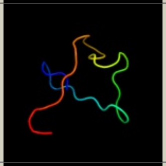
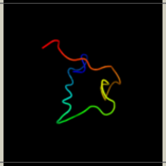
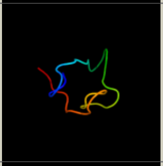
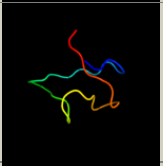
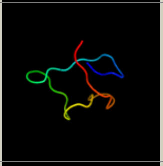
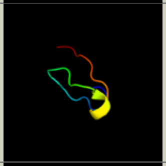
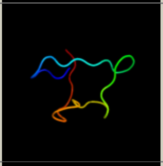
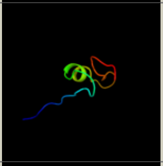
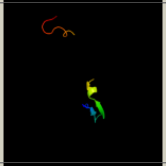
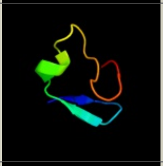
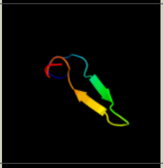
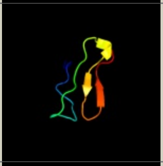
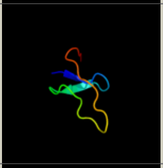
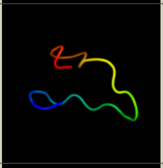
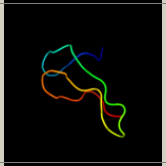
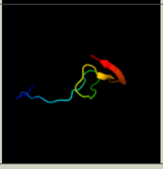
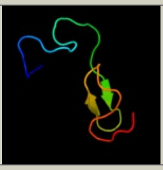
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFL9
Date	Thu Jan 5 11:26:42 GMT 2012
Unique Job ID	a786d72efde76f4c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pptA_	Alignment		94.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
2	d1akya2	Alignment		92.4	9	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
3	d2ak3a2	Alignment		92.1	9	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
4	d1p3ja2	Alignment		91.9	22	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
5	d1zina2	Alignment		91.7	22	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
6	d1s3ga2	Alignment		91.6	19	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
7	c2lcqA_	Alignment		90.5	33	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
8	d1e4va2	Alignment		90.1	9	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
9	c2kdxA_	Alignment		89.0	13	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
10	c3a44D_	Alignment		88.9	24	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
11	d1k3xa3	Alignment		88.1	23	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins

12	d2gmga1	Alignment		87.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
13	c2f9iD_	Alignment		86.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
14	c2gb5B_	Alignment		86.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
15	d1ee8a3	Alignment		86.4	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
16	d1dl6a_	Alignment		86.0	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
17	c3lpeF_	Alignment		85.8	21	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
18	c1yuzB_	Alignment		84.9	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
19	d1pfta_	Alignment		84.8	24	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
20	d2dkta1	Alignment		84.7	25	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
21	d1yc5a1	Alignment	not modelled	84.5	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
22	c3k7aM_	Alignment	not modelled	84.2	18	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
23	d1tdza3	Alignment	not modelled	83.9	22	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
24	d2ayja1	Alignment		83.8	24	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e
25	d1m2ka_	Alignment	not modelled	82.6	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
26	d1lkoa2	Alignment	not modelled	82.4	21	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
27	d2j0151	Alignment	not modelled	82.4	21	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
						Fold: Rubredoxin-like

28	d2zjrz1	Alignment	not modelled	82.1	28	**Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
29	d1k82a3	Alignment	not modelled	82.0	16	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
30	d1l1ta3	Alignment	not modelled	81.8	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
31	c2f9yB_	Alignment	not modelled	81.6	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
32	d2f9yb1	Alignment	not modelled	81.6	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
33	c3glsC_	Alignment	not modelled	81.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
34	d1ryqa_	Alignment	not modelled	81.3	28	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
35	d1r2za3	Alignment	not modelled	80.6	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
36	c3k35D_	Alignment	not modelled	79.0	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
37	c2ja6L_	Alignment	not modelled	78.7	27	**PDB header:**transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
38	d2ct7a1	Alignment	not modelled	78.4	30	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
39	d1qxfa_	Alignment	not modelled	78.0	17	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
40	c3p2aB_	Alignment	not modelled	76.8	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
41	d1yuza2	Alignment	not modelled	76.3	35	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
42	c2odxA_	Alignment	not modelled	76.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase polypeptide iv; **PDBTitle:** solution structure of zn(ii)cox4
43	c1dvbA_	Alignment	not modelled	76.0	29	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
44	d1q1aa_	Alignment	not modelled	76.0	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
45	c2hr5B_	Alignment	not modelled	75.6	24	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
46	d2dsxa1	Alignment	not modelled	75.0	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
47	d2gnra1	Alignment	not modelled	75.0	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
48	c1i3ql_	Alignment	not modelled	74.3	15	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
49	c3h0gL_	Alignment	not modelled	74.0	23	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
50	d6rxna_	Alignment	not modelled	73.8	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
51	c2x5cB_	Alignment	not modelled	73.8	60	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
52	d4rxna_	Alignment	not modelled	73.6	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	d1qcva_	Alignment	not modelled	73.5	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
54	d2k4xa1	Alignment	not modelled	73.3	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a

55	d2apob1	Alignment	not modelled	73.3	24	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
56	d2ey4e1	Alignment	not modelled	73.2	31	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
57	c3axtA_	Alignment	not modelled	72.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable n(2),n(2)-dimethylguanosine trna methyltransferase **PDBTitle:** complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine
58	d1iroa_	Alignment	not modelled	72.6	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
59	c2aklA_	Alignment	not modelled	72.2	32	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
60	d2akla2	Alignment	not modelled	72.2	32	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
61	c3pkiF_	Alignment	not modelled	71.8	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
62	d1s24a_	Alignment	not modelled	70.8	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
63	c1s24A_	Alignment	not modelled	70.8	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
64	c3cngC_	Alignment	not modelled	70.1	34	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
65	d1nnqa2	Alignment	not modelled	69.5	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
66	d1weoa_	Alignment	not modelled	69.4	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
67	c1q14A_	Alignment	not modelled	69.3	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
68	c3iz6X_	Alignment	not modelled	69.2	20	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein s27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
69	c2kn9A_	Alignment	not modelled	68.9	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
70	d2qam01	Alignment	not modelled	67.3	4	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
71	d1iu5a_	Alignment	not modelled	67.1	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
72	c3p2aA_	Alignment	not modelled	66.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
73	d1dx8a_	Alignment	not modelled	66.1	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
74	c2v3bB_	Alignment	not modelled	65.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
75	d2fiya1	Alignment	not modelled	65.1	13	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
76	c3izbX_	Alignment	not modelled	65.0	17	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**40s ribosomal protein rps27 (s27e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
77	d1h7va_	Alignment	not modelled	64.8	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
78	d2cona1	Alignment	not modelled	62.3	24	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
79	c2xzm6_	Alignment	not modelled	62.0	17	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**rps27e; **PDBTitle:** 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 1
80	c3jwpA_	Alignment	not modelled	62.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein sir2 homologue; **PDBTitle:** crystal structure of plasmodium falciparum sir2a

						(pf13_0152) in2 complex with amp
81	d2rdva_	Alignment	not modelled	61.8	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
82	c1hk8A_	Alignment	not modelled	61.6	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
83	d1hk8a_	Alignment	not modelled	61.6	24	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
84	c3h7hA_	Alignment	not modelled	60.9	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
85	d1ibia1	Alignment	not modelled	60.2	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
86	c3floD_	Alignment	not modelled	59.9	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
87	c2pziA_	Alignment	not modelled	59.5	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable serine/threonine-protein kinase pkng; **PDBTitle:** crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
88	c3gn5B_	Alignment	not modelled	59.3	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
89	d1rb9a_	Alignment	not modelled	59.3	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
90	d1brfa_	Alignment	not modelled	57.0	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
91	c3na7A_	Alignment	not modelled	55.5	30	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
92	d1ctla1	Alignment	not modelled	55.3	43	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
93	c2yucA_	Alignment	not modelled	54.7	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**tnf receptor-associated factor 4; **PDBTitle:** solution structure of the traf-type zinc finger domains2 (102-164) from human tnf receptor associated factor 4
94	c2bx9J_	Alignment	not modelled	54.5	24	**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
95	c3g9yA_	Alignment	not modelled	53.2	28	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**zinc finger ran-binding domain-containing protein 2; **PDBTitle:** crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt ssrna sequence agguaa
96	d1x6ma_	Alignment	not modelled	52.9	19	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
97	c3h0gI_	Alignment	not modelled	52.8	18	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
98	c2lk0A_	Alignment	not modelled	52.5	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein 5; **PDBTitle:** solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
99	d1pfva3	Alignment	not modelled	50.7	33	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
100	d1p91a_	Alignment	not modelled	50.6	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
101	c2jrpA_	Alignment	not modelled	49.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cytoplasmic protein; **PDBTitle:** solution nmr structure of yfgj from salmonella typhimurium2 modeled with two zn+2 bound, northeast structural genomics3 consortium target str86
102	d2jnea1	Alignment	not modelled	48.9	43	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
103	c2jneA_	Alignment	not modelled	48.9	43	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein yfgj; **PDBTitle:** nmr structure of e.coli yfgj modelled with two zn+2 bound.2 northeast structural genomics consortium target er317.
104	c2d9kA_	Alignment	not modelled	48.7	23	**PDB header:**immune system **Chain:** A: **PDB Molecule:**fln29 gene product; **PDBTitle:** solution structure of the zf-traf domain of fln29 gene2 product

105	d1dgsa1	Alignment	not modelled	47.6	55	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
106	d1ma3a_	Alignment	not modelled	46.7	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
107	d2ct1a1	Alignment	not modelled	45.9	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
108	d1j8fa_	Alignment	not modelled	45.4	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
109	c3tsuA_	Alignment	not modelled	45.3	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
110	d2pk7a1	Alignment	not modelled	44.2	15	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
111	c2js4A_	Alignment	not modelled	44.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
112	c3ir9A_	Alignment	not modelled	43.3	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**peptide chain release factor subunit 1; **PDBTitle:** c-terminal domain of peptide chain release factor from2 methanosarcina mazei.
113	d2hf1a1	Alignment	not modelled	43.1	15	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
114	c2jr6A_	Alignment	not modelled	42.5	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein nma0874; **PDBTitle:** solution structure of upf0434 protein nma0874. northeast structural2 genomics target mr32
115	c2y69S_	Alignment	not modelled	42.2	50	**PDB header:**electron transport **Chain:** S: **PDB Molecule:**cytochrome c oxidase subunit 5b; **PDBTitle:** bovine heart cytochrome c oxidase re-refined with molecular2 oxygen
116	c2hjhB_	Alignment	not modelled	41.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
117	d2jnya1	Alignment	not modelled	40.9	20	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
118	c1ltlE_	Alignment	not modelled	40.6	22	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
119	c3ld0Q_	Alignment	not modelled	40.1	21	**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
120	c2yqqA_	Alignment	not modelled	40.0	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**zinc finger hit domain-containing protein 3; **PDBTitle:** solution structure of the zf-hit domain in zinc finger hit2 domain-containing protein 3 (trip-3)