Phyre^2

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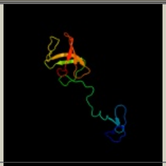
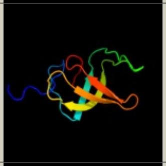
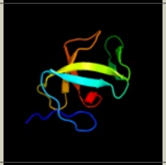
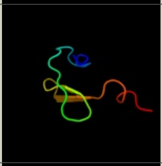
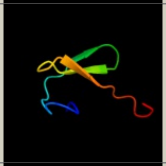
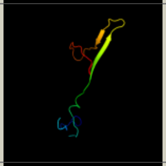
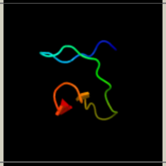
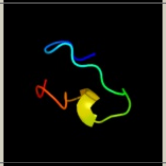
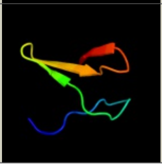
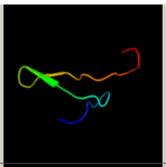
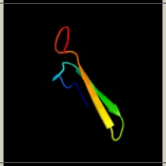
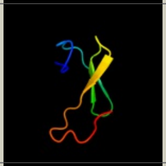
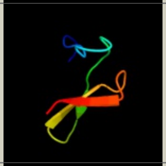
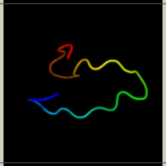
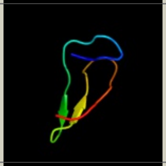
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2aklA_	Alignment		100.0	68	**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
2	d2akla1	Alignment		100.0	70	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
3	d2akka1	Alignment		100.0	48	**Fold:**SH3-like barrel **Superfamily:**Prokaryotic SH3-related domain **Family:**PhnA-like
4	d2akla2	Alignment		99.5	59	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
5	d1twfi2	Alignment		89.0	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
6	c2gb5B_	Alignment		87.9	13	**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
7	c2jr6A_	Alignment		87.6	10	**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
8	c2f9iD_	Alignment		87.5	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
9	d1tfia_	Alignment		87.0	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
10	c2js4A_	Alignment		86.7	13	**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
11	d2jnya1	Alignment		86.4	13	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like

12	c2riqA_	Alignment		85.1	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
13	c2jvnA_	Alignment		84.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
14	c1i3ql_	Alignment		84.1	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
15	c2kdxA_	Alignment		83.5	18	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
16	d2pk7a1	Alignment		82.4	13	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
17	d2ct7a1	Alignment		82.4	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
18	d1qypa_	Alignment		82.4	36	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
19	d1pfta_	Alignment		82.4	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
20	d2hf1a1	Alignment		80.5	17	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
21	d1dl6a_	Alignment	not modelled	79.9	43	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
22	c2kpiA_	Alignment	not modelled	78.9	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
23	c3cngC_	Alignment	not modelled	78.2	26	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
24	d2f9yb1	Alignment	not modelled	77.4	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
25	c2f9yB_	Alignment	not modelled	77.4	21	**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
26	c3gn5B_	Alignment	not modelled	74.0	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)
27	d2gmga1	Alignment	not modelled	71.8	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
28	c3k7aM_	Alignment	not modelled	70.9	30	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex

29	c3a44D_	Alignment	not modelled	65.5	41	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
30	d1pfva3	Alignment	not modelled	64.9	44	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
31	d1p91a_	Alignment	not modelled	64.3	45	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
32	d1nuia2	Alignment	not modelled	62.8	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
33	d2fiya1	Alignment	not modelled	62.7	33	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
34	d2apob1	Alignment	not modelled	62.6	53	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
35	c2k5rA_	Alignment	not modelled	61.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
36	c2pziA_	Alignment	not modelled	60.3	21	**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
37	d1k3xa3	Alignment	not modelled	60.0	29	**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	c3bvoA_	Alignment	not modelled	59.4	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
39	c3tsuA_	Alignment	not modelled	59.2	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
40	d2ey4e1	Alignment	not modelled	58.8	47	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
41	d2f4ma1	Alignment	not modelled	57.9	33	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
42	c1hk8A_	Alignment	not modelled	53.9	21	**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
43	d1hk8a_	Alignment	not modelled	53.9	21	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
44	c3u50C_	Alignment	not modelled	52.0	13	**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
45	d1tdza3	Alignment	not modelled	50.4	28	**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
46	c1dvbA_	Alignment	not modelled	49.0	38	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
47	c2ja6L_	Alignment	not modelled	47.7	22	**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
48	c1nuiA_	Alignment	not modelled	47.4	25	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
49	d1l1oc_	Alignment	not modelled	47.4	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
50	d2j0151	Alignment	not modelled	46.3	39	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
51	d1h7va_	Alignment	not modelled	46.1	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
52	d1tiea_	Alignment	not modelled	45.4	18	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
53	d1ee8a3	Alignment	not modelled	45.4	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
						PDB header:transcription

54	c3h0gL_	Alignment	not modelled	44.6	26	**Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
55	d1vd4a_	Alignment	not modelled	43.3	31	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
56	d1dgsa1	Alignment	not modelled	42.6	28	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
57	d1dx8a_	Alignment	not modelled	42.5	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
58	c2qkdA_	Alignment	not modelled	42.1	22	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
59	d3bx1c1	Alignment	not modelled	41.7	18	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
60	d1qcva_	Alignment	not modelled	41.1	5	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
61	d1wd2a_	Alignment	not modelled	39.3	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
62	c3eswA_	Alignment	not modelled	39.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
63	d2rdva_	Alignment	not modelled	38.7	35	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
64	d1iu5a_	Alignment	not modelled	38.5	18	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
65	d1k82a3	Alignment	not modelled	38.3	17	**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
66	d1r2za3	Alignment	not modelled	38.2	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
67	d1l1ta3	Alignment	not modelled	38.2	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
68	d1iroa_	Alignment	not modelled	38.1	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
69	d1x3za1	Alignment	not modelled	38.1	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
70	c2dreA_	Alignment	not modelled	38.0	28	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**water-soluble chlorophyll protein; **PDBTitle:** crystal structure of water-soluble chlorophyll protein from2 lepidium virginicum at 2.00 angstrom resolution
71	c2kn9A_	Alignment	not modelled	37.9	24	**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
72	d1brfa_	Alignment	not modelled	37.8	14	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
73	d2dsxa1	Alignment	not modelled	36.9	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
74	c2j6aA_	Alignment	not modelled	36.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein trm112; **PDBTitle:** crystal structure of s. cerevisiae ynr046w, a zinc finger2 protein from the erf1 methyltransferase complex.
75	d1rb9a_	Alignment	not modelled	36.0	35	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
76	d4rxna_	Alignment	not modelled	35.3	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
77	c2v3bB_	Alignment	not modelled	34.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
78	c3floD_	Alignment	not modelled	33.4	21	**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
79	c3lpeF_	Alignment	not modelled	33.3	35	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
80	d2zjrz1	Alignment	not modelled	32.5	39	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins

						Family: Ribosomal protein L32p
81	d1s24a_	Alignment	not modelled	32.4	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
82	c1s24A_	Alignment	not modelled	32.4	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
83	c3ndjA_	Alignment	not modelled	32.3	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
84	c3egxB_	Alignment	not modelled	31.8	18	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
85	d1eyla_	Alignment	not modelled	31.3	19	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
86	c2qn4B_	Alignment	not modelled	31.3	18	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**alpha-amylase/subtilisin inhibitor; **PDBTitle:** structure and function study of rice bifunctional alpha-2 amylase/subtilisin inhibitor from oryza sativa
87	c2qa4Z_	Alignment	not modelled	30.8	26	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
88	d1vqoz1	Alignment	not modelled	29.9	26	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
89	c1yshD_	Alignment	not modelled	29.8	19	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
90	c1v9pB_	Alignment	not modelled	29.7	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
91	c2ba1B_	Alignment	not modelled	29.7	32	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
92	d1ffkw_	Alignment	not modelled	29.6	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
93	c2zkrz_	Alignment	not modelled	29.4	19	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
94	c3f2cA_	Alignment	not modelled	29.1	24	**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
95	d2k4xa1	Alignment	not modelled	28.9	32	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
96	c3axtA_	Alignment	not modelled	28.9	23	**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
97	c2k5cA_	Alignment	not modelled	28.8	44	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
98	d1jj2y_	Alignment	not modelled	28.6	26	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
99	d1imla1	Alignment	not modelled	27.9	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
100	c3iirA_	Alignment	not modelled	27.4	21	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor; **PDBTitle:** crystal structure of miraculin like protein from seeds of murraya2 koenigii
101	c2l43A_	Alignment	not modelled	27.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n-teminal domain from histone h3.3, linker, phd1 domain **PDBTitle:** structural basis for histone code recognition by brpf2-phd1 finger
102	d2jnea1	Alignment	not modelled	26.9	28	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
103	c2jneA_	Alignment	not modelled	26.9	28	**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	c3pihA_	Alignment	not modelled	26.1	33	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
105	d1yuza2	Alignment	not modelled	26.0	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
						Fold:ISP domain

106	d1fqta_	Alignment	not modelled	25.9	11	**Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
107	c2yt5A_	Alignment	not modelled	25.8	34	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the phd domain of metal-response2 element-binding transcription factor 2
108	d1r8na_	Alignment	not modelled	25.5	23	**Fold:**beta-Trefoil **Superfamily:**STI-like **Family:**Kunitz (STI) inhibitors
109	c3jyw9_	Alignment	not modelled	25.0	19	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
110	d1cwva2	Alignment	not modelled	24.9	25	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
111	c2jrpA_	Alignment	not modelled	24.8	24	**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
112	c1r8oA_	Alignment	not modelled	24.2	24	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**kunitz trypsin inhibitor; **PDBTitle:** crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifera langsdorffii seeds
113	c4a17Y_	Alignment	not modelled	24.1	23	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** 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.
114	c2ktvA_	Alignment	not modelled	23.7	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
115	c3cc4Z_	Alignment	not modelled	23.7	27	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
116	c1dgsB_	Alignment	not modelled	23.6	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
117	c1s1i9_	Alignment	not modelled	23.5	19	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 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.
118	d2gvia2	Alignment	not modelled	23.5	70	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**FwdE C-terminal domain-like
119	d1weva_	Alignment	not modelled	23.3	24	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
120	d1lkoa2	Alignment	not modelled	23.1	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin