


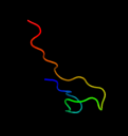

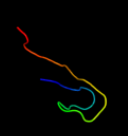













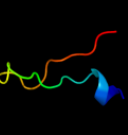


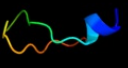


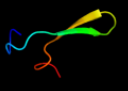

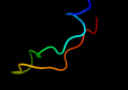

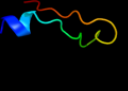



# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q9DB75
Date	Tue Jul 30 13:11:58 BST 2013
Unique Job ID	b5a3457121c54f90

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2joxA_</a>	 Alignment		72.5	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> churchill protein; <b>PDBTitle:</b> embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
2	<a href="#">c1hk8A_</a>	 Alignment		59.7	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic ribonucleotide-triphosphate reductase; <b>PDBTitle:</b> structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dntp
3	<a href="#">d1hk8a_</a>	 Alignment		59.7	32	<b>Fold:</b> PFL-like glycy radical enzymes <b>Superfamily:</b> PFL-like glycy radical enzymes <b>Family:</b> Class III anaerobic ribonucleotide reductase NRDD subunit
4	<a href="#">d2ct1a1</a>	 Alignment		57.4	28	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> Classic zinc finger, C2H2
5	<a href="#">c2opfA_</a>	 Alignment		54.4	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> endonuclease viii; <b>PDBTitle:</b> crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
6	<a href="#">c3eb6A_</a>	 Alignment		53.6	23	<b>PDB header:</b> apoptosis, ligase <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 3; <b>PDBTitle:</b> structure of the ciap2 ring domain bound to ubch5b
7	<a href="#">c1k82D_</a>	 Alignment		46.7	23	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> D: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
8	<a href="#">c4a17Y_</a>	 Alignment		46.5	20	<b>PDB header:</b> ribosome <b>Chain:</b> Y: <b>PDB Molecule:</b> rpl37a; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
9	<a href="#">c3fl2A_</a>	 Alignment		45.3	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase uhrf1; <b>PDBTitle:</b> crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
10	<a href="#">c3zf7o_</a>	 Alignment		44.4	17	<b>PDB header:</b> ribosome <b>Chain:</b> O: <b>PDB Molecule:</b> 60s ribosomal protein l13a, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
11	<a href="#">c2yhoE_</a>	 Alignment		43.3	12	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase mylip; <b>PDBTitle:</b> the idol-ube2d complex mediates sterol-dependent degradation of the2 ldl receptor

12	<a href="#">c3cc4Z_</a>	Alignment		43.1	26	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> co-crystal structure of anisomycin bound to the 50s ribosomal subunit
13	<a href="#">c2kdxA_</a>	Alignment		42.8	27	<b>PDB header:</b> metal-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hydrogenase/urease nickel incorporation protein <b>PDBTitle:</b> solution structure of hypa protein
14	<a href="#">d2cona1</a>	Alignment		40.1	18	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> NOB1 zinc finger-like <b>Family:</b> NOB1 zinc finger-like
15	<a href="#">c2f5qA_</a>	Alignment		39.7	46	<b>PDB header:</b> hydrolase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosidase; <b>PDBTitle:</b> catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
16	<a href="#">c2ea5A_</a>	Alignment		39.1	23	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell growth regulator with ring finger domain <b>PDBTitle:</b> solution structure of the ring domain of the human cell2 growth regulator with ring finger domain 1 protein
17	<a href="#">c2qa4Z_</a>	Alignment		38.9	26	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 50s ribosomal protein l37ae; <b>PDBTitle:</b> a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
18	<a href="#">c1z6uA_</a>	Alignment		35.8	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> np95-like ring finger protein isoform b; <b>PDBTitle:</b> np95-like ring finger protein isoform b [homo sapiens]
19	<a href="#">d1ffkw_</a>	Alignment		35.7	22	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
20	<a href="#">c2djba_</a>	Alignment		35.1	19	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> polycomb group ring finger protein 6; <b>PDBTitle:</b> solution structure of the ring domain of the human polycomb2 group ring finger protein 6
21	<a href="#">d1v87a_</a>	Alignment	not modelled	34.9	36	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
22	<a href="#">d1x63a2</a>	Alignment	not modelled	34.3	50	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
23	<a href="#">d1fbva4</a>	Alignment	not modelled	34.2	20	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
24	<a href="#">c2lo2A_</a>	Alignment	not modelled	34.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> saga-associated factor 11; <b>PDBTitle:</b> solution structure of sgf11(63-99) zinc finger domain
25	<a href="#">c2eclA_</a>	Alignment	not modelled	34.1	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring-box protein 2; <b>PDBTitle:</b> solution structure of the ring domain of the human ring-box2 protein 2
26	<a href="#">c2ecgA_</a>	Alignment	not modelled	33.6	15	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> baculoviral iap repeat-containing protein 4; <b>PDBTitle:</b> solution structure of the ring domain of the baculoviral2 iap repeat-containing protein 4 from homo sapiens
27	<a href="#">c2bi6H_</a>	Alignment	not modelled	33.4	26	<b>PDB header:</b> cysteine protease inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> bromelain inhibitor vi; <b>PDBTitle:</b> nmr study of bromelain inhibitor vi from pineapple stem
28	<a href="#">c3twkB_</a>	Alignment	not modelled	33.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase 1; <b>PDBTitle:</b> crystal structure of arabidopsis thaliana fpg
						<b>PDB header:</b> immune system, membrane protein

29	<a href="#">c2kluA_</a>	Alignment	not modelled	33.1	13	<b>Chain:</b> A: <b>PDB Molecule:</b> t-cell surface glycoprotein cd4; <b>PDBTitle:</b> nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
30	<a href="#">c1bi6H_</a>	Alignment	not modelled	32.2	26	<b>PDB header:</b> cysteine protease inhibitor <b>Chain:</b> H: <b>PDB Molecule:</b> bromelain inhibitor vi; <b>PDBTitle:</b> nmr structure of bromelain inhibitor vi from pineapple stem
31	<a href="#">d1iyma_</a>	Alignment	not modelled	32.1	21	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
32	<a href="#">d1lv3a_</a>	Alignment	not modelled	31.8	18	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Hypothetical zinc finger protein YacG
33	<a href="#">c2d8tA_</a>	Alignment	not modelled	31.6	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger protein 146; <b>PDBTitle:</b> solution structure of the ring domain of the human ring2 finger protein 146
34	<a href="#">c2jvxA_</a>	Alignment	not modelled	31.3	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> solution structure of human nemo zinc finger
35	<a href="#">d1jj2y_</a>	Alignment	not modelled	30.1	26	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
36	<a href="#">c1nnjA_</a>	Alignment	not modelled	29.9	46	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> formamidopyrimidine-dna glycosylase; <b>PDBTitle:</b> crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
37	<a href="#">c2jmdA_</a>	Alignment	not modelled	29.8	30	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 6; <b>PDBTitle:</b> solution structure of the ring domain of human traf6
38	<a href="#">d1vdda_</a>	Alignment	not modelled	29.1	29	<b>Fold:</b> Recombination protein RecR <b>Superfamily:</b> Recombination protein RecR <b>Family:</b> Recombination protein RecR
39	<a href="#">d1x6ma_</a>	Alignment	not modelled	28.5	27	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> Glutathione-dependent formaldehyde-activating enzyme, Gfa
40	<a href="#">c2lqcA_</a>	Alignment	not modelled	28.4	25	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative toxin vapc6; <b>PDBTitle:</b> solution structure of the endonuclease nob1 from p.horikoshii
41	<a href="#">d1vqoz1</a>	Alignment	not modelled	28.2	27	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zn-binding ribosomal proteins <b>Family:</b> Ribosomal protein L37ae
42	<a href="#">c1yshD_</a>	Alignment	not modelled	27.9	18	<b>PDB header:</b> structural protein/rna <b>Chain:</b> D: <b>PDB Molecule:</b> ribosomal protein l37a; <b>PDBTitle:</b> localization and dynamic behavior of ribosomal protein l30e
43	<a href="#">c1vddC_</a>	Alignment	not modelled	27.7	29	<b>PDB header:</b> recombination <b>Chain:</b> C: <b>PDB Molecule:</b> recombination protein recr; <b>PDBTitle:</b> crystal structure of recombinational repair protein recr
44	<a href="#">c4epoL_</a>	Alignment	not modelled	27.7	32	<b>PDB header:</b> protein binding/ligase <b>Chain:</b> L: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf8; <b>PDBTitle:</b> crystal structure of rnf8 bound to the ubc13/mms2 heterodimer
45	<a href="#">c3vk6A_</a>	Alignment	not modelled	27.2	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase hakai; <b>PDBTitle:</b> crystal structure of a phosphotyrosine binding domain
46	<a href="#">c4b6ap_</a>	Alignment	not modelled	26.9	22	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17-a; <b>PDBTitle:</b> cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
47	<a href="#">c2h0dB_</a>	Alignment	not modelled	25.4	21	<b>PDB header:</b> metal binding protein/ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin ligase protein ring2; <b>PDBTitle:</b> structure of a bmi-1-ring1b polycomb group ubiquitin ligase complex
48	<a href="#">d1wiia_</a>	Alignment	not modelled	25.4	23	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Zinc beta-ribbon <b>Family:</b> Putative zinc binding domain
49	<a href="#">c2hdpB_</a>	Alignment	not modelled	24.9	19	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin-protein ligase e3 mdm2; <b>PDBTitle:</b> solution structure of hdm2 ring finger domain
50	<a href="#">c1ee8A_</a>	Alignment	not modelled	24.7	35	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mutm (fpg) protein; <b>PDBTitle:</b> crystal structure of mutm (fpg) protein from thermus thermophilus hb8
51	<a href="#">c3j39p_</a>	Alignment	not modelled	24.7	19	<b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> 60s ribosomal protein l17; <b>PDBTitle:</b> structure of the d. melanogaster 60s ribosomal proteins
52	<a href="#">c3na7A_</a>	Alignment	not modelled	24.5	31	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
53	<a href="#">c2lo4A_</a>	Alignment	not modelled	24.4	36	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> optineurin; <b>PDBTitle:</b> nmr solution structure of optineurin zinc-finger domain
54	<a href="#">c1s1i9_</a>	Alignment	not modelled	24.0	13	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from 2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
						<b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> Z: <b>PDB Molecule:</b> e site t-rna;

55	<a href="#">c2zkrz_</a>	Alignment	not modelled	23.8	25	<b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
56	<a href="#">c2jvyA_</a>	Alignment	not modelled	23.7	27	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> solution structure of the eda-id-related c417f mutant of2 human nemo zinc finger
57	<a href="#">c2vjfB_</a>	Alignment	not modelled	23.5	24	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> mdm4 protein; <b>PDBTitle:</b> crystal structure of the mdm2-mdmx ring domain heterodimer
58	<a href="#">c3jyw9_</a>	Alignment	not modelled	23.2	13	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> 60s ribosomal protein l43; <b>PDBTitle:</b> structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
59	<a href="#">c2l0bA_</a>	Alignment	not modelled	23.2	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase praja-1; <b>PDBTitle:</b> solution nmr structure of zinc finger domain of e3 ubiquitin-protein2 ligase praja-1 from homo sapiens, northeast structural genomics3 consortium (nesg) target hr4710b
60	<a href="#">c3j2i_</a>	Alignment	not modelled	23.1	31	<b>PDB header:</b> ribosome <b>Chain:</b> l: <b>PDB Molecule:</b> 50s ribosomal protein l13p; <b>PDBTitle:</b> promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
61	<a href="#">c3l11A_</a>	Alignment	not modelled	22.6	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf168; <b>PDBTitle:</b> crystal structure of the ring domain of rnf168
62	<a href="#">c2ecyA_</a>	Alignment	not modelled	22.2	20	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 3; <b>PDBTitle:</b> solution structure of the zinc finger, c3hc4 type (ring2 finger)" domain of tnf receptor-associated factor 3
63	<a href="#">d1qf8a_</a>	Alignment	not modelled	21.5	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Casein kinase II beta subunit <b>Family:</b> Casein kinase II beta subunit
64	<a href="#">c2ecmA_</a>	Alignment	not modelled	21.5	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 structure of the ring domain of the ring finger2 and chy zinc finger domain-containing protein 1 from mus3 musculus
65	<a href="#">c3izrm_</a>	Alignment	not modelled	21.3	13	<b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein l23 (l14p); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
66	<a href="#">d1g25a_</a>	Alignment	not modelled	21.1	21	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
67	<a href="#">d1e4ua_</a>	Alignment	not modelled	21.1	25	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> RING finger domain, C3HC4
68	<a href="#">d2fu5a1</a>	Alignment	not modelled	20.9	11	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> RabGEF Mss4
69	<a href="#">c3facE_</a>	Alignment	not modelled	20.7	25	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides protein2 rsp 2168. northeast structural genomics target rhr83.
70	<a href="#">c1x4jA_</a>	Alignment	not modelled	20.7	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger protein 38; <b>PDBTitle:</b> solution structure of ring finger in ring finger protein 38
71	<a href="#">c2ep4A_</a>	Alignment	not modelled	20.4	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger protein 24; <b>PDBTitle:</b> solution structure of ring finger from human ring finger2 protein 24
72	<a href="#">c2kn9A_</a>	Alignment	not modelled	20.3	24	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
73	<a href="#">d1rb9a_</a>	Alignment	not modelled	20.3	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
74	<a href="#">d1zvfa1</a>	Alignment	not modelled	19.7	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
75	<a href="#">c1zzaA_</a>	Alignment	not modelled	19.5	15	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> stannin; <b>PDBTitle:</b> solution nmr structure of the membrane protein stannin
76	<a href="#">d2dsxa1</a>	Alignment	not modelled	19.3	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
77	<a href="#">d1hxra_</a>	Alignment	not modelled	19.1	11	<b>Fold:</b> Mss4-like <b>Superfamily:</b> Mss4-like <b>Family:</b> RabGEF Mss4
78	<a href="#">d1s24a_</a>	Alignment	not modelled	19.1	33	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
79	<a href="#">c1s24A_</a>	Alignment	not modelled	19.1	33	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin 2; <b>PDBTitle:</b> rubredoxin domain ii from pseudomonas oleovorans
80	<a href="#">c2m4yA_</a>	Alignment	not modelled	19.0	25	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin; <b>PDBTitle:</b> rubredoxin type protein from mycobacterium ulcerans

81	<a href="#">d1qcva_</a>	Alignment	not modelled	18.8	29	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
82	<a href="#">d2rdva_</a>	Alignment	not modelled	18.6	43	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
83	<a href="#">d4rxna_</a>	Alignment	not modelled	18.2	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
84	<a href="#">c2kizA_</a>	Alignment	not modelled	18.1	21	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase arkadia; <b>PDBTitle:</b> solution structure of arkadia ring-h2 finger domain
85	<a href="#">d1dx8a_</a>	Alignment	not modelled	18.1	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
86	<a href="#">d1ee8a3</a>	Alignment	not modelled	17.8	50	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> C-terminal, Zn-finger domain of MutM-like DNA repair proteins
87	<a href="#">c2cklB_</a>	Alignment	not modelled	17.7	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> ubiquitin ligase protein ring2; <b>PDBTitle:</b> ring1b-bmi1 e3 catalytic domain structure
88	<a href="#">c2m0eA_</a>	Alignment	not modelled	17.7	40	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger and btb domain-containing protein 17; <b>PDBTitle:</b> solution structure of miz-1 zinc finger 6
89	<a href="#">d1brfa_</a>	Alignment	not modelled	17.7	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
90	<a href="#">c3vhsB_</a>	Alignment	not modelled	17.6	55	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> atpase wrnip1; <b>PDBTitle:</b> crystal structure of ubz of human wrnip1
91	<a href="#">c2xeuA_</a>	Alignment	not modelled	17.5	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ring finger protein 4; <b>PDBTitle:</b> ring domain
92	<a href="#">c3vhsA_</a>	Alignment	not modelled	17.5	55	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase wrnip1; <b>PDBTitle:</b> crystal structure of ubz of human wrnip1
93	<a href="#">d1iroa_</a>	Alignment	not modelled	17.4	38	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
94	<a href="#">d1h7va_</a>	Alignment	not modelled	17.4	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
95	<a href="#">c2ysoA_</a>	Alignment	not modelled	17.3	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 95 homolog; <b>PDBTitle:</b> solution structure of the c2h2 type zinc finger (region 656-2 688) of human zinc finger protein 95 homolog
96	<a href="#">c1z60A_</a>	Alignment	not modelled	17.2	38	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tfiih basal transcription factor complex p44 <b>PDBTitle:</b> solution structure of the carboxy-terminal domain of human2 tfiih p44 subunit
97	<a href="#">d1z60a1</a>	Alignment	not modelled	17.2	38	<b>Fold:</b> Cysteine-rich domain <b>Superfamily:</b> Cysteine-rich domain <b>Family:</b> TFIIH p44 subunit cysteine-rich domain
98	<a href="#">d1iu5a_</a>	Alignment	not modelled	17.1	43	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
99	<a href="#">d1jwhc_</a>	Alignment	not modelled	17.0	35	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Casein kinase II beta subunit <b>Family:</b> Casein kinase II beta subunit