Phyre^2

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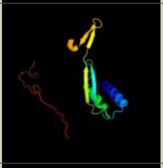
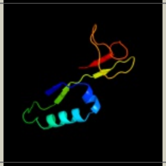
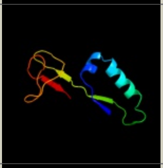
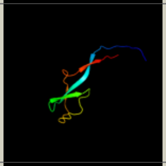
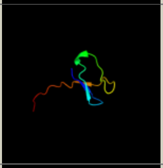
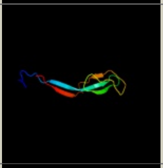
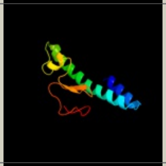
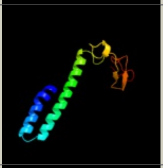
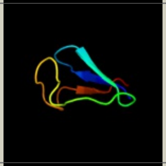
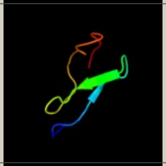
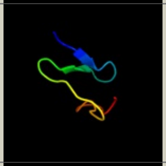
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kdxA_	Alignment		100.0	22	**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	26	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
3	d1hk8a_	Alignment		97.1	12	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
4	c1hk8A_	Alignment		97.1	12	**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
5	d2gmga1	Alignment		95.4	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PF0610-like
6	d1ltla_	Alignment		95.0	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA replication initiator (cdc21/cdc54) N-terminal domain
7	c2k2dA_	Alignment		94.9	13	**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
8	c1ltlE_	Alignment		94.7	15	**PDB header:**replication **Chain:** E: **PDB Molecule:**dna replication initiator (cdc21/cdc54); **PDBTitle:** the dodecamer structure of mcm from archaeal m.2 thermoautotrophicum
9	c2hr5B_	Alignment		94.6	14	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
10	c1dvbA_	Alignment		94.3	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
11	c2lcqA_	Alignment		93.8	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		93.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
13	d1brfa_	Alignment		92.5	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
14	d1lkoa2	Alignment		92.2	25	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
15	d1h7va_	Alignment		92.1	23	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
16	c2kn9A_	Alignment		92.1	22	**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
17	d1qcva_	Alignment		92.0	11	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
18	d1iu5a_	Alignment		91.5	21	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
19	c2v3bB_	Alignment		91.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rubredoxin 2; **PDBTitle:** crystal structure of the electron transfer complex2 rubredoxin - rubredoxin reductase from pseudomonas3 aeruginosa.
20	d1s24a_	Alignment		91.3	30	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
21	c1s24A_	Alignment	not modelled	91.3	30	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin 2; **PDBTitle:** rubredoxin domain ii from pseudomonas oleovorans
22	d1dx8a_	Alignment	not modelled	91.3	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
23	d2cona1	Alignment	not modelled	91.0	19	**Fold:**Rubredoxin-like **Superfamily:**NOB1 zinc finger-like **Family:**NOB1 zinc finger-like
24	d1iroa_	Alignment	not modelled	91.0	21	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
25	d6rxna_	Alignment	not modelled	90.7	18	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
26	d1rb9a_	Alignment	not modelled	90.6	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
27	d2rdva_	Alignment	not modelled	90.5	21	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
28	d4rxna_	Alignment	not modelled	89.9	17	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
29	d2dsxa1	Alignment	not modelled	89.7	16	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like

						Family: Rubredoxin
30	c2aklA_	Alignment	not modelled	89.2	27	**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
31	d2gnra1	Alignment	not modelled	89.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**SSO2064-like
32	d2akla2	Alignment	not modelled	87.0	27	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
33	d1nnqa2	Alignment	not modelled	85.8	20	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
34	d2fiya1	Alignment	not modelled	85.6	16	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
35	c3tsuA_	Alignment	not modelled	84.9	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
36	d1yuza2	Alignment	not modelled	83.3	19	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
37	c2vl6C_	Alignment	not modelled	83.1	10	**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	c3f9vA_	Alignment	not modelled	79.6	11	**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
39	c3floD_	Alignment	not modelled	79.6	20	**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
40	d1m2ka_	Alignment	not modelled	78.8	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
41	c3k35D_	Alignment	not modelled	77.7	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** crystal structure of human sirt6
42	c3pihA_	Alignment	not modelled	77.4	28	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
43	c3glsC_	Alignment	not modelled	77.2	37	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nad-dependent deacetylase sirtuin-3, **PDBTitle:** crystal structure of human sirt3
44	c3bvoA_	Alignment	not modelled	77.1	26	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
45	c1q14A_	Alignment	not modelled	75.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hst2 protein; **PDBTitle:** structure and autoregulation of the yeast hst2 homolog of sir2
46	d1yc5a1	Alignment	not modelled	74.8	30	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
47	c2gb5B_	Alignment	not modelled	74.7	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
48	c3pkiF_	Alignment	not modelled	74.6	27	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**nad-dependent deacetylase sirtuin-6; **PDBTitle:** human sirt6 crystal structure in complex with adp ribose
49	c3ir9A_	Alignment	not modelled	74.3	14	**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.
50	d2dkta1	Alignment	not modelled	73.9	22	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
51	c2f9iD_	Alignment	not modelled	73.5	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
52	c3cngC_	Alignment	not modelled	73.3	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
53	d2j0151	Alignment	not modelled	73.2	19	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
54	d1q1aa_	Alignment	not modelled	73.1	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
55	d1qxfa_	Alignment	not modelled	72.6	11	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins

						Family: Ribosomal protein S27e
56	d2apob1	Alignment	not modelled	72.6	37	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
57	c1i3ql_	Alignment	not modelled	72.4	30	**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
58	d2zjrz1	Alignment	not modelled	72.4	19	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
59	c3ky9B_	Alignment	not modelled	71.7	17	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
60	c3h0gL_	Alignment	not modelled	71.7	30	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
61	c3iz6X_	Alignment	not modelled	70.6	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
62	c3lpeF_	Alignment	not modelled	70.3	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
63	c3axtA_	Alignment	not modelled	70.1	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
64	d2ey4e1	Alignment	not modelled	70.0	37	**Fold:**Rubredoxin-like **Superfamily:**Nop10-like SnoRNP **Family:**Nucleolar RNA-binding protein Nop10-like
65	c2ba1B_	Alignment	not modelled	68.5	20	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
66	c3izbX_	Alignment	not modelled	68.0	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
67	c2ktvA_	Alignment	not modelled	68.0	9	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor subunit 1; **PDBTitle:** human erf1 c-domain, "open" conformer
68	d2jnea1	Alignment	not modelled	67.6	23	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
69	c2jneA_	Alignment	not modelled	67.6	23	**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.
70	d1ma3a_	Alignment	not modelled	67.0	17	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
71	c1m2oA_	Alignment	not modelled	66.2	14	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
72	c2j6aA_	Alignment	not modelled	65.8	22	**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.
73	c2nn6I_	Alignment	not modelled	65.2	24	**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
74	c2k5cA_	Alignment	not modelled	65.2	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
75	c2ja6L_	Alignment	not modelled	64.8	25	**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
76	c2kwqA_	Alignment	not modelled	64.2	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** mcm10 c-terminal dna binding domain
77	d1s5pa_	Alignment	not modelled	63.6	21	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
78	d1ryqa_	Alignment	not modelled	62.8	41	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
79	d2f9yb1	Alignment	not modelled	62.2	29	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
80	c2f9yB_	Alignment	not modelled	62.2	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
						PDB header:ribosome **Chain:** 6: **PDB Molecule:**rps27e;

81	c2xzm6_	Alignment	not modelled	62.1	20	**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
82	c2vrwB_	Alignment	not modelled	61.0	17	**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
83	d1x6ha1	Alignment	not modelled	60.4	23	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
84	d2qtva5	Alignment	not modelled	60.3	14	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
85	c2pziA_	Alignment	not modelled	60.2	24	**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
86	d1vd4a_	Alignment	not modelled	60.0	31	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
87	d2nn6i1	Alignment	not modelled	59.7	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
88	c1jocA_	Alignment	not modelled	59.2	29	**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
89	c3h0gI_	Alignment	not modelled	59.0	30	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
90	d1dl6a_	Alignment	not modelled	58.7	24	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
91	d2qam01	Alignment	not modelled	58.3	8	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
92	c3gn5B_	Alignment	not modelled	57.6	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)
93	c3jwpA_	Alignment	not modelled	57.1	30	**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
94	c1ee8A_	Alignment	not modelled	57.1	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
95	c3zyqA_	Alignment	not modelled	57.0	24	**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
96	c3bjiA_	Alignment	not modelled	56.6	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
97	d1k81a_	Alignment	not modelled	56.2	16	**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
98	d2ayja1	Alignment	not modelled	54.8	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e
99	c2jrpA_	Alignment	not modelled	54.7	29	**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
100	c2e9hA_	Alignment	not modelled	54.5	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
101	c2emcA_	Alignment	not modelled	53.3	13	**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
102	d1pfta_	Alignment	not modelled	53.2	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
103	c2hjhB_	Alignment	not modelled	52.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nad-dependent histone deacetylase sir2; **PDBTitle:** crystal structure of the sir2 deacetylase
104	c2bx9J_	Alignment	not modelled	52.0	27	**PDB header:**transcription regulation **Chain:** J: **PDB Molecule:**tryptophan rna-binding attenuator protein-inhibitory **PDBTitle:** crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
105	c2epqA_	Alignment	not modelled	52.0	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

106	d1nuia2	Alignment	not modelled	51.8	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
107	c2opfA_	Alignment	not modelled	51.6	36	**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
108	c3f2cA_	Alignment	not modelled	50.9	18	**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
109	c1nnjA_	Alignment	not modelled	50.4	22	**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
110	c2e2zA_	Alignment	not modelled	50.4	24	**PDB header:**protein transport, chaperone regulator **Chain:** A: **PDB Molecule:**tim15; **PDBTitle:** solution nmr structure of yeast tim15, co-chaperone of2 mitochondrial hsp70
111	d1pfva3	Alignment	not modelled	50.3	21	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
112	c3ld0Q_	Alignment	not modelled	50.2	27	**PDB header:**gene regulation **Chain:** Q: **PDB Molecule:**inhibitor of trap, regulated by t-box (trp) sequence rtpa; **PDBTitle:** crystal structure of b.licheniformis anti-trap protein, an antagonist2 of trap-rna interactions
113	d1p91a_	Alignment	not modelled	49.8	26	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
114	c1dvpA_	Alignment	not modelled	48.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
115	d2ct7a1	Alignment	not modelled	48.3	28	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
116	c1k82D_	Alignment	not modelled	47.5	27	**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
117	c2f5qA_	Alignment	not modelled	46.5	23	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
118	c3mv2A_	Alignment	not modelled	46.2	7	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
119	d1wfka_	Alignment	not modelled	46.2	27	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
120	c2qkdA_	Alignment	not modelled	46.0	12	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains