Phyre2

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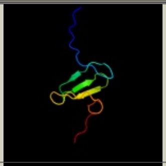
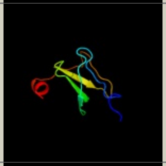
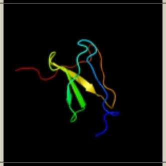
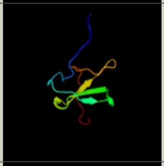
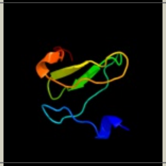
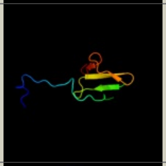
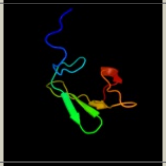
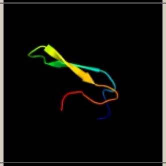
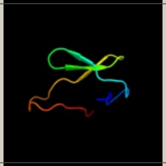
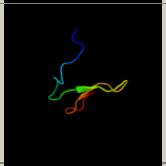
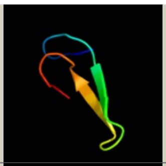
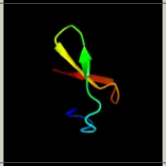
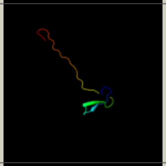
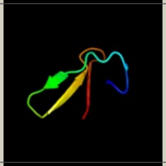
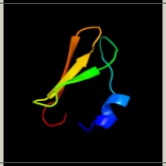
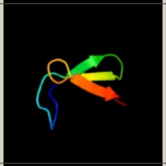
Description	P0AAZ7
Date	Thu Jan 5 11:14:13 GMT 2012
Unique Job ID	81dfbf7044774b9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2js4A_	Alignment		99.9	50	**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
2	c2jr6A_	Alignment		99.9	48	**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
3	d2jnya1	Alignment		99.9	44	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
4	d2hf1a1	Alignment		99.9	55	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
5	d2pk7a1	Alignment		99.9	57	**Fold:**Trm112p-like **Superfamily:**Trm112p-like **Family:**Trm112p-like
6	c2k5rA_	Alignment		99.8	33	**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
7	c2kpiA_	Alignment		99.8	44	**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
8	c2j6aA_	Alignment		98.5	28	**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.
9	d1p91a_	Alignment		97.6	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase RlmA
10	d1dl6a_	Alignment		95.7	22	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
11	c3k7aM_	Alignment		95.0	26	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex

12	d1pfta_	Alignment		94.5	31	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
13	c2aklA_	Alignment		92.9	26	**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
14	c2gb5B_	Alignment		92.4	9	**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
15	d2akla2	Alignment		92.4	26	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**PhnA zinc-binding domain
16	c3q87A_	Alignment		90.1	50	**PDB header:**transferase activator/transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ecu08_1170; **PDBTitle:** structure of eukaryotic translation termination complex2 methyltransferase mtq2-trm112
17	d2fiya1	Alignment		83.2	21	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
18	c2jneA_	Alignment		82.1	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.
19	d2jnea1	Alignment		82.1	17	**Fold:**Rubredoxin-like **Superfamily:**YfgJ-like **Family:**YfgJ-like
20	c2dcuB_	Alignment		80.9	23	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
21	c1neeA_	Alignment	not modelled	80.6	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
22	d2ct7a1	Alignment	not modelled	77.7	27	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**IBR domain
23	c2e9hA_	Alignment	not modelled	77.2	26	**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
24	c2jrpA_	Alignment	not modelled	75.7	34	**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
25	c3cw2M_	Alignment	not modelled	74.3	18	**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 .
26	c3gceA_	Alignment	not modelled	73.5	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
27	c2k5cA_	Alignment	not modelled	70.7	30	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
28	c3cngC_	Alignment	not modelled	69.6	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase;

28	c3cngC_	Alignment	not modelled	69.6	19	**PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
29	d1k81a_	Alignment	not modelled	67.8	24	**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
30	c2f9iD_	Alignment	not modelled	66.7	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
31	d1vm9a_	Alignment	not modelled	66.6	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
32	d1dgsa1	Alignment	not modelled	65.5	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**NAD+-dependent DNA ligase, domain 3
33	c1i3ql_	Alignment	not modelled	63.3	18	**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
34	c2i7fB_	Alignment	not modelled	60.7	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
35	c2owoA_	Alignment	not modelled	59.7	24	**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
36	c2f9yB_	Alignment	not modelled	58.9	16	**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
37	d2f9yb1	Alignment	not modelled	58.9	16	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
38	c3h0gI_	Alignment	not modelled	58.7	19	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb9; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
39	d1l1oc_	Alignment	not modelled	57.7	37	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
40	d3c0da1	Alignment	not modelled	56.5	16	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
41	d1bora_	Alignment	not modelled	55.8	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
42	c2f5qA_	Alignment	not modelled	55.4	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
43	d1jm7b_	Alignment	not modelled	55.2	21	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
44	d1rfsa_	Alignment	not modelled	54.6	12	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
45	c2opfA_	Alignment	not modelled	54.6	13	**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
46	d1g8kb_	Alignment	not modelled	53.5	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
47	d2jzaa1	Alignment	not modelled	52.7	25	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
48	d1wiia_	Alignment	not modelled	52.2	23	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
49	c1nnjA_	Alignment	not modelled	51.9	12	**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
50	c1ee8A_	Alignment	not modelled	51.8	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**mutm (fpg) protein; **PDBTitle:** crystal structure of mutm (fpg) protein from thermus thermophilus hb8
51	c2kdxA_	Alignment	not modelled	48.1	34	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
52	c1k82D_	Alignment	not modelled	48.0	21	**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
53	c2yu4A_	Alignment	not modelled	48.0	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**e3 sumo-protein ligase nse2; **PDBTitle:** solution structure of the sp-ring domain in non-smc element2 2 homolog (mms21, s. cerevisiae)
54	c2gajA_	Alignment	not modelled	47.8	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase i; **PDBTitle:** structure of full length topoisomerase i from thermotoga

						maritima in2 monoclinic crystal form
55	d1q90c_	Alignment	not modelled	46.9	6	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
56	c3ztgA_	Alignment	not modelled	46.2	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase rbbp6; **PDBTitle:** solution structure of the ring finger-like domain of2 retinoblastoma binding protein-6 (rbbp6)
57	d1vd4a_	Alignment	not modelled	46.1	21	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
58	d1ibia2	Alignment	not modelled	46.0	26	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
59	c3bvoA_	Alignment	not modelled	44.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
60	d2jo6a1	Alignment	not modelled	44.6	28	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
61	c2ba1B_	Alignment	not modelled	44.3	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**archaeal exosome rna binding protein csl4; **PDBTitle:** archaeal exosome core
62	c2riqA_	Alignment	not modelled	44.3	24	**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
63	c2jvnA_	Alignment	not modelled	44.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
64	c3lrqB_	Alignment	not modelled	43.3	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase trim37; **PDBTitle:** crystal structure of the u-box domain of human ubiquitin-2 protein ligase (e3), northeast structural genomics3 consortium target hr4604d.
65	c2de7E_	Alignment	not modelled	42.7	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
66	d1fqta_	Alignment	not modelled	42.4	23	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
67	c2qpzA_	Alignment	not modelled	42.1	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
68	c3d89A_	Alignment	not modelled	41.3	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
69	d2baya1	Alignment	not modelled	40.8	9	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
70	c3cc4Z_	Alignment	not modelled	40.5	26	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
71	c4a17Y_	Alignment	not modelled	39.9	19	**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.
72	d1ffkw_	Alignment	not modelled	39.0	19	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
73	d1tdza3	Alignment	not modelled	38.9	12	**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
74	d1weva_	Alignment	not modelled	38.6	22	**Fold:**FYVE/PHD zinc finger **Superfamily:**FYVE/PHD zinc finger **Family:**PHD domain
75	c2nn6I_	Alignment	not modelled	38.5	8	**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
76	d1k82a3	Alignment	not modelled	38.5	21	**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
77	c2qa4Z_	Alignment	not modelled	38.2	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
78	d1k3xa3	Alignment	not modelled	37.6	13	**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
79	c1dgsB_	Alignment	not modelled	37.6	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
80	d1r2za3	Alignment	not modelled	37.4	13	**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
81	d2k4xa1	Alignment	not modelled	37.4	15	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27a
82	d1z01a1	Alignment	not modelled	37.3	22	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
83	d1l1ta3	Alignment	not modelled	37.0	13	**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
84	c2e76D_	Alignment	not modelled	36.4	12	**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
85	c2qkdA_	Alignment	not modelled	35.6	27	**PDB header:**signaling protein, cell cycle **Chain:** A: **PDB Molecule:**zinc finger protein zpr1; **PDBTitle:** crystal structure of tandem zpr1 domains
86	c2y43B_	Alignment	not modelled	35.2	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**e3 ubiquitin-protein ligase rad18; **PDBTitle:** rad18 ubiquitin ligase ring domain structure
87	c3floD_	Alignment	not modelled	35.1	34	**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
88	d1vqoz1	Alignment	not modelled	34.9	26	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
89	c1rmdA_	Alignment	not modelled	34.6	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**rag1; **PDBTitle:** rag1 dimerization domain
90	c1yshD_	Alignment	not modelled	34.6	15	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
91	c1v9pB_	Alignment	not modelled	33.7	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
92	c2zkrz_	Alignment	not modelled	33.7	11	**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
93	d1jj2y_	Alignment	not modelled	33.6	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
94	c3a44D_	Alignment	not modelled	33.6	14	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
95	d2de6a1	Alignment	not modelled	33.1	19	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
96	c3ndjA_	Alignment	not modelled	33.0	33	**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
97	c2hl7A_	Alignment	not modelled	32.7	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
98	c2f6nA_	Alignment	not modelled	32.4	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**bromodomain phd finger transcription factor; **PDBTitle:** crystal structure of phd finger-linker-bromodomain fragment2 of human bptf in the free form
99	d1ee8a3	Alignment	not modelled	31.1	19	**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
100	d1jm7a_	Alignment	not modelled	30.4	25	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
101	c2cklA_	Alignment	not modelled	30.3	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb group ring finger protein 4; **PDBTitle:** ring1b-bmi1 e3 catalytic domain structure
102	c2ct2A_	Alignment	not modelled	29.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tripartite motif protein 32; **PDBTitle:** solution structure of the ring domain of the tripartite2 motif protein 32
103	c2ecwA_	Alignment	not modelled	28.9	19	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**tripartite motif-containing protein 30; **PDBTitle:** solution structure of the zinc finger, c3hc4 type (ring2 finger) domain tripartite motif protein 30
104	d1p3ja2	Alignment	not modelled	28.8	20	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
105	c1nuiA_	Alignment	not modelled	28.7	8	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of

						bacteriophage t7 primase-2 helicase protein
106	c3dqyA_	Alignment	not modelled	28.4	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin **PDBTitle:** crystal structure of toluene 2,3-dioxygenase ferredoxin
107	d1akya2	Alignment	not modelled	27.8	16	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
108	d1s3ga2	Alignment	not modelled	27.8	27	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
109	d1lv3a_	Alignment	not modelled	27.5	19	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Hypothetical zinc finger protein YacG
110	c3hi2C_	Alignment	not modelled	26.8	29	**PDB header:**dna binding protein/toxin **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit); **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
111	c2kw0A_	Alignment	not modelled	26.5	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
112	c2xb1A_	Alignment	not modelled	26.4	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**pygopus homolog 2, b-cell cll/lymphoma 9-like protein; **PDBTitle:** crystal structure of the human pygo2 phd finger in complex with the2 b9l hd1 domain
113	c3nw0A_	Alignment	not modelled	26.4	20	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**non-structural maintenance of chromosomes element 1 **PDBTitle:** crystal structure of mageg1 and nse1 complex
114	c1s1i9_	Alignment	not modelled	26.4	15	**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.
115	d1g25a_	Alignment	not modelled	24.9	13	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4
116	c3u50C_	Alignment	not modelled	24.9	8	**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
117	d1e4va2	Alignment	not modelled	24.5	5	**Fold:**Rubredoxin-like **Superfamily:**Microbial and mitochondrial ADK, insert "zinc finger" domain **Family:**Microbial and mitochondrial ADK, insert "zinc finger" domain
118	c3jyw9_	Alignment	not modelled	24.5	15	**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
119	d2dkta1	Alignment	not modelled	24.1	12	**Fold:**CHY zinc finger-like **Superfamily:**CHY zinc finger-like **Family:**CHY zinc finger
120	c3gn5B_	Alignment	not modelled	23.8	37	**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)