




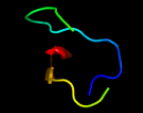







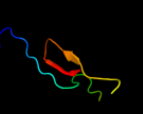






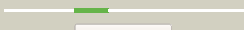
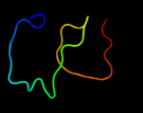


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A0PK84
Date	Wed Jul 10 14:28:08 BST 2013
Unique Job ID	8b671c3d7f6075cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ky9B_</a>	 Alignment		84.8	7	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> autoinhibited vav1
2	<a href="#">c2vrwB_</a>	 Alignment		81.3	7	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> critical structural role for the ph and c1 domains of the2 vav1 exchange factor
3	<a href="#">c3bjjA_</a>	 Alignment		72.9	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> proto-oncogene vav; <b>PDBTitle:</b> structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
4	<a href="#">c1jocA_</a>	 Alignment		68.4	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> early endosomal autoantigen 1; <b>PDBTitle:</b> eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
5	<a href="#">c3zyqA_</a>	 Alignment		61.3	15	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine kinase <b>PDBTitle:</b> crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
6	<a href="#">c3okyA_</a>	 Alignment		58.8	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> plexin-a2; <b>PDBTitle:</b> plexin a2 in complex with semaphorin 6a
7	<a href="#">c1dvpA_</a>	 Alignment		58.1	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte growth factor-regulated tyrosine <b>PDBTitle:</b> crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
8	<a href="#">c1x4uA_</a>	 Alignment		53.6	10	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger, fyve domain containing 27 isoform b; <b>PDBTitle:</b> solution structure of the fyve domain from human fyve2 domain containing 27 isoform b protein
9	<a href="#">d2pg3a1</a>	 Alignment		53.5	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
10	<a href="#">c2yqmA_</a>	 Alignment		53.5	17	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> run and fyve domain-containing protein 1; <b>PDBTitle:</b> solution structure of the fyve domain in zinc finger fyve2 domain-containing protein 12
11	<a href="#">c2k2cA_</a>	 Alignment		50.8	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger and chy zinc finger domain- <b>PDBTitle:</b> solution nmr structure of n-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2a

12	<a href="#">c3a19B_</a>	Alignment		50.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> plexin-a2; <b>PDBTitle:</b> mouse plexin a2 extracellular domain
13	<a href="#">c3a18B_</a>	Alignment		49.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> plexin-a2; <b>PDBTitle:</b> plexin a2 / semaphorin 6a complex
14	<a href="#">c2a20A_</a>	Alignment		47.6	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> regulating synaptic membrane exocytosis protein <b>PDBTitle:</b> solution structure of rim2 zinc finger domain
15	<a href="#">d2dkta2</a>	Alignment		45.0	17	<b>Fold:</b> Zinc hairpin stack <b>Superfamily:</b> Zinc hairpin stack <b>Family:</b> Zinc hairpin stack
16	<a href="#">c1z2qA_</a>	Alignment		44.7	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lm5-1; <b>PDBTitle:</b> high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
17	<a href="#">d1olza3</a>	Alignment		44.5	25	<b>Fold:</b> Trefoil/Plexin domain-like <b>Superfamily:</b> Plexin repeat <b>Family:</b> Plexin repeat
18	<a href="#">c3ol2B_</a>	Alignment		43.1	18	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> plexin-b1; <b>PDBTitle:</b> receptor-ligand structure of human semaphorin 4d with plexin b1.
19	<a href="#">d1joca1</a>	Alignment		43.0	13	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
20	<a href="#">c3nvnB_</a>	Alignment		42.9	19	<b>PDB header:</b> viral protein/signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> plexin-c1; <b>PDBTitle:</b> molecular mechanism of guidance cue recognition
21	<a href="#">c3nvgE_</a>	Alignment	not modelled	42.8	15	<b>PDB header:</b> signaling protein/protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> semaphorin-7a; <b>PDBTitle:</b> molecular mechanism of guidance cue recognition
22	<a href="#">d1wfkA_</a>	Alignment	not modelled	42.8	10	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
23	<a href="#">c4gz8A_</a>	Alignment	not modelled	42.1	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> semaphorin-3a; <b>PDBTitle:</b> mouse semaphorin 3a, domains sema-psi-ig
24	<a href="#">c2uzxB_</a>	Alignment	not modelled	41.6	12	<b>PDB header:</b> signaling protein/receptor <b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte growth factor receptor; <b>PDBTitle:</b> structure of the human receptor tyrosine kinase met in2 complex with the listeria monocytogenes invasion protein3 inlb: crystal form i
25	<a href="#">c2cszA_</a>	Alignment	not modelled	40.6	15	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> synaptotagmin-like protein 4; <b>PDBTitle:</b> solution structure of the ring domain of the synaptotagmin-2 like protein 4
26	<a href="#">c1olzB_</a>	Alignment	not modelled	40.3	18	<b>PDB header:</b> developmental protein <b>Chain:</b> B: <b>PDB Molecule:</b> semaphorin 4d; <b>PDBTitle:</b> the ligand-binding face of the semaphorins revealed by the2 high resolution crystal structure of sema4d
27	<a href="#">c3okyB_</a>	Alignment	not modelled	40.3	19	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> plexin a2 in complex with semaphorin 6a
28	<a href="#">d2ayja1</a>	Alignment	not modelled	39.3	17	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L40e <b>PDB header:</b> signaling protein/receptor

29	<a href="#">c2uzyB_</a>	Alignment	not modelled	38.7	12	<b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte growth factor receptor; <b>PDBTitle:</b> structure of the human receptor tyrosine kinase met in2 complex with the listeria monocytogenes invasion protein3 inlb: low resolution, crystal form ii
30	<a href="#">c3oktA_</a>	Alignment	not modelled	38.4	23	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> plexin-a2; <b>PDBTitle:</b> mouse plexin a2, extracellular domains 1-4
31	<a href="#">d2mda2</a>	Alignment	not modelled	38.3	43	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
32	<a href="#">c3t7IA_</a>	Alignment	not modelled	38.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger fyve domain-containing protein 16; <b>PDBTitle:</b> crystal structure of the fyve domain of endofin (zfyve16) at 1.1a2 resolution
33	<a href="#">c4fwwA_</a>	Alignment	not modelled	37.5	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> macrophage-stimulating protein receptor; <b>PDBTitle:</b> crystal structure of the sema-psi extracellular domains of human ron2 receptor tyrosine kinase
34	<a href="#">c3l0aA_</a>	Alignment	not modelled	37.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative exonuclease; <b>PDBTitle:</b> crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
35	<a href="#">d1njqa_</a>	Alignment	not modelled	36.8	42	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Plant C2H2 finger (QALGGH zinc finger)
36	<a href="#">d1dvpa2</a>	Alignment	not modelled	35.9	22	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
37	<a href="#">c1shyB_</a>	Alignment	not modelled	34.0	13	<b>PDB header:</b> growth factor/growth factor receptor <b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte growth factor receptor; <b>PDBTitle:</b> the crystal structure of hgf beta-chain in complex with the sema2 domain of the met receptor.
38	<a href="#">c2yw8A_</a>	Alignment	not modelled	32.8	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> run and fyve domain-containing protein 1; <b>PDBTitle:</b> crystal structure of human run and fyve domain-containing2 protein
39	<a href="#">d2adra2</a>	Alignment	not modelled	31.6	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
40	<a href="#">c1y02A_</a>	Alignment	not modelled	30.9	9	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fyve-ring finger protein sakura; <b>PDBTitle:</b> crystal structure of a fyve-type domain from caspase2 regulator carp2
41	<a href="#">d1paaa_</a>	Alignment	not modelled	30.2	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
42	<a href="#">c2gb5B_</a>	Alignment	not modelled	30.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh pyrophosphatase; <b>PDBTitle:</b> crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
43	<a href="#">d1wfla_</a>	Alignment	not modelled	28.8	14	<b>Fold:</b> AN1-like Zinc finger <b>Superfamily:</b> AN1-like Zinc finger <b>Family:</b> AN1-like Zinc finger
44	<a href="#">d1vfya_</a>	Alignment	not modelled	28.1	19	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
45	<a href="#">c3bl5E_</a>	Alignment	not modelled	26.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> queuosine biosynthesis protein quec; <b>PDBTitle:</b> crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
46	<a href="#">c3izbP_</a>	Alignment	not modelled	25.1	56	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein rps11 (s17p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
47	<a href="#">d1zbdb_</a>	Alignment	not modelled	24.9	10	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger <b>Family:</b> FYVE, a phosphatidylinositol-3-phosphate binding domain
48	<a href="#">d2fiya1</a>	Alignment	not modelled	24.6	7	<b>Fold:</b> FdhE-like <b>Superfamily:</b> FdhE-like <b>Family:</b> FdhE-like
49	<a href="#">c3goxB_</a>	Alignment	not modelled	24.1	13	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> restriction endonuclease hpy99i; <b>PDBTitle:</b> crystal structure of the beta-beta-alpha-me type ii restriction2 endonuclease hpy99i in the absence of edta
50	<a href="#">c2cr8A_</a>	Alignment	not modelled	23.1	22	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> mdm4 protein; <b>PDBTitle:</b> solution structure of the zf-ranbp domain of p53-binding2 protein mdm4
51	<a href="#">c3iz6P_</a>	Alignment	not modelled	22.6	56	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 40s ribosomal protein s11 (s17p); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
52	<a href="#">c2ysmA_</a>	Alignment	not modelled	22.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> myeloid/lymphoid or mixed-lineage leukemia <b>PDBTitle:</b> solution structure of the first and second phd domain from2 myeloid/lymphoid or mixed-lineage leukemia protein 33 homolog
53	<a href="#">c2c6bA_</a>	Alignment	not modelled	21.5	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin-protein ligase e3 mdm2; <b>PDBTitle:</b> solution structure of the c4 zinc-finger domain of hdm2
54	<a href="#">d1wila_</a>	Alignment	not modelled	20.9	24	<b>Fold:</b> FYVE/PHD zinc finger <b>Superfamily:</b> FYVE/PHD zinc finger

						<b>Family:</b> variant PHD-like domain
55	<a href="#">c3swrA_</a>	Alignment	not modelled	20.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1; <b>PDBTitle:</b> structure of human dnmt1 (601-1600) in complex with sinefungin
56	<a href="#">c3iz5p_</a>	Alignment	not modelled	20.4	20	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l15 (l15e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
57	<a href="#">d1shyb2</a>	Alignment	not modelled	19.2	12	<b>Fold:</b> Trefoil/Plexin domain-like <b>Superfamily:</b> Plexin repeat <b>Family:</b> Plexin repeat
58	<a href="#">c3j21g_</a>	Alignment	not modelled	18.1	17	<b>PDB header:</b> ribosome <b>Chain:</b> G: <b>PDB Molecule:</b> 50s ribosomal protein l7ae; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
59	<a href="#">d2it8a1</a>	Alignment	not modelled	17.6	47	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
60	<a href="#">c2it8A_</a>	Alignment	not modelled	17.6	47	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin inhibitor 2; <b>PDBTitle:</b> solution structure of a linear analog of the cyclic squash2 trypsin inhibitor mcoi-ii
61	<a href="#">c2kfqA_</a>	Alignment	not modelled	17.5	31	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> fp1; <b>PDBTitle:</b> nmr structure of fp1
62	<a href="#">c3cezA_</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine-r-sulfoxide reductase; <b>PDBTitle:</b> crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
63	<a href="#">d1lpva_</a>	Alignment	not modelled	17.2	29	<b>Fold:</b> Cysteine-rich DNA binding domain, (DM domain) <b>Superfamily:</b> Cysteine-rich DNA binding domain, (DM domain) <b>Family:</b> Cysteine-rich DNA binding domain, (DM domain)
64	<a href="#">c1lpvA_</a>	Alignment	not modelled	17.2	29	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> doublesex protein; <b>PDBTitle:</b> drosophila melanogaster doublesex (dsx), nmr, 18 structures
65	<a href="#">c2zetD_</a>	Alignment	not modelled	17.0	23	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> melanophilin; <b>PDBTitle:</b> crystal structure of the small gtpase rab27b complexed with2 the slp homology domain of slac2-a/melanophilin
66	<a href="#">d2epra1</a>	Alignment	not modelled	16.8	15	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
67	<a href="#">c3j3aL_</a>	Alignment	not modelled	16.6	67	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 40s ribosomal protein s11; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
68	<a href="#">c3j20R_</a>	Alignment	not modelled	16.4	44	<b>PDB header:</b> ribosome <b>Chain:</b> R: <b>PDB Molecule:</b> 30s ribosomal protein s17p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
69	<a href="#">c4a1dK_</a>	Alignment	not modelled	16.4	26	<b>PDB header:</b> ribosome <b>Chain:</b> K: <b>PDB Molecule:</b> ubiquitin-60s ribosomal protein l40; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
70	<a href="#">c2xzn5_</a>	Alignment	not modelled	16.4	29	<b>PDB header:</b> ribosome <b>Chain:</b> 5: <b>PDB Molecule:</b> ribosomal protein s26e containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
71	<a href="#">c1nj3A_</a>	Alignment	not modelled	16.0	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> npl4; <b>PDBTitle:</b> structure and ubiquitin interactions of the conserved nzf2 domain of npl4
72	<a href="#">c3zeyV_</a>	Alignment	not modelled	16.0	29	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> ribosomal protein s26, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
73	<a href="#">c3j38a_</a>	Alignment	not modelled	15.8	21	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein sa; <b>PDBTitle:</b> structure of the d. melanogaster 40s ribosomal proteins
74	<a href="#">d2yt9a1</a>	Alignment	not modelled	15.7	38	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
75	<a href="#">c3u5ga_</a>	Alignment	not modelled	15.6	27	<b>PDB header:</b> ribosome <b>Chain:</b> A: <b>PDB Molecule:</b> 40s ribosomal protein s0-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
76	<a href="#">d1ha9a_</a>	Alignment	not modelled	15.2	47	<b>Fold:</b> Knottins (small inhibitors, toxins, lectins) <b>Superfamily:</b> Plant inhibitors of proteinases and amylases <b>Family:</b> Plant inhibitors of proteinases and amylases
77	<a href="#">c3j39m_</a>	Alignment	not modelled	15.0	21	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l14; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
78	<a href="#">c2po8A_</a>	Alignment	not modelled	14.9	47	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> mcoi-ii; <b>PDBTitle:</b> the structure of a two-disulfide intermediate of mcoi-ii
79	<a href="#">c3zeyE_</a>	Alignment	not modelled	14.7	56	<b>PDB header:</b> ribosome <b>Chain:</b> E: <b>PDB Molecule:</b> 40s ribosomal proteins s11, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome

80	<a href="#">d1fcda3</a>	Alignment	not modelled	14.5	27	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
81	<a href="#">c2eluA</a>	Alignment	not modelled	14.5	43	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 406; <b>PDBTitle:</b> solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406
82	<a href="#">d1zu1a2</a>	Alignment	not modelled	14.4	27	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
83	<a href="#">d1llmc2</a>	Alignment	not modelled	13.6	28	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
84	<a href="#">c3hcjB</a>	Alignment	not modelled	13.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase; <b>PDBTitle:</b> structure of msrb from xanthomonas campestris (oxidized2 form)
85	<a href="#">c3bvoA</a>	Alignment	not modelled	13.0	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> co-chaperone protein hscb, mitochondrial precursor; <b>PDBTitle:</b> crystal structure of human co-chaperone protein hscb
86	<a href="#">c2xznQ</a>	Alignment	not modelled	12.9	56	<b>PDB header:</b> ribosome <b>Chain:</b> Q: <b>PDB Molecule:</b> ribosomal protein s17 containing protein; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
87	<a href="#">c2k8dA</a>	Alignment	not modelled	12.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peptide methionine sulfoxide reductase msrb; <b>PDBTitle:</b> solution structure of a zinc-binding methionine sulfoxide reductase
88	<a href="#">d2dlqa2</a>	Alignment	not modelled	12.4	30	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
89	<a href="#">c3eh2B</a>	Alignment	not modelled	12.4	17	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> protein transport protein sec24c; <b>PDBTitle:</b> crystal structure of the human copii-coat protein sec24c
90	<a href="#">c2k85A</a>	Alignment	not modelled	12.1	4	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> glucocorticoid receptor dna-binding factor 1; <b>PDBTitle:</b> p190-a rhogap ff1 domain
91	<a href="#">d1wg2a</a>	Alignment	not modelled	12.1	8	<b>Fold:</b> AN1-like Zinc finger <b>Superfamily:</b> AN1-like Zinc finger <b>Family:</b> AN1-like Zinc finger
92	<a href="#">c3u5gL</a>	Alignment	not modelled	11.8	56	<b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 40s ribosomal protein s11-a; <b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
93	<a href="#">d1u85a1</a>	Alignment	not modelled	11.8	28	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
94	<a href="#">c2ljsA</a>	Alignment	not modelled	11.6	47	<b>PDB header:</b> hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> trypsin inhibitor 3; <b>PDBTitle:</b> solution structure of mcoti-v
95	<a href="#">c1d4uA</a>	Alignment	not modelled	11.4	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleotide excision repair protein xpa (xpa-mbd); <b>PDBTitle:</b> interactions of human nucleotide excision repair protein2 xpa with rpa70 and dna: chemical shift mapping and 15n nmr3 relaxation studies
96	<a href="#">d1xm0a1</a>	Alignment	not modelled	11.3	11	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SeIR domain
97	<a href="#">d1l1da</a>	Alignment	not modelled	11.1	17	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> SeIR domain
98	<a href="#">c2voyK</a>	Alignment	not modelled	10.8	15	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
99	<a href="#">c3pt6B</a>	Alignment	not modelled	10.7	17	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna (cytosine-5)-methyltransferase 1; <b>PDBTitle:</b> crystal structure of mouse dnmt1(650-1602) in complex with dna