Phyre2

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Description	P76102
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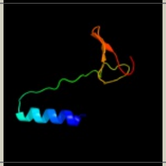
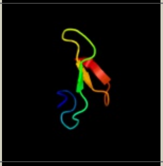
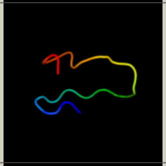
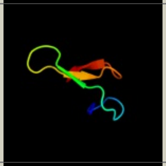
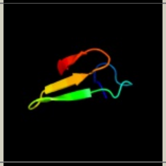
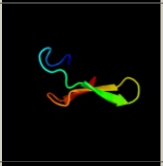
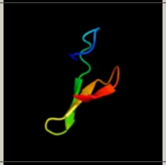
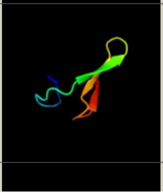
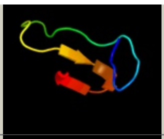
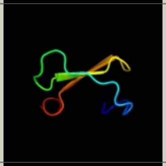
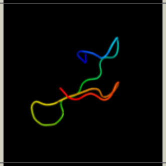
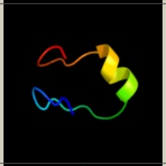
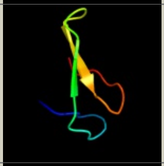
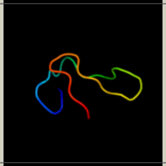
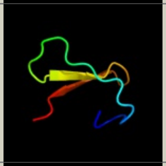
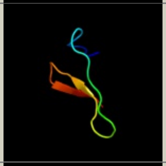
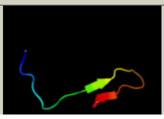
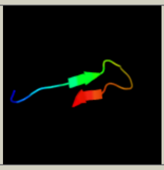
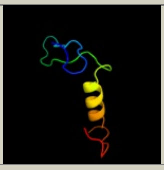
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hk8a_	Alignment		95.0	20	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
2	c1hk8A_	Alignment		95.0	20	**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
3	c2gb5B_	Alignment		94.7	23	**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
4	c2qa4Z_	Alignment		94.4	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
5	c1yuzB_	Alignment		94.2	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
6	d1ffkw_	Alignment		94.1	41	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
7	d1jj2y_	Alignment		94.1	33	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
8	d1vqoz1	Alignment		94.0	26	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
9	c2zkrz_	Alignment		93.9	30	**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
10	c1yshD_	Alignment		93.9	26	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
11	c3cc4Z_	Alignment		93.9	26	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit

12	c4a17Y_	Alignment		93.7	26	**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.
13	d2akla2	Alignment		93.6	13	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
14	c1s1i9_	Alignment		93.5	26	**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.
15	c2hr5B_	Alignment		93.5	41	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
16	d1pfta_	Alignment		93.1	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
17	c3jyw9_	Alignment		92.9	26	**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
18	c2aklA_	Alignment		92.5	14	**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
19	d1dl6a_	Alignment		92.3	14	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
20	d2fiya1	Alignment		92.2	15	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
21	c2opfA_	Alignment	not modelled	92.1	28	**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
22	c2lcqA_	Alignment	not modelled	91.5	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
23	c1ee8A_	Alignment	not modelled	91.4	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
24	c2f5qA_	Alignment	not modelled	91.4	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
25	c1nnjA_	Alignment	not modelled	91.2	24	**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
26	c3ky9B_	Alignment	not modelled	91.1	16	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
27	c3k7aM_	Alignment	not modelled	91.0	23	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
28	c1kcfB_	Alignment		90.9	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2

						junction resolvase, ydc2
29	c1k82D_	Alignment	not modelled	90.8	28	**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
30	c1dvbA_	Alignment	not modelled	90.6	26	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
31	c3cngC_	Alignment	not modelled	90.5	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
32	d1twfi2	Alignment	not modelled	90.4	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
33	c3bjiA_	Alignment	not modelled	89.9	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
34	c2vrwB_	Alignment	not modelled	89.2	16	**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
35	c1y1yS_	Alignment	not modelled	89.1	18	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
36	c1i3ql_	Alignment	not modelled	89.0	24	**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
37	c3ndjA_	Alignment	not modelled	88.2	31	**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
38	d1kcfa2	Alignment		87.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Mitochondrial resolvase ydc2 catalytic domain
39	c3pfqA_	Alignment	not modelled	87.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
40	c1pqvS_	Alignment	not modelled	87.0	19	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
41	d1tdza3	Alignment	not modelled	86.9	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
42	d1ee8a3	Alignment	not modelled	86.6	20	**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
43	d1k3xa3	Alignment	not modelled	86.3	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
44	d1r2za3	Alignment	not modelled	85.7	20	**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
45	d1l1ta3	Alignment	not modelled	85.6	20	**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	c2f9iD_	Alignment	not modelled	85.2	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
47	d1k82a3	Alignment	not modelled	85.0	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
48	c2k5cA_	Alignment	not modelled	84.7	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
49	d1yuza2	Alignment	not modelled	84.6	27	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
50	c2f9yB_	Alignment	not modelled	84.6	24	**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
51	d2f9yb1	Alignment	not modelled	84.6	24	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
52	d1nnqa2	Alignment	not modelled	84.3	41	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
53	c2qkdA_	Alignment	not modelled	84.2	28	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1;

						PDBTitle: crystal structure of tandem zpr1 domains
54	d1qypa_	Alignment	not modelled	84.0	36	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
55	d1tfia_	Alignment	not modelled	83.6	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
56	c3zyqA_	Alignment	not modelled	83.6	22	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
57	c1nuiA_	Alignment	not modelled	82.8	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
58	c3h0gI_	Alignment	not modelled	82.7	22	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
59	c1dvpA_	Alignment	not modelled	82.6	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
60	c3na7A_	Alignment	not modelled	82.4	21	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
61	d1iv0a_	Alignment	not modelled	81.4	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
62	d1nu0a_	Alignment	not modelled	81.4	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
63	d1lkoa2	Alignment	not modelled	80.8	26	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
64	d1vm9a_	Alignment	not modelled	80.5	15	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
65	d2k4xa1	Alignment	not modelled	80.1	35	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
66	c2kdxA_	Alignment	not modelled	79.0	30	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
67	d1pfva3	Alignment	not modelled	78.3	30	**Fold:**Rubredoxin-like **Superfamily:**Methionyl-tRNA synthetase (MetRS), Zn-domain **Family:**Methionyl-tRNA synthetase (MetRS), Zn-domain
68	d2ct7a1	Alignment	not modelled	78.2	29	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
69	d2j0151	Alignment	not modelled	77.8	30	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
70	c1z2qA_	Alignment	not modelled	76.8	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lm5-1; **PDBTitle:** high-resolution solution structure of the lm5-1 fyve domain2 from leishmania major
71	c3gn5B_	Alignment	not modelled	75.9	18	**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)
72	d2zjrz1	Alignment	not modelled	75.5	36	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
73	d1tbna_	Alignment	not modelled	74.4	15	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
74	c1jocA_	Alignment	not modelled	73.6	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**early endosomal autoantigen 1; **PDBTitle:** homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate
75	d1vhxa_	Alignment	not modelled	73.4	7	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
76	d1wiia_	Alignment	not modelled	73.1	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
77	c2owoA_	Alignment		72.4	18	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
						PDB header:transferase

78	c2rowA_	Alignment	not modelled	72.4	14	**Chain:** A: **PDB Molecule:**rho-associated protein kinase 2; **PDBTitle:** the c1 domain of rock ii
79	c2e9hA_	Alignment	not modelled	72.4	23	**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
80	c2ba1B_	Alignment	not modelled	72.1	22	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
81	c3t7lA_	Alignment	not modelled	72.0	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**zinc finger fyve domain-containing protein 16; **PDBTitle:** crystal structure of the fyve domain of endofin (zfyve16) at 1.1a2 resolution
82	c3a44D_	Alignment	not modelled	71.6	24	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
83	d1ptqa_	Alignment	not modelled	71.0	21	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
84	d1joca1	Alignment	not modelled	71.0	26	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**FYVE, a phosphatidylinositol-3-phosphate binding domain
85	c2enzA_	Alignment	not modelled	70.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c theta type; **PDBTitle:** solution structure of the second c1 domain from human2 protein kinase c theta
86	d1vd4a_	Alignment	not modelled	70.3	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
87	c1y8fA_	Alignment	not modelled	70.0	21	**PDB header:**endocytosis/exocytosis,signaling protein **Chain:** A: **PDB Molecule:**unc-13 homolog a; **PDBTitle:** solution structure of the munc13-1 c1-domain
88	d1l1oc_	Alignment	not modelled	69.8	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
89	c2eliA_	Alignment	not modelled	69.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c alpha type; **PDBTitle:** solution structure of the second phorbol2 esters/diacylglycerol binding domain of human protein3 kinase c alpha type
90	d1p91a_	Alignment	not modelled	69.7	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
91	d1x3za1	Alignment	not modelled	68.9	37	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
92	d2j9ub1	Alignment	not modelled	68.9	26	**Fold:**Rubredoxin-like **Superfamily:**Ran binding protein zinc finger-like **Family:**Ran binding protein zinc finger-like
93	c2j9uB_	Alignment	not modelled	68.9	26	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 36; **PDBTitle:** 2 angstrom x-ray structure of the yeast escrt-i vps28 c-2 terminus in complex with the nzf-n domain from escrt-ii
94	d1wffa_	Alignment	not modelled	68.6	38	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
95	c2dcuB_	Alignment	not modelled	67.9	22	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
96	c2nn6I_	Alignment	not modelled	67.9	7	**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
97	c3cw2M_	Alignment	not modelled	67.9	19	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
98	d1xa6a3	Alignment	not modelled	67.8	23	**Fold:**Cysteine-rich domain **Superfamily:**Cysteine-rich domain **Family:**Protein kinase cysteine-rich domain (cys2, phorbol-binding domain)
99	c2i7fB_	Alignment	not modelled	67.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
100	d1k81a_	Alignment	not modelled	67.3	22	**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
101	c3dqyA_	Alignment	not modelled	67.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin **PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin
102	c2de7E_	Alignment	not modelled	65.5	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ferredoxin component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
103	d1dgsa1	Alignment	not modelled	65.4	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like

						Family:NAD+-dependent DNA ligase, domain 3
104	c2ennA_	Alignment	not modelled	65.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c theta type; **PDBTitle:** solution structure of the first c1 domain from human2 protein kinase c theta
105	c2js4A_	Alignment	not modelled	64.8	19	**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
106	c1neeA_	Alignment	not modelled	64.8	22	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
107	c1dgsB_	Alignment	not modelled	64.8	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
108	c3egxB_	Alignment	not modelled	64.5	24	**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
109	c1p84E_	Alignment	not modelled	64.1	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
110	d1wfpa_	Alignment	not modelled	64.0	41	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
111	d1pvma3	Alignment	not modelled	64.0	35	**Fold:**Rubredoxin-like **Superfamily:**Hypothetical protein Ta0289 C-terminal domain **Family:**Hypothetical protein Ta0289 C-terminal domain
112	c2e73A_	Alignment	not modelled	64.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c gamma type; **PDBTitle:** solution structure of the phorbol esters/diacylglycerol2 binding domain of protein kinase c gamma
113	c3bvoA_	Alignment	not modelled	64.0	31	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
114	c2gajA_	Alignment	not modelled	63.4	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga maritima in2 monoclinic crystal form
115	c1x4uA_	Alignment	not modelled	63.2	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**zinc finger, fyve domain containing 27 isoform b; **PDBTitle:** solution structure of the fyve domain from human fyve2 domain containing 27 isoform b protein
116	c3eswA_	Alignment	not modelled	63.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
117	c2jr6A_	Alignment	not modelled	62.9	4	**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
118	c2pziA_	Alignment	not modelled	62.4	25	**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
119	c2e76D_	Alignment	not modelled	62.4	22	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
120	d1d0qa_	Alignment	not modelled	62.0	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger