Phyre2

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Description	P50465
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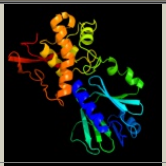
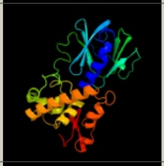
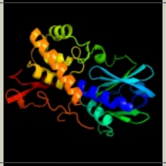
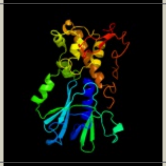
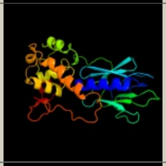
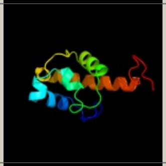
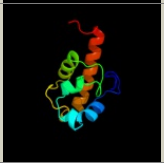
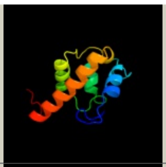
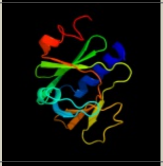
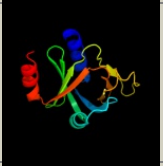
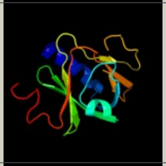
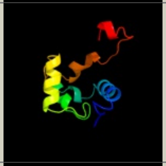
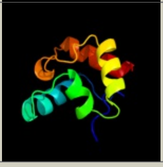
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2opfA_	Alignment		100.0	98	**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
2	c2f5qA_	Alignment		100.0	30	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
3	c1nnjA_	Alignment		100.0	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
4	c1k82D_	Alignment		100.0	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
5	c1ee8A_	Alignment		100.0	27	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
6	c3a46B_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of mvnei1/thf complex
7	c1tdhA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nei endonuclease viii-like 1; **PDBTitle:** crystal structure of human endonuclease viii-like 1 (neil1)
8	d1k3xa1	Alignment		100.0	100	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
9	d1k3xa2	Alignment		100.0	98	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
10	d1r2za1	Alignment		100.0	27	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
11	d1k82a1	Alignment		100.0	22	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins

12	d1ee8a1	Alignment		100.0	28	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
13	d1tdza1	Alignment		100.0	25	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
14	d1r2za2	Alignment		99.9	27	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
15	d1ee8a2	Alignment		99.9	25	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
16	d1tdza2	Alignment		99.9	20	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
17	d1k82a2	Alignment		99.9	22	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
18	d1tdha1	Alignment		99.8	30	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
19	d1tdha2	Alignment		99.8	20	**Fold:**N-terminal domain of MutM-like DNA repair proteins **Superfamily:**N-terminal domain of MutM-like DNA repair proteins **Family:**N-terminal domain of MutM-like DNA repair proteins
20	d2hkja1	Alignment		99.6	20	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
21	d1k3xa3	Alignment	not modelled	99.5	100	**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
22	d1ee8a3	Alignment	not modelled	99.5	32	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
23	d1tdza3	Alignment	not modelled	99.5	34	**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
24	d1r2za3	Alignment	not modelled	99.5	42	**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
25	d1k82a3	Alignment	not modelled	99.5	36	**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
26	d1l1ta3	Alignment	not modelled	99.4	46	**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
27	d2uubm1	Alignment	not modelled	96.8	24	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
28	c2zkqm_	Alignment	not modelled	96.6	14	**PDB header:**ribosomal protein/rna **Chain:** M: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

29	c3iz6M_	Alignment	not modelled	96.5	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**40s ribosomal protein s18 (s13p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
30	d1i94m_	Alignment	not modelled	96.4	27	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
31	d2gy9m1	Alignment	not modelled	96.4	24	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
32	c2xznM_	Alignment	not modelled	96.3	20	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**rps18e; **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 2
33	c3doaA_	Alignment	not modelled	96.1	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fibrinogen binding protein; **PDBTitle:** the crystal structure of the fibrinogen binding protein from2 staphylococcus aureus
34	d2i0za2	Alignment	not modelled	94.0	21	**Fold:**HI0933 insert domain-like **Superfamily:**HI0933 insert domain-like **Family:**HI0933 insert domain-like
35	c1mx0D_	Alignment	not modelled	93.6	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**type ii dna topoisomerase vi subunit b; **PDBTitle:** structure of topoisomerase subunit
36	d1qyra_	Alignment	not modelled	90.9	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA adenine dimethylase-like
37	c2gb5B_	Alignment	not modelled	88.3	20	**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
38	c3uzuA_	Alignment	not modelled	88.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** the structure of the ribosomal rna small subunit methyltransferase a2 from burkholderia pseudomallei
39	c3fuxB_	Alignment	not modelled	85.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** t. thermophilus 16s rrna a1518 and a1519 methyltransferase (ksga) in2 complex with 5'-methylthioadenosine in space group p212121
40	c3fteA_	Alignment	not modelled	85.3	15	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**dimethyladenosine transferase; **PDBTitle:** crystal structure of a. aeolicus ksga in complex with rna
41	c1yuzB_	Alignment	not modelled	85.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
42	c3tqsB_	Alignment	not modelled	82.1	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal rna small subunit methyltransferase a; **PDBTitle:** structure of the dimethyladenosine transferase (ksga) from coxiella2 burnetii
43	c3bbnM_	Alignment	not modelled	78.7	23	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**ribosomal protein s13; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
44	d2fiya1	Alignment	not modelled	78.1	23	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
45	c1dvbA_	Alignment	not modelled	77.4	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
46	d1twfi2	Alignment	not modelled	74.7	29	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
47	d2gqfa2	Alignment	not modelled	74.4	15	**Fold:**HI0933 insert domain-like **Superfamily:**HI0933 insert domain-like **Family:**HI0933 insert domain-like
48	c2jneA_	Alignment	not modelled	74.0	17	**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.
49	d2jnea1	Alignment	not modelled	74.0	17	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
50	c2jrpA_	Alignment	not modelled	73.5	17	**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
51	d2f4ma1	Alignment	not modelled	73.4	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
52	c3u50C_	Alignment	not modelled	70.8	27	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**telomerase-associated protein 82; **PDBTitle:** crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-c
53	d2akla2	Alignment	not modelled	70.5	42	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
						Fold: Rubredoxin-like

54	d1qypa_	Alignment	not modelled	69.9	32	**Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
55	c2owoA_	Alignment	not modelled	65.1	38	**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
56	c2hr5B_	Alignment	not modelled	62.7	29	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
57	d1pfta_	Alignment	not modelled	61.8	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
58	c3eg9B_	Alignment	not modelled	61.7	23	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
59	c2kpiA_	Alignment	not modelled	61.6	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco3027; **PDBTitle:** solution nmr structure of streptomyces coelicolor sco30272 modeled with zn+2 bound, northeast structural genomics3 consortium target rr58
60	d1l1oc_	Alignment	not modelled	61.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
61	c3egxB_	Alignment	not modelled	61.2	29	**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
62	c2h1rA_	Alignment	not modelled	61.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dimethyladenosine transferase, putative; **PDBTitle:** crystal structure of a dimethyladenosine transferase from2 plasmodium falciparum
63	c1dgsB_	Alignment	not modelled	60.8	35	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
64	c1pd0A_	Alignment	not modelled	60.7	27	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
65	c2lcqA_	Alignment	not modelled	60.1	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
66	d1tfia_	Alignment	not modelled	59.7	30	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
67	d1qf8a_	Alignment	not modelled	59.5	30	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
68	d1odha_	Alignment	not modelled	57.7	13	**Fold:**GCM domain **Superfamily:**GCM domain **Family:**GCM domain
69	c3h0gI_	Alignment	not modelled	57.6	28	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
70	c3eh2B_	Alignment	not modelled	55.8	19	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
71	c1m2vB_	Alignment	not modelled	54.9	27	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
72	c1i3qI_	Alignment	not modelled	53.4	29	**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
73	c2js4A_	Alignment	not modelled	53.0	17	**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
74	c3na7A_	Alignment	not modelled	52.5	24	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
75	d1x3za1	Alignment	not modelled	52.2	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
76	c2zbkB_	Alignment	not modelled	52.1	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**type 2 dna topoisomerase 6 subunit b; **PDBTitle:** crystal structure of an intact type ii dna topoisomerase:2 insights into dna transfer mechanisms
77	c2jr6A_	Alignment	not modelled	51.6	13	**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
78	c1m2oA_	Alignment	not modelled	51.3	23	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
79	c2riqA_	Alignment	not modelled	50.7	25	**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
80	d2ct7a1	Alignment	not modelled	50.1	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
81	d1pd0a5	Alignment	not modelled	49.8	27	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
82	d2avue1	Alignment	not modelled	49.1	20	**Fold:**FlhC-like **Superfamily:**FlhC-like **Family:**FlhC-like
83	c2jvnA_	Alignment	not modelled	48.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
84	c3eswA_	Alignment	not modelled	46.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
85	c2avuF_	Alignment	not modelled	45.0	20	**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
86	d2jnya1	Alignment	not modelled	44.5	13	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
87	c2ba1B_	Alignment	not modelled	44.1	23	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
88	d1u5ka2	Alignment	not modelled	43.8	21	**Fold:**ArfGap/RecO-like zinc finger **Superfamily:**ArfGap/RecO-like zinc finger **Family:**RecO C-terminal domain-like
89	c3kp9A_	Alignment	not modelled	43.1	67	**PDB header:**blood coagulation,oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** structure of a bacterial homolog of vitamin k epoxide reductase
90	d2b9da1	Alignment	not modelled	42.7	28	**Fold:**E7 C-terminal domain-like **Superfamily:**E7 C-terminal domain-like **Family:**E7 C-terminal domain-like
91	c1u5kA_	Alignment	not modelled	41.6	23	**PDB header:**recombination,replication **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** recombinational repair protein reco
92	d2k4xa1	Alignment	not modelled	41.6	32	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
93	d1ctla1	Alignment	not modelled	41.5	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
94	d1ibia1	Alignment	not modelled	39.3	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
95	d1wd2a_	Alignment	not modelled	39.3	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
96	d1dl6a_	Alignment	not modelled	39.2	22	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
97	c1nypA_	Alignment	not modelled	39.1	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**pinch protein; **PDBTitle:** 4th lim domain of pinch protein
98	c3d00A_	Alignment	not modelled	39.0	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**tungsten formylmethanofuran dehydrogenase subunit e; **PDBTitle:** crystal structure of a tungsten formylmethanofuran dehydrogenase2 subunit e (fmde)-like protein (syn_00638) from syntrophus3 aciditrophicus at 1.90 a resolution
99	d2pk7a1	Alignment	not modelled	38.3	13	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
100	d2hf1a1	Alignment	not modelled	38.3	22	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
101	d1nuia2	Alignment	not modelled	37.4	30	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
102	c2qkdA_	Alignment	not modelled	37.1	16	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
103	c2yrcA_	Alignment	not modelled	36.8	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** solution structure of the zf-sec23_sec24 from human sec23a
104	d1lkoa2	Alignment	not modelled	36.3	41	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
105	d1vd4a_	Alignment	not modelled	36.1	33	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
						PDB header:oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein

106	c2hl7A_	Alignment	not modelled	35.8	67	ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
107	c2d56A_	Alignment	not modelled	34.5	26	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**asabf; **PDBTitle:** solution structure of asabf, antibacterial peptide isolated2 from a nematode, ascaris suum
108	d2qtva5	Alignment	not modelled	34.3	23	**Fold:**Rubredoxin-like **Superfamily:**Zn-finger domain of Sec23/24 **Family:**Zn-finger domain of Sec23/24
109	c3zvzB_	Alignment	not modelled	33.9	38	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** phd finger of human uhrf1
110	c3a44D_	Alignment	not modelled	32.7	23	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
111	c1pqvS_	Alignment	not modelled	30.6	19	**PDB header:**transferase/transcription **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis complex
112	c1y1yS_	Alignment	not modelled	30.6	22	**PDB header:**transferase/transcription/dna-rna hybrid **Chain:** S: **PDB Molecule:**transcription elongation factor s-ii; **PDBTitle:** rna polymerase ii-tfiis-dna/rna complex
113	c2qneA_	Alignment	not modelled	30.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
114	c2nn6I_	Alignment	not modelled	30.1	23	**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
115	d2ct1a1	Alignment	not modelled	29.9	38	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
116	c2yg8B_	Alignment	not modelled	29.3	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna-3-methyladenine glycosidase ii, putative; **PDBTitle:** structure of an unusual 3-methyladenine dna glycosylase ii (2 alka) from deinococcus radiodurans
117	c2o10A_	Alignment	not modelled	29.1	24	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**muscle lim protein; **PDBTitle:** solution structure of the n-terminal lim domain of mlp/crp3
118	c2kw0A_	Alignment	not modelled	29.1	67	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
119	c2k5rA_	Alignment	not modelled	28.9	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein xf2673; **PDBTitle:** solution nmr structure of xf2673 from xylella fastidiosa.2 northeast structural genomics consortium target xfr39
120	c1x6aA_	Alignment	not modelled	28.7	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lim domain kinase 2; **PDBTitle:** solution structures of the second lim domain of human lim-2 kinase 2 (limk2)