignment		9.5	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 24; **PDBTitle:** solution structure of human j-protein co-chaperone, dph4
20	c1ce0B_	Alignment		9.5	33	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
21	c2ovcA_	Alignment	not modelled	9.4	64	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily kqt member 4; **PDBTitle:** crystal structure of a coiled-coil tetramerization domain from kv7.42 channels
22	d2bcgg2	Alignment	not modelled	8.9	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
23	c2khfA_	Alignment	not modelled	8.7	20	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in dpc-micelles
24	c2w0cR_	Alignment	not modelled	8.4	71	**PDB header:**virus **Chain:** R: **PDB Molecule:**protein p3; **PDBTitle:** x-ray structure of the entire lipid-containing2 bacteriophage pm2
25	c2voiB_	Alignment	not modelled	8.2	33	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**bh3-interacting domain death agonist p13; **PDBTitle:** structure of mouse a1 bound to the bid bh3-domain
26	d1nz6a_	Alignment	not modelled	8.2	45	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
27	c2o37A_	Alignment	not modelled	8.1	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein sis1; **PDBTitle:** j-domain of sis1 protein, hsp40 co-chaperone from2 saccharomyces cerevisiae.
28	c2g7rA_	Alignment	not modelled	7.7	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mucosa-associated lymphoid tissue lymphoma translocation **PDBTitle:** x-ray structure of the death domain of the human mucosa

						associated2 lymphoid tissue lymphoma translocation protein 1
29	c3ag7A_	Alignment	not modelled	7.2	11	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein f9e10.5; **PDBTitle:** an auxilin-like j-domain containing protein, jac1 j-domain
30	c2ys8A_	Alignment	not modelled	7.2	27	**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
31	c2l06A_	Alignment	not modelled	7.0	86	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phycobilisome lcm core-membrane linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
32	c2guzO_	Alignment	not modelled	6.8	36	**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
33	c2ochA_	Alignment	not modelled	6.8	36	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hypothetical protein dnj-12; **PDBTitle:** j-domain of dnj-12 from caenorhabditis elegans
34	c2ctrA_	Alignment	not modelled	6.6	36	**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
35	c2ky4A_	Alignment	not modelled	6.4	56	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
36	d1fd3a_	Alignment	not modelled	6.4	67	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
37	c2xzrA_	Alignment	not modelled	6.3	24	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**immunoglobulin-binding protein eibd; **PDBTitle:** escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
38	c2dn9A_	Alignment	not modelled	6.3	55	**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
39	c2khgA_	Alignment	not modelled	6.3	20	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**plnj; **PDBTitle:** plantaricin j in tfe
40	d1xbla_	Alignment	not modelled	6.1	27	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
41	c1bq0A_	Alignment	not modelled	6.1	27	**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
42	c2d96A_	Alignment	not modelled	6.0	29	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p100 subunit; **PDBTitle:** solution structure of the death domain of nuclear factor nf-2 kappa-b p100
43	d1fafa_	Alignment	not modelled	6.0	36	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
44	d1ni7a_	Alignment	not modelled	5.8	20	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SufE-like
45	d1qmga2	Alignment	not modelled	5.8	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
46	c2ctqA_	Alignment	not modelled	5.7	27	**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
47	c2pjwV_	Alignment	not modelled	5.7	22	**PDB header:**endocytosis/exocytosis **Chain:** V: **PDB Molecule:**vacuolar protein sorting-associated protein 27; **PDBTitle:** the vps27/hse1 complex is a gat domain-based scaffold for2 ubiquitin-dependent sorting
48	d1e3ha6	Alignment	not modelled	5.6	17	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
49	c2a3dA_	Alignment	not modelled	5.4	35	**PDB header:**three-helix bundle **Chain:** A: **PDB Molecule:**protein (de novo three-helix bundle); **PDBTitle:** solution structure of a de novo designed single chain three-2 helix bundle (a3d)
50	c2o7hF_	Alignment	not modelled	5.4	33	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
51	c2cugA_	Alignment	not modelled	5.3	36	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**mkiaa0962 protein; **PDBTitle:** solution structure of the j domain of the pseudo dnaj2 protein, mouse hypothetical mkiaa0962