Phyre^2

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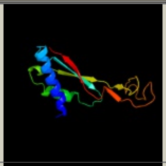
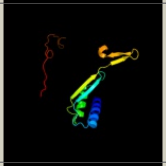
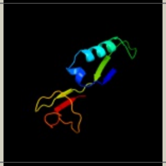
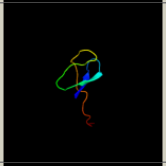
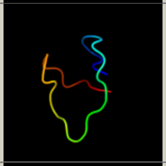
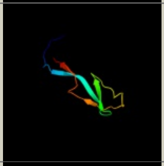
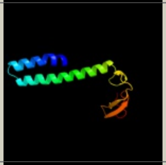
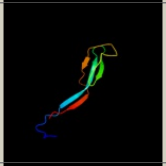
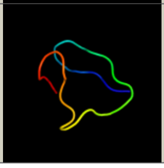
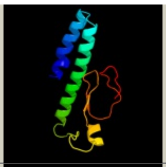
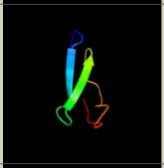
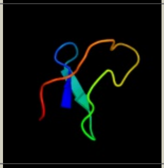
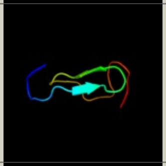
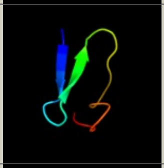
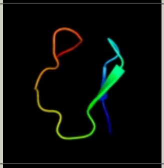
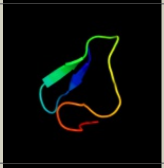
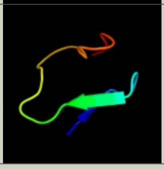
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kdxA_	Alignment		100.0	26	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
2	c3a44D_	Alignment		100.0	30	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
3	c1hk8A_	Alignment		97.1	11	**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
4	d1hk8a_	Alignment		97.1	11	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
5	c2hr5B_	Alignment		95.1	20	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
6	c2k2dA_	Alignment		95.0	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ring finger and chy zinc finger domain- **PDBTitle:** solution nmr structure of c-terminal domain of human pirh2.2 northeast structural genomics consortium (nesg) target ht2c
7	d2gmga1	Alignment		95.0	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
8	d1ltla_	Alignment		94.9	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
9	c1dvbA_	Alignment		94.9	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
10	c1ltlE_	Alignment		94.4	18	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
11	c2lcqA_	Alignment		94.2	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii

12	c1yuzB_	Alignment		94.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
13	d1lkoa2	Alignment		93.9	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
14	d2gnra1	Alignment		92.0	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
15	d1h7va_	Alignment		91.9	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
16	d1iu5a_	Alignment		91.9	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
17	d1qcva_	Alignment		91.8	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
18	c2kn9A_	Alignment		91.7	23	**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
19	d2dsxa1	Alignment		91.6	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
20	d1iroa_	Alignment		91.4	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
21	d1brfa_	Alignment	not modelled	91.2	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
22	d4rxna_	Alignment	not modelled	90.6	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
23	d1dx8a_	Alignment	not modelled	90.2	16	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
24	c2v3bB_	Alignment	not modelled	90.1	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
25	c1s24A_	Alignment	not modelled	90.1	23	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
26	d1s24a_	Alignment	not modelled	90.1	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
27	d6rxna_	Alignment	not modelled	90.1	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
28	d1rb9a_	Alignment	not modelled	89.8	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
29	d2rdva_	Alignment	not modelled	89.7	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like

						Family: Rubredoxin
30	d1nnqa2	Alignment	not modelled	89.1	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
31	d1yuza2	Alignment	not modelled	87.9	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
32	d2cona1	Alignment	not modelled	87.8	16	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
33	c2f9iD_	Alignment	not modelled	87.8	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
34	d1qxfa_	Alignment	not modelled	87.7	20	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
35	c3iz6X_	Alignment	not modelled	86.7	23	**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
36	c3floD_	Alignment	not modelled	84.3	17	**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
37	c2vl6C_	Alignment	not modelled	83.9	12	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain
38	c3izbX_	Alignment	not modelled	83.8	20	**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
39	d2fiya1	Alignment	not modelled	83.5	16	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
40	c3f9vA_	Alignment	not modelled	82.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
41	c2xzm6_	Alignment	not modelled	80.8	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
42	d2f9yb1	Alignment	not modelled	80.3	29	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
43	c2f9yB_	Alignment	not modelled	80.3	29	**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
44	c2ba1B_	Alignment	not modelled	79.6	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
45	c3glsC_	Alignment	not modelled	78.8	35	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
46	c3k35D_	Alignment	not modelled	78.6	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
47	c3pkiF_	Alignment	not modelled	78.4	24	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
48	d1m2ka_	Alignment	not modelled	78.0	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
49	c2nn6I_	Alignment	not modelled	77.6	30	**PDB header:**hydrolase/transferase **Chain:** I: **PDB Molecule:**3'-5' exoribonuclease csl4 homolog; **PDBTitle:** structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
50	d1q1aa_	Alignment	not modelled	77.5	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
51	c3lpeF_	Alignment	not modelled	77.4	30	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
52	c1q14A_	Alignment	not modelled	76.3	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
53	d2jnea1	Alignment	not modelled	76.1	26	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
54	c2jneA_	Alignment	not modelled	76.1	26	**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.
55	c2k5cA_	Alignment	not modelled	75.9	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
56	d2dkta1	Alignment	not modelled	75.8	21	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
57	c2aklA_	Alignment	not modelled	75.1	24	**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
58	c3tsuA_	Alignment	not modelled	74.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
59	d2akla2	Alignment	not modelled	73.3	24	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
60	c1i3qI_	Alignment	not modelled	73.2	31	**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
61	d1yc5a1	Alignment	not modelled	72.5	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
62	c3cngC_	Alignment	not modelled	72.3	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
63	d1s5pa_	Alignment	not modelled	71.4	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
64	d2zjrz1	Alignment	not modelled	71.3	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
65	d1ryqa_	Alignment	not modelled	70.8	29	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
66	d2j0151	Alignment	not modelled	70.6	23	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
67	d2nn6i1	Alignment	not modelled	70.3	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
68	c2gb5B_	Alignment	not modelled	69.9	17	**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
69	d1p91a_	Alignment	not modelled	68.5	22	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
70	d2apob1	Alignment	not modelled	67.7	26	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
71	c2ktvA_	Alignment	not modelled	66.6	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
72	d2ey4e1	Alignment	not modelled	65.8	26	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
73	c2j6aA_	Alignment	not modelled	65.6	17	**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.
74	c3h0gI_	Alignment	not modelled	65.4	30	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
75	c3ky9B_	Alignment	not modelled	64.3	13	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
76	c2jrpA_	Alignment	not modelled	64.2	21	**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
77	c3axtA_	Alignment	not modelled	63.5	19	**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
78	c2opfA_	Alignment	not modelled	63.1	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
79	c1ee8A_	Alignment	not modelled	63.1	38	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
80	d2qtva5	Alignment	not modelled	62.5	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24

81	d1ma3a_	Alignment	not modelled	62.3	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
82	d1vd4a_	Alignment	not modelled	61.9	26	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
83	c3bvoA_	Alignment	not modelled	61.7	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
84	d1nuia2	Alignment	not modelled	61.5	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
85	c1m2oA_	Alignment	not modelled	61.5	24	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
86	c2emcA_	Alignment	not modelled	60.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 641-2 673) of human zinc finger protein 473
87	c1jocA_	Alignment	not modelled	59.3	19	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
88	c3mv2A_	Alignment	not modelled	58.9	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
89	c2epqA_	Alignment	not modelled	58.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the third zinc finger domain of zinc2 finger protein 278
90	d2ct7a1	Alignment	not modelled	57.6	39	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
91	c3h0gL_	Alignment	not modelled	57.3	27	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
92	c1k82D_	Alignment	not modelled	56.9	24	**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
93	c2e2zA_	Alignment	not modelled	56.8	38	**PDB header:**protein transport, chaperone regulator **Chain:** A: **PDB Molecule:**tim15; **PDBTitle:** solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
94	c2drpD_	Alignment	not modelled	56.6	33	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**protein (tramtrack dna-binding domain); **PDBTitle:** the crystal structure of a two zinc-finger peptide reveals2 an extension to the rules for zinc-finger/dna recognition
95	c2hjhB_	Alignment	not modelled	56.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
96	c1nnjA_	Alignment	not modelled	56.2	23	**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
97	c3mkrB_	Alignment	not modelled	56.0	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
98	c2f5qA_	Alignment	not modelled	55.3	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
99	c2qkdA_	Alignment	not modelled	55.1	18	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
100	c3jwpA_	Alignment	not modelled	54.9	31	**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
101	c3ir9A_	Alignment	not modelled	54.6	18	**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.
102	d2qam01	Alignment	not modelled	54.1	4	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
103	c2kwqA_	Alignment	not modelled	53.3	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** mcm10 c-terminal dna binding domain
104	c2e9hA_	Alignment	not modelled	53.0	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
105	c3zyqA_	Alignment	not modelled	52.7	19	**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
106	c2en8A_	Alignment	not modelled	52.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 224; **PDBTitle:** solution structure of the c2h2 type zinc finger (region

						171-2 203) of human zinc finger protein 224
107	c2eozA_	Alignment	not modelled	52.4	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 809-2 841) of human zinc finger protein 473
108	c1nltA_	Alignment	not modelled	52.0	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
109	d1dl6a_	Alignment	not modelled	51.9	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
110	c2ctdA_	Alignment	not modelled	51.7	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 512; **PDBTitle:** solution structure of two zf-c2h2 domains from human zinc2 finger protein 512
111	c2avuF_	Alignment	not modelled	51.7	30	**PDB header:**transcription activator **Chain:** F: **PDB Molecule:**flagellar transcriptional activator flhc; **PDBTitle:** structure of the escherichia coli flhdc complex, a2 prokaryotic heteromeric regulator of transcription
112	d2avue1	Alignment	not modelled	51.7	30	**Fold:**FlhC-like **Superfamily:**FlhC-like **Family:**FlhC-like
113	d1zina2	Alignment	not modelled	51.6	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
114	d1p3ja2	Alignment	not modelled	51.2	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
115	d1s3ga2	Alignment	not modelled	51.2	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
116	c2vrwB_	Alignment	not modelled	50.7	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** critical structural role for the ph and c1 domains of the2 vav1 exchange factor
117	c2epsA_	Alignment	not modelled	50.5	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**poz-, at hook-, and zinc finger-containing **PDBTitle:** solution structure of the 4th zinc finger domain of zinc2 finger protein 278
118	c3f2cA_	Alignment	not modelled	50.1	21	**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
119	d1pfva3	Alignment	not modelled	50.1	21	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
120	d1k81a_	Alignment	not modelled	49.9	10	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta