Phyre2

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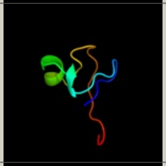
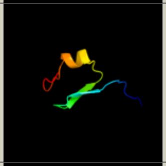
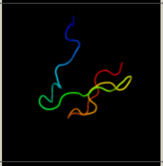
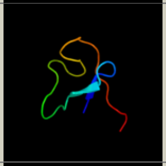
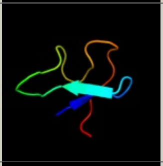
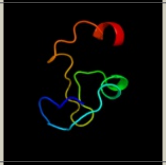
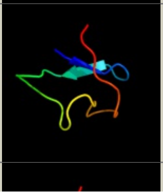
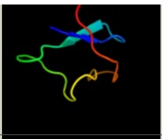
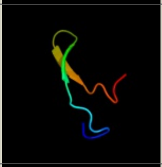
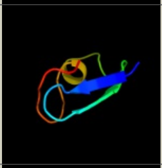
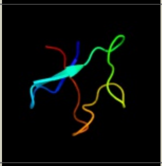
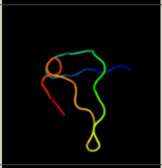
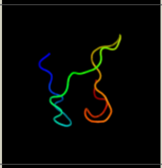
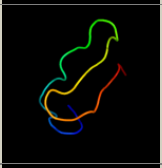
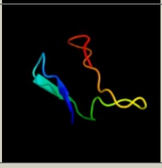
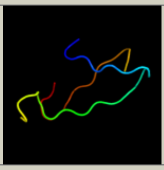
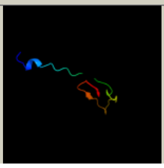
Description	P0AD03
Date	Thu Jan 5 11:19:33 GMT 2012
Unique Job ID	27829163bd5e48f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pptA_	Alignment		94.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
2	c2lcqA_	Alignment		92.8	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
3	c2hr5B_	Alignment		92.0	30	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
4	d1dl6a_	Alignment		91.1	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
5	c2f9iD_	Alignment		90.8	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
6	d1akya2	Alignment		90.5	5	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
7	d2ak3a2	Alignment		89.8	6	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
8	d1p3ja2	Alignment		89.4	12	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
9	d2f9yb1	Alignment		89.1	22	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
10	c2f9yB_	Alignment		89.1	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
11	d1zina2	Alignment		88.9	15	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain

12	d1s3ga2	Alignment		88.8	12	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
13	c1dvbA_	Alignment		87.6	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
14	d1k3xa3	Alignment		87.4	27	**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
15	d1yc5a1	Alignment		87.3	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
16	d1e4va2	Alignment		86.7	0	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
17	c1hk8A_	Alignment		86.4	14	**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
18	d1hk8a_	Alignment		86.4	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
19	c2gb5B_	Alignment		86.0	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
20	d2gnra1	Alignment		86.0	29	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
21	d1ee8a3	Alignment	not modelled	85.5	26	**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
22	c3na7A_	Alignment	not modelled	85.4	18	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
23	d1pfta_	Alignment	not modelled	84.9	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
24	d1m2ka_	Alignment	not modelled	84.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
25	d2gmga1	Alignment	not modelled	84.0	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
26	c3glsC_	Alignment	not modelled	83.7	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
27	c2kdxA_	Alignment	not modelled	83.5	29	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
28	c3a44D_	Alignment	not modelled	83.4	30	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
29	d1tdza3	Alignment	not modelled	83.2	26	**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	c3lpeF_	Alignment	not modelled	82.1	24	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
31	c3k7aM_	Alignment	not modelled	81.9	24	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
32	d1lkoa2	Alignment	not modelled	81.5	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
33	c3k35D_	Alignment	not modelled	81.4	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
34	c3p2aB_	Alignment	not modelled	81.3	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
35	d2ct7a1	Alignment	not modelled	80.6	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
36	d1k82a3	Alignment	not modelled	80.5	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
37	d1l1ta3	Alignment	not modelled	80.5	32	**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
38	d1q1aa_	Alignment	not modelled	80.4	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
39	d1r2za3	Alignment	not modelled	79.2	32	**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
40	d1weoa_	Alignment	not modelled	78.7	22	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
41	c2ja6L_	Alignment	not modelled	77.6	26	**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
42	c3h0gL_	Alignment	not modelled	77.5	19	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
43	d2akla2	Alignment	not modelled	76.3	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
44	c2aklA_	Alignment	not modelled	76.0	28	**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
45	c3pkiF_	Alignment	not modelled	75.9	16	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
46	c1i3ql_	Alignment	not modelled	75.2	19	**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
47	c3axtA_	Alignment	not modelled	75.1	22	**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
48	d1yuza2	Alignment	not modelled	74.5	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
49	c3p2aA_	Alignment	not modelled	73.1	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
50	d6rxna_	Alignment	not modelled	72.9	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
51	c2jrpA_	Alignment	not modelled	72.2	37	**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
52	d2dsxa1	Alignment	not modelled	72.2	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	c3cngC_	Alignment	not modelled	72.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
54	d1qcva_	Alignment	not modelled	71.7	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
55	c1q14A_	Alignment	not modelled	71.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2

56	d2dkta1	Alignment	not modelled	71.2	24	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
57	d4rxna_	Alignment	not modelled	70.9	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
58	c2x5cB_	Alignment	not modelled	70.5	60	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hypothetical protein orf131; **PDBTitle:** crystal structure of hypothetical protein orf131 from2 pyrobaculum spherical virus
59	d1iroa_	Alignment	not modelled	70.0	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
60	c3jwpA_	Alignment	not modelled	68.9	15	**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
61	d2k4xa1	Alignment	not modelled	68.6	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
62	c2v3bB_	Alignment	not modelled	68.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
63	d2cona1	Alignment		68.0	28	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
64	c1s24A_	Alignment	not modelled	68.0	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
65	d1s24a_	Alignment	not modelled	68.0	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
66	c2js4A_	Alignment	not modelled	67.8	17	**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
67	c2odxA_	Alignment		67.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase polypeptide iv; **PDBTitle:** solution structure of zn(ii)cox4
68	d2ey4e1	Alignment	not modelled	67.1	22	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
69	d1p91a_	Alignment	not modelled	67.0	33	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
70	d1nnqa2	Alignment	not modelled	66.8	35	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
71	c1yuzB_	Alignment		66.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
72	d1qxfa_	Alignment	not modelled	66.3	14	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
73	d2apob1	Alignment	not modelled	66.2	27	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
74	d2pk7a1	Alignment	not modelled	66.0	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
75	c2kn9A_	Alignment	not modelled	66.0	33	**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
76	c2jr6A_	Alignment	not modelled	65.9	14	**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
77	c3zyqA_	Alignment		65.6	22	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution

78	c2pziA_	Alignment	not modelled	65.2	18	**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
79	c3floD_	Alignment	not modelled	64.8	29	**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
80	d1ryqa_	Alignment		64.6	36	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
81	d2jnya1	Alignment	not modelled	64.5	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
82	d2fiya1	Alignment	not modelled	64.3	22	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
83	c3ky9B_	Alignment		63.8	29	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
84	d1dx8a_	Alignment	not modelled	63.3	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
85	d1h7va_	Alignment	not modelled	62.0	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
86	c3gn5B_	Alignment	not modelled	61.3	25	**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)
87	d1iu5a_	Alignment	not modelled	61.0	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
88	d2rdva_	Alignment	not modelled	58.8	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
89	d2j0151	Alignment	not modelled	57.6	27	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
90	c3iz6X_	Alignment	not modelled	57.3	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
91	d2hf1a1	Alignment	not modelled	57.0	19	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
92	c3f2cA_	Alignment	not modelled	56.6	22	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
93	d1rb9a_	Alignment	not modelled	56.3	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
94	c3h0gI_	Alignment	not modelled	55.0	15	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
95	d1brfa_	Alignment	not modelled	54.9	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
96	d2zjrz1	Alignment	not modelled	54.4	33	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
97	d1j8fa_	Alignment	not modelled	53.8	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
98	c2opfA_	Alignment	not modelled	53.7	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
99	d1ibia1	Alignment	not modelled	53.6	30	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
100	c1k82D_	Alignment	not modelled	53.4	20	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
101	d2ayja1	Alignment	not modelled	53.3	24	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e

102	d1l1oc_	Alignment	not modelled	52.0	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
103	c2kpiA_	Alignment	not modelled	51.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
104	c1nnjA_	Alignment	not modelled	51.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
105	d2jnea1	Alignment	not modelled	50.7	24	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
106	c2jneA_	Alignment	not modelled	50.7	24	**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.
107	d1x6ma_	Alignment	not modelled	50.4	15	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**Glutathione-dependent formaldehyde-activating enzyme, Gfa
108	c3ir9A_	Alignment	not modelled	50.0	15	**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.
109	c3nw0A_	Alignment	not modelled	48.7	25	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
110	d1ma3a_	Alignment	not modelled	47.4	18	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
111	c3u50C_	Alignment	not modelled	46.7	28	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**telomerase-associated protein 82; **PDBTitle:** crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
112	d2qam01	Alignment	not modelled	46.5	11	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
113	c3h7hA_	Alignment	not modelled	46.5	25	**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)
114	c2f5qA_	Alignment	not modelled	46.3	27	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
115	d1pfva3	Alignment	not modelled	45.9	29	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
116	d1ctla1	Alignment	not modelled	45.8	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
117	c1ee8A_	Alignment	not modelled	45.8	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
118	d1dgsa1	Alignment	not modelled	45.4	27	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
119	c3izbX_	Alignment	not modelled	45.2	14	**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
120	c1ltlE_	Alignment	not modelled	43.5	14	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum