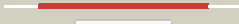
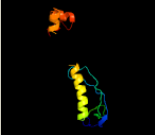
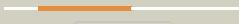
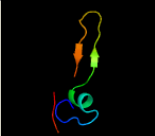
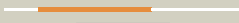









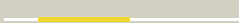


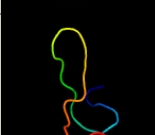

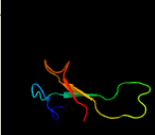

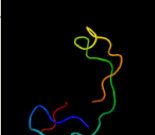



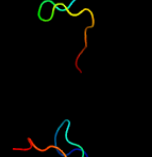
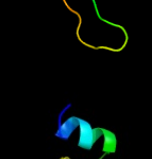

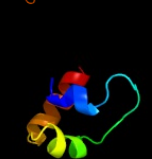

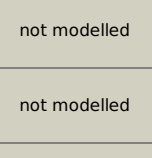


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0850 (-) _947315_947647
Date	Fri Jul 26 01:50:44 BST 2019
Unique Job ID	e79e87f9b81d5dd4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gn5B_	 Alignment		93.7	13	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)
2	c2qkdA_	 Alignment		89.1	19	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
3	c2hu9B_	 Alignment		87.6	19	PDB header: metal transport Chain: B: PDB Molecule: mercuric transport protein periplasmic component; PDBTitle: x-ray structure of the archaeoglobus fulgidus copz n-2 terminal domain
4	d1dgsa1	 Alignment		87.1	32	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
5	c5fjaL_	 Alignment		78.5	32	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase iii subunit rpc10; PDBTitle: cryo-em structure of yeast rna polymerase iii at 4.7 a
6	d1pvma3	 Alignment		76.7	39	Fold: Rubredoxin-like Superfamily: Hypothetical protein Ta0289 C-terminal domain Family: Hypothetical protein Ta0289 C-terminal domain
7	c1dgsB_	 Alignment		74.7	32	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
8	d2fiya1	 Alignment		73.3	29	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
9	c1v9pB_	 Alignment		69.3	32	PDB header: ligase Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
10	c5flmL_	 Alignment		65.7	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
11	d1x3za1	 Alignment		64.0	16	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core

12	c3floD	Alignment		59.5	18	PDB header: transferase Chain: D: PDB Molecule: dna polymerase alpha catalytic subunit a; PDBTitle: crystal structure of the carboxyl-terminal domain of yeast dna2 polymerase alpha in complex with its b subunit
13	d1k78a1	Alignment		58.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
14	c2owoA	Alignment		57.1	32	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
15	c4qiwP	Alignment		54.0	28	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
16	c4glxA	Alignment		53.0	37	PDB header: ligase/ligase inhibitor/dna Chain: A: PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
17	d1qpza1	Alignment		52.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
18	d1qypa	Alignment		51.0	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
19	d2dk5a1	Alignment		50.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RPO3F domain-like
20	d1twfi2	Alignment		50.5	13	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
21	c3j39p	Alignment	not modelled	49.9	23	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
22	d2hsga1	Alignment	not modelled	47.7	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
23	d1lcda	Alignment	not modelled	47.5	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
24	d2bjca1	Alignment	not modelled	46.7	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
25	d1luxca	Alignment	not modelled	45.7	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
26	d1hlva1	Alignment	not modelled	44.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
27	d1a1ha1	Alignment	not modelled	44.3	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
28	c2lcvA	Alignment	not modelled	44.2	18	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
29	c3jzrm	Alignment	not modelled	43.4	23	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p);

29	c2zfm_	Alignment	not modelled	43.4	33	PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
30	d1efaa1	Alignment	not modelled	43.3	4	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
31	d2jneA1	Alignment	not modelled	43.0	33	Fold: Rubredoxin-like Superfamily: YfgJ-like Family: YfgJ-like
32	c2jneA_	Alignment	not modelled	43.0	33	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. northeast2 structural genomics consortium target er317.
33	d1luxda_	Alignment	not modelled	43.0	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
34	c4bs9A_	Alignment	not modelled	42.6	36	PDB header: isomerase Chain: A: PDB Molecule: trud; PDBTitle: structure of the heterocyclase trud
35	d2akla2	Alignment	not modelled	42.2	43	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: PhnA zinc-binding domain
36	c3h0gl_	Alignment	not modelled	41.5	24	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
37	c5a3aA_	Alignment	not modelled	41.5	36	PDB header: transferase Chain: A: PDB Molecule: sir2 family protein; PDBTitle: crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
38	c2gb5B_	Alignment	not modelled	41.0	24	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
39	c4c2mX_	Alignment	not modelled	41.0	34	PDB header: transcription Chain: X: PDB Molecule: dna-directed rna polymerase i subunit rpa12; PDBTitle: structure of rna polymerase i at 2.8 a resolution
40	c3cngC_	Alignment	not modelled	40.5	37	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
41	c3j2i1_	Alignment	not modelled	39.4	45	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
42	d1ubdc3	Alignment	not modelled	39.2	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
43	d6paxa1	Alignment	not modelled	38.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
44	d1u86a1	Alignment	not modelled	37.5	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
45	c2yu3A_	Alignment	not modelled	36.8	18	PDB header: transcription Chain: A: PDB Molecule: dna-directed rna polymerase iii 39 kda PDBTitle: solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide
46	d2j0151	Alignment	not modelled	36.6	71	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
47	c3j3v0_	Alignment	not modelled	36.5	43	PDB header: ribosome Chain: O: PDB Molecule: 50s ribosomal protein l32; PDBTitle: atomic model of the immature 50s subunit from bacillus subtilis (state2 i-a)
48	c4y97H_	Alignment	not modelled	36.4	34	PDB header: transferase Chain: H: PDB Molecule: dna polymerase alpha catalytic subunit; PDBTitle: crystal structure of human pol alpha b-subunit in complex with c-2 terminal domain of catalytic subunit
49	c2nb9A_	Alignment	not modelled	35.9	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
50	c2odxA_	Alignment	not modelled	35.9	22	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c oxidase polypeptide iv; PDBTitle: solution structure of zn(ii)cox4
51	d1jj2y_	Alignment	not modelled	34.9	34	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
52	d1m2ka_	Alignment	not modelled	34.2	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
53	c1yshD_	Alignment	not modelled	34.1	30	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
54	d1a1a1a1	Alignment	not modelled	33.9	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
55	c2zkrz_	Alignment	not modelled	33.8	27	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna

						and proteins into an 3.8.7 a cryo-em map
56	d2zjrz1	Alignment	not modelled	33.6	71	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
57	c4rulA_	Alignment	not modelled	33.4	30	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
58	d1vqoz1	Alignment	not modelled	32.9	33	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
59	c3glsC_	Alignment	not modelled	32.8	27	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
60	d1yuza2	Alignment	not modelled	32.7	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
61	d1zyba1	Alignment	not modelled	32.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
62	d1aaya1	Alignment	not modelled	31.5	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
63	c2l8nA_	Alignment	not modelled	31.3	17	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
64	c5xonU_	Alignment	not modelled	30.9	17	PDB header: transcription/rna Chain: U: PDB Molecule: general transcription elongation factor tfiis; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
65	d1lkoa2	Alignment	not modelled	30.8	27	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
66	d1nnqa2	Alignment	not modelled	30.4	36	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
67	d1ubdc4	Alignment	not modelled	30.3	31	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
68	d1tf3a2	Alignment	not modelled	29.9	14	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
69	c1i3ql_	Alignment	not modelled	29.8	17	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
70	d2ey4e1	Alignment	not modelled	29.6	27	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
71	c3hhgF_	Alignment	not modelled	29.5	11	PDB header: transcription regulator Chain: F: PDB Molecule: transcriptional regulator, lysr family; PDBTitle: structure of crga, a lysr-type transcriptional regulator from 2 neisseria meningitidis.
72	c2aklA_	Alignment	not modelled	29.2	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phna-like protein pa0128; PDBTitle: solution structure for phn-a like protein pa0128 from 2 pseudomonas aeruginosa
73	d2f4ma1	Alignment	not modelled	29.0	13	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
74	c1s1i9_	Alignment	not modelled	28.8	17	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
75	c2qa4Z_	Alignment	not modelled	28.0	33	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
76	d1imla1	Alignment	not modelled	27.6	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
77	d2dlqa2	Alignment	not modelled	27.3	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
78	d2cona1	Alignment	not modelled	27.1	25	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
79	d1yc5a1	Alignment	not modelled	26.9	27	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
80	c3eswA_	Alignment	not modelled	26.8	18	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
81	d1ffkw_	Alignment	not modelled	26.3	27	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae

82	d2gaua1	Alignment	not modelled	25.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
83	c1nuia_	Alignment	not modelled	25.8	13	PDB header: replication Chain: A: PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
84	clareA_	Alignment	not modelled	25.8	22	PDB header: transcription regulation Chain: A: PDB Molecule: yeast transcription factor adr1; PDBTitle: structures of dna-binding mutant zinc finger domains: implications for2 dna binding
85	d1tdza3	Alignment	not modelled	25.5	29	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
86	c5fo5A_	Alignment	not modelled	25.3	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
87	d1u85a1	Alignment	not modelled	24.9	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
88	c3iz5i_	Alignment	not modelled	24.9	25	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein l10 (l10e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
89	c3lsgD_	Alignment	not modelled	24.9	15	PDB header: transcription regulator Chain: D: PDB Molecule: two-component response regulator yesn; PDBTitle: the crystal structure of the c-terminal domain of the two-2 component response regulator yesn from fusobacterium3 nucleatum subsp. nucleatum atcc 25586
90	c3j21d_	Alignment	not modelled	24.5	33	PDB header: ribosome Chain: D: PDB Molecule: 50s ribosomal protein l4p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
91	d1x6ea2	Alignment	not modelled	24.5	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
92	d2esna1	Alignment	not modelled	24.4	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LysR-like transcriptional regulators
93	c5y9sD_	Alignment	not modelled	24.4	14	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
94	c3j39g_	Alignment	not modelled	24.1	17	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l7a; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
95	d1q1aa_	Alignment	not modelled	23.7	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
96	d2apob1	Alignment	not modelled	23.6	27	Fold: Rubredoxin-like Superfamily: Nop10-like SnoRNP Family: Nucleolar RNA-binding protein Nop10-like
97	c3izci_	Alignment	not modelled	23.3	33	PDB header: ribosome Chain: I: PDB Molecule: 60s ribosomal protein rpl10 (l10e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
98	c2elpA_	Alignment	not modelled	23.3	33	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
99	d1sp2a_	Alignment	not modelled	23.2	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
100	c2m6nA_	Alignment	not modelled	23.1	17	PDB header: cell cycle Chain: A: PDB Molecule: tf-box only protein 5; PDBTitle: 3d solution structure of emi1 (early mitotic inhibitor 1)
101	d2coha1	Alignment	not modelled	23.0	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
102	d2yt9a1	Alignment	not modelled	22.9	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
103	c3jyw9_	Alignment	not modelled	22.8	18	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
104	c6f40P_	Alignment	not modelled	22.7	20	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase iii subunit rpc6; PDBTitle: rna polymerase iii open complex
105	c4b6ap_	Alignment	not modelled	22.6	18	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
106	c3ispA_	Alignment	not modelled	22.5	14	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator PDBTitle: crystal structure of argp from mycobacterium tuberculosis
107	d1a1ia2	Alignment	not modelled	22.4	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers

						Family: Classic zinc finger, C2H2
108	d1f2ig1	Alignment	not modelled	22.4	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
109	d3e5ua1	Alignment	not modelled	22.4	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
110	c1xf7A_	Alignment	not modelled	22.3	25	PDB header: transcription Chain: A: PDB Molecule: wilms' tumor protein; PDBTitle: high resolution nmr structure of the wilms' tumor2 suppressor protein (wt1) finger 3
111	d1xf7a_	Alignment	not modelled	22.3	25	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
112	d1a1ga1	Alignment	not modelled	22.2	29	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
113	c4ce45_	Alignment	not modelled	22.1	27	PDB header: ribosome Chain: 5: PDB Molecule: mrp132; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
114	c3k1nB_	Alignment	not modelled	21.9	8	PDB header: transcription Chain: B: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of full-length benm
115	d2oz6a1	Alignment	not modelled	21.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
116	c1va1A_	Alignment	not modelled	21.7	21	PDB header: transcription Chain: A: PDB Molecule: transcription factor sp1; PDBTitle: solution structure of transcription factor sp1 dna binding2 domain (zinc finger 1)
117	c3m8jA_	Alignment	not modelled	21.5	8	PDB header: transcription Chain: A: PDB Molecule: focb protein; PDBTitle: crystal structure of e.coli focb at 1.4 a resolution
118	d2ct1a1	Alignment	not modelled	21.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
119	c5z4yB_	Alignment	not modelled	21.5	8	PDB header: dna binding protein Chain: B: PDB Molecule: cys regulon transcriptional activator; PDBTitle: crystal structure of pacysb ntd domain with space group p4
120	c5ol0B_	Alignment	not modelled	21.4	15	PDB header: hydrolase Chain: B: PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide