Phyre2

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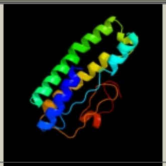
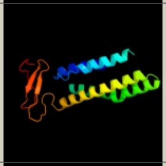
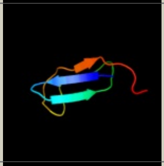
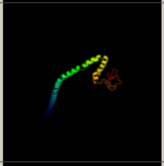
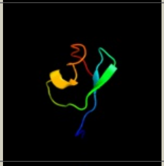
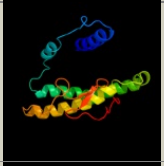
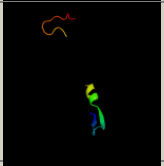
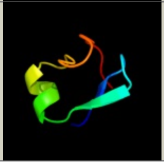
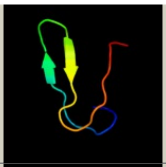
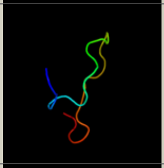
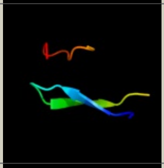
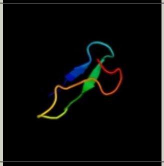
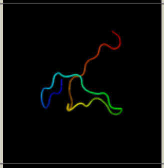
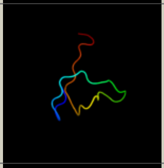
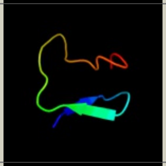
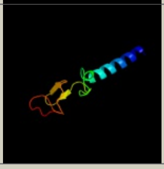
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yuzB_	Alignment		94.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
2	c2kdxA_	Alignment		94.4	19	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
3	c1dvbA_	Alignment		94.2	13	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
4	c2kwqA_	Alignment		93.7	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** mcm10 c-terminal dna binding domain
5	c3na7A_	Alignment		93.5	12	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
6	d1ltla_	Alignment		93.1	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
7	c2hr5B_	Alignment		92.8	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
8	c3a44D_	Alignment		91.7	24	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
9	c3glsC_	Alignment		91.5	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
10	d1m2ka_	Alignment		91.5	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
11	c1ltlE_	Alignment		91.4	28	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum

12	c2gb5B_	Alignment		89.7	21	**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
13	d1yc5a1	Alignment		89.4	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
14	d1q1aa_	Alignment		88.6	24	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
15	c3jwpA_	Alignment		87.0	21	**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
16	d1ma3a_	Alignment		86.7	29	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
17	c1hk8A_	Alignment		85.4	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
18	d1hk8a_	Alignment		85.4	21	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
19	c1q14A_	Alignment		85.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
20	c3floD_	Alignment		84.3	16	**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
21	c2lcqA_	Alignment	not modelled	84.1	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
22	d1s5pa_	Alignment	not modelled	83.7	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
23	d1j8fa_	Alignment	not modelled	83.1	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
24	d1p3ja2	Alignment	not modelled	81.2	27	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
25	c3pkiF_	Alignment	not modelled	81.1	26	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
26	c3k35D_	Alignment	not modelled	81.0	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
27	d1zina2	Alignment	not modelled	79.8	30	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
28	d1s3ga2	Alignment	not modelled	79.7	30	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger"

						domain
29	d1lkoa2	Alignment	not modelled	78.8	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
30	d2akla2	Alignment	not modelled	78.8	31	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
31	c3axtA_	Alignment	not modelled	78.0	20	**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
32	c3f2cA_	Alignment	not modelled	76.9	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
33	d1akya2	Alignment	not modelled	74.3	18	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
34	d1e4va2	Alignment	not modelled	74.1	18	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
35	d2gmga1	Alignment	not modelled	72.8	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
36	c3ir9A_	Alignment	not modelled	72.5	23	**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.
37	d2b4ya1	Alignment	not modelled	70.6	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
38	c2opfA_	Alignment	not modelled	70.2	22	**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
39	d1nnqa2	Alignment	not modelled	68.2	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
40	c3nw0A_	Alignment	not modelled	67.7	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
41	c2xf5C_	Alignment	not modelled	67.6	25	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**gp23.1; **PDBTitle:** crystal structure of bacillus subtilis spp1 phage gp23.1, a2 putative chaperone.
42	d1h7va_	Alignment	not modelled	67.3	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
43	d1yuza2	Alignment	not modelled	67.3	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
44	c2vl6C_	Alignment	not modelled	67.1	25	**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
45	d1ryqa_	Alignment	not modelled	66.2	27	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
46	c2riqA_	Alignment	not modelled	64.4	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
47	c3h0gL_	Alignment	not modelled	63.8	35	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
48	c2hjhB_	Alignment	not modelled	62.7	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
49	d2gnra1	Alignment	not modelled	62.2	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
50	c2jvnA_	Alignment	not modelled	62.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
51	d1dx8a_	Alignment	not modelled	61.1	28	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
52	c3lpeF_	Alignment	not modelled	59.3	33	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
53	c2kn9A_	Alignment	not modelled	58.7	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

54	d2dkta1	Alignment	not modelled	57.3	18	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
55	c2ds8A_	Alignment	not modelled	54.6	25	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
56	c1nl0G_	Alignment	not modelled	53.5	44	**PDB header:**immune system **Chain:** G: **PDB Molecule:**factor ix; **PDBTitle:** crystal structure of human factor ix gla domain in complex2 of an inhibitory antibody, 10c12
57	c2ba1B_	Alignment	not modelled	53.0	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
58	d1nuia2	Alignment	not modelled	53.0	38	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
59	c1pqvS_	Alignment	not modelled	53.0	17	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
60	d2dlqa2	Alignment	not modelled	52.4	55	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
61	c2emcA_	Alignment	not modelled	52.3	16	**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
62	c2nn6I_	Alignment	not modelled	51.8	25	**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
63	d2cona1	Alignment	not modelled	51.1	18	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
64	c1y1yS_	Alignment	not modelled	51.1	17	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
65	c3f9vA_	Alignment	not modelled	50.6	24	**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
66	c3iz6X_	Alignment	not modelled	50.2	19	**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
67	c2j6aA_	Alignment	not modelled	49.8	27	**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.
68	d1qxfa_	Alignment	not modelled	48.6	27	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
69	d2ds5a1	Alignment	not modelled	47.8	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
70	c1ovxB_	Alignment	not modelled	47.8	25	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
71	c2ja6L_	Alignment	not modelled	47.3	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
72	c2epqA_	Alignment	not modelled	45.2	29	**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
73	c1k82D_	Alignment	not modelled	44.2	19	**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
74	d2ak3a2	Alignment	not modelled	44.1	15	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
75	d1dl6a_	Alignment	not modelled	43.6	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
76	d1zbdb_	Alignment	not modelled	43.2	26	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
77	c1s24A_	Alignment	not modelled	43.0	22	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
78	d1s24a_	Alignment	not modelled	43.0	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
79	d2dsxa1	Alignment	not modelled	41.9	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like

						Family: Rubredoxin
80	d6rxna_	Alignment	not modelled	41.6	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
81	d2c4fl3	Alignment	not modelled	41.3	28	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
82	c1tjlD_	Alignment	not modelled	41.2	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dnak suppressor protein; **PDBTitle:** crystal structure of transcription factor dksa from e. coli
83	d1brfa_	Alignment	not modelled	41.1	29	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
84	d4rxna_	Alignment	not modelled	41.0	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
85	c3ermD_	Alignment	not modelled	41.0	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved protein with unknown function2 from pseudomonas syringae pv. tomato str. dc3000
86	c2ktvA_	Alignment	not modelled	40.9	26	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
87	d1x3za1	Alignment	not modelled	40.7	30	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
88	c2en8A_	Alignment	not modelled	40.7	22	**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
89	c2v3bB_	Alignment	not modelled	40.5	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
90	c2xgvA_	Alignment	not modelled	40.0	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**psiv capsid n-terminal domain; **PDBTitle:** structure of the n-terminal domain of capsid protein from2 rabbit endogenous lentivirus (relik)
91	d1iu5a_	Alignment	not modelled	40.0	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
92	c2lk0A_	Alignment	not modelled	39.9	38	**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
93	c2e2zA_	Alignment	not modelled	39.5	31	**PDB header:**protein transport, chaperone regulator **Chain:** A: **PDB Molecule:**tim15; **PDBTitle:** solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
94	c3izbX_	Alignment	not modelled	39.2	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
95	d1kbea_	Alignment	not modelled	38.3	14	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
96	c2avuF_	Alignment	not modelled	38.1	26	**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
97	d1danl3	Alignment	not modelled	36.9	28	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
98	d1pfta_	Alignment	not modelled	36.8	42	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
99	d1iroa_	Alignment	not modelled	36.8	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
100	d2avue1	Alignment	not modelled	36.7	26	**Fold:**FlhC-like **Superfamily:**FlhC-like **Family:**FlhC-like
101	d1qcva_	Alignment	not modelled	36.1	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
102	c2rowA_	Alignment	not modelled	35.1	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rho-associated protein kinase 2; **PDBTitle:** the c1 domain of rock ii
103	d2fiya1	Alignment	not modelled	34.8	26	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
104	c3g9yA_	Alignment	not modelled	34.7	31	**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
105	d1rb9a_	Alignment	not modelled	33.9	31	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin

106	d2ayja1	Alignment	not modelled	33.7	35	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e
107	c3h0gN_	Alignment	not modelled	33.6	14	**PDB header:**transcription **Chain:** N: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb2; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
108	d1ctla1	Alignment	not modelled	33.6	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
109	c2xzm6_	Alignment	not modelled	32.9	23	**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
110	c2yu5A_	Alignment	not modelled	32.8	33	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the zf-c2h2 domain (669-699aa) in2 zinc finger protein 473
111	c2js4A_	Alignment	not modelled	31.4	21	**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	c2en3A_	Alignment	not modelled	31.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 95 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 796-2 828) of human zinc finger protein 95 homolog
113	c2eozA_	Alignment	not modelled	31.0	19	**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
114	c3ky9B_	Alignment	not modelled	30.9	14	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
115	d1jj2y_	Alignment	not modelled	30.6	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
116	c1i3ql_	Alignment	not modelled	30.6	44	**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
117	c3pihA_	Alignment	not modelled	30.6	30	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
118	d1imla1	Alignment	not modelled	30.4	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
119	c2kpiA_	Alignment	not modelled	30.3	28	**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
120	d1vqoz1	Alignment	not modelled	29.6	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae