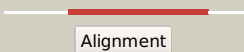

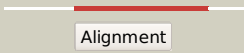



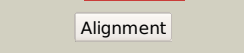



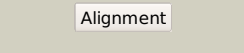

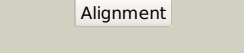



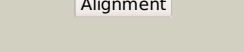

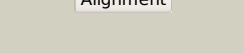
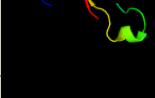
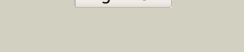

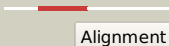
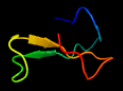

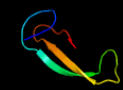

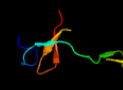

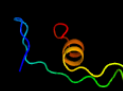

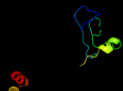



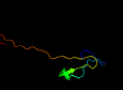




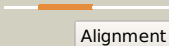
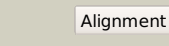
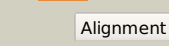
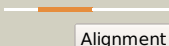

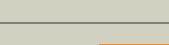
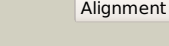
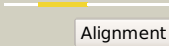


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2718c_(-)_3030423_3030887
Date	Wed Aug 7 12:50:37 BST 2019
Unique Job ID	d163f1997e7203ba

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5im3A_	 Alignment		99.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase; PDBTitle: crystal structure of the class i ribonucleotide reductase from2 pseudomonas aeruginosa in complex with datp
2	c5olkD_	 Alignment		99.5	27	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase, beta subunit 1; PDBTitle: crystal structure of the atp-cone-containing nrdb from2 leeuwenhoekiella blandensis
3	c3r1rB_	 Alignment		98.6	27	PDB header: complex (oxidoreductase/peptide) Chain: B: PDB Molecule: ribonucleotide reductase r1 protein; PDBTitle: ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
4	d1r1ra1	 Alignment		98.0	23	Fold: R1 subunit of ribonucleotide reductase, N-terminal domain Superfamily: R1 subunit of ribonucleotide reductase, N-terminal domain Family: R1 subunit of ribonucleotide reductase, N-terminal domain
5	c3pawD_	 Alignment		97.6	19	PDB header: oxidoreductase Chain: D: PDB Molecule: ribonucleoside-diphosphate reductase large chain 1; PDBTitle: low resolution x-ray crystal structure of yeast rnr1p with datp bound2 in the a-site
6	d1qypa_	 Alignment		96.1	26	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
7	d1twfi2	 Alignment		95.8	24	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
8	c1i3ql_	 Alignment		95.1	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
9	d1tfia_	 Alignment		94.6	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
10	c4c2mX_	 Alignment		94.1	31	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
11	c3k7aM_	 Alignment		94.0	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of an rna polymerase ii-tfiib complex

12	c4v1oM_	 Alignment		93.7	31	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: architecture of the rna polymerase ii-mediator core transcription2 initiation complex
13	c3h0gI_	 Alignment		93.4	27	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
14	c3gn5B_	 Alignment		93.1	25	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
15	c5iy9M_	 Alignment		92.9	41	PDB header: transcription, transferase/dna/rna Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: human holo-pic in the initial transcribing state (no iis)
16	c5fz5M_	 Alignment		91.9	11	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
17	c5flmI_	 Alignment		91.2	32	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: structure of transcribing mammalian rna polymerase ii
18	c2gb5B_	 Alignment		90.9	16	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
19	d1wiia_	 Alignment		90.3	29	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
20	c5xogM_	 Alignment		89.6	29	PDB header: transcription Chain: M: PDB Molecule: transcription elongation factor 1 homolog; PDBTitle: rna polymerase ii elongation complex bound with spt5 kow5 and elf1
21	d2fiya1	 Alignment	not modelled	87.8	22	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
22	d1dl6a_	 Alignment	not modelled	87.1	42	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
23	c3k1fM_	 Alignment	not modelled	85.4	21	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: crystal structure of rna polymerase ii in complex with tfiib
24	c5fjal_	 Alignment	not modelled	84.8	13	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
25	c2e9hA_	 Alignment	not modelled	83.8	33	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
26	c3hnfA_	 Alignment	not modelled	81.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ribonucleoside-diphosphate reductase large subunit; PDBTitle: crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
27	c3cngC_	 Alignment	not modelled	79.5	23	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
28	d1ls1a1	 Alignment	not modelled	77.9	14	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins

29	d1rj9b1	Alignment	not modelled	77.2	13	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
30	c2nb9A	Alignment	not modelled	76.5	39	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
31	c3ndjA	Alignment	not modelled	76.5	23	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
32	c2qkdA	Alignment	not modelled	75.2	23	PDB header: signaling protein, cell cycle Chain: A: PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
33	c1nuiA	Alignment	not modelled	75.2	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
34	d1pfva3	Alignment	not modelled	74.7	33	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
35	c3izrm	Alignment	not modelled	73.0	35	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
36	d1pfta	Alignment	not modelled	72.1	31	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
37	d1vqoz1	Alignment	not modelled	71.7	43	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
38	c3j39p	Alignment	not modelled	71.3	35	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
39	c3j21i	Alignment	not modelled	71.1	48	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)
40	d2k4xa1	Alignment	not modelled	70.8	41	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
41	c4a17Y	Alignment	not modelled	70.6	35	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.
42	c5vkyB	Alignment	not modelled	70.1	21	PDB header: protein binding Chain: B: PDB Molecule: topoisomerase i damage affected protein 2; PDBTitle: yeast tda2 (yer071c) - a dynein light chain family member that works2 independently of the dynein motor complex and microtubules.
43	c2qa4Z	Alignment	not modelled	69.8	43	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
44	c2zkrz	Alignment	not modelled	69.7	29	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 an3 8.7 a cryo-em map
45	c4bpo9	Alignment	not modelled	69.7	31	PDB header: ribosome Chain: 9: PDB Molecule: 40s ribosomal protein rps31e; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 3
46	c1yshD	Alignment	not modelled	69.4	35	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
47	d1wgwa	Alignment	not modelled	69.1	14	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
48	c3zf7o	Alignment	not modelled	68.8	35	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
49	d1jj2y	Alignment	not modelled	68.5	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
50	c4b6ap	Alignment	not modelled	68.0	26	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
51	c6f5zC	Alignment	not modelled	67.5	13	PDB header: transferase Chain: C: PDB Molecule: upf0434 family protein; PDBTitle: complex between the haloferax volcanii trm112 methyltransferase2 activator and the hvo_0019 putative methyltransferase
52	d1j8yf1	Alignment	not modelled	67.2	9	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
53	c2elpA	Alignment	not modelled	66.6	50	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 PDB header: ribosome

54	c3cc4Z_	Alignment	not modelled	66.2	43	Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
55	c6cnbR_	Alignment	not modelled	66.0	22	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
56	d1ffkw_	Alignment	not modelled	65.9	29	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L37ae
57	c1s1i9_	Alignment	not modelled	64.6	26	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.
58	c4rvga_	Alignment	not modelled	64.3	21	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
59	c2xzn9_	Alignment	not modelled	63.1	31	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; 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
60	c2xzm9_	Alignment	not modelled	63.1	31	PDB header: ribosome Chain: 9: PDB Molecule: rps31e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
61	c3jyw9_	Alignment	not modelled	61.9	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
62	c6f42V_	Alignment	not modelled	60.6	22	PDB header: transcription Chain: V: PDB Molecule: transcription factor iiib 70 kda subunit; PDBTitle: rna polymerase iii closed complex cc1.
63	c3hkzP_	Alignment	not modelled	60.4	43	PDB header: transferase Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
64	c5ijlA_	Alignment	not modelled	59.9	22	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
65	c6g5iy_	Alignment	not modelled	59.6	29	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state r
66	c4qiwp_	Alignment	not modelled	57.4	38	PDB header: transcription Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: crystal structure of euryarchaeal rna polymerase from thermococcus2 kodakarensis
67	c2hu9B_	Alignment	not modelled	57.2	46	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
68	c6hmsB_	Alignment	not modelled	57.2	22	PDB header: replication Chain: B: PDB Molecule: dna polymerase ii large subunit,dna polymerase ii large PDBTitle: cryo-em map of dna polymerase d from pyrococcus abyssi in complex with2 dna
69	d1q2ra_	Alignment	not modelled	53.3	12	Fold: YlxR-like Superfamily: YlxR-like Family: YlxR-like
70	c1x6eA_	Alignment	not modelled	52.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: zinc finger protein 24; PDBTitle: solution structures of the c2h2 type zinc finger domain of2 human zinc finger protein 24
71	d1x3za1	Alignment	not modelled	52.7	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
72	c2l7xA_	Alignment	not modelled	52.3	44	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crimean congo hemorrhagic fever gn zinc finger
73	d1qzxa1	Alignment	not modelled	51.9	10	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
74	c3eswA_	Alignment	not modelled	51.6	23	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
75	c6iieA_	Alignment	not modelled	51.1	18	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase alpha; PDBTitle: crystal structure of human diacylglycerol kinase alpha ef-hand domains2 bound to ca2+
76	d2cona1	Alignment	not modelled	50.3	19	Fold: Rubredoxin-like Superfamily: NOB1 zinc finger-like Family: NOB1 zinc finger-like
77	c2f9iD_	Alignment	not modelled	49.0	18	PDB header: transferase Chain: D: PDB Molecule: acetyl-coenzyme a carboxylase carboxyl transferase subunit PDBTitle: crystal structure of the carboxyltransferase subunit of acc from2 staphylococcus aureus
78	d1vd4a_	Alianment	not modelled	49.0	50	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon

						Family: Transcriptional factor domain
79	c5iy9Q_	Alignment	not modelled	48.0	50	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
80	c3ja82_	Alignment	not modelled	47.0	17	PDB header: hydrolase Chain: 2: PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
81	c4kisA_	Alignment	not modelled	46.6	13	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
82	c2akIA_	Alignment	not modelled	46.2	30	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
83	c3x38B_	Alignment	not modelled	46.2	8	PDB header: replication regulator Chain: B: PDB Molecule: mitochondrial morphogenesis protein sld7; PDBTitle: crystal structure of the c-terminal domain of sld7
84	c2jq5A_	Alignment	not modelled	45.8	30	PDB header: structural genomics Chain: A: PDB Molecule: sec-c motif; PDBTitle: solution structure of rpa3114, a sec-c motif containing protein from2 rhodopseudomonas palustris; northeast structural genomics consortium3 target rpt5 / ontario center for structural proteomics target rp3097
85	c2cotA_	Alignment	not modelled	45.3	23	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 435; PDBTitle: solution structure of the first and second zf-c2h2 domain2 of zinc finger protein 435
86	d2f9yb1	Alignment	not modelled	44.9	21	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
87	c2f9yB_	Alignment	not modelled	44.9	21	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
88	c2kvfA_	Alignment	not modelled	44.7	60	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 32; PDBTitle: structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
89	c6ny5A_	Alignment	not modelled	44.4	19	PDB header: rna binding protein/rna Chain: A: PDB Molecule: pumilio domain-containing protein c56f2.08c; PDBTitle: crystal structure of the pum-hd domain of s. pombe puf1 in complex2 with rna
90	c3u5cf_	Alignment	not modelled	44.2	44	PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein s5; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
91	c4uer9_	Alignment	not modelled	44.2	44	PDB header: translation Chain: 9: PDB Molecule: es31; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
92	c4byt5_	Alignment	not modelled	44.2	44	PDB header: ribosome Chain: 5: PDB Molecule: ubiquitin-40s ribosomal protein s31; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
93	c4byl5_	Alignment	not modelled	44.2	44	PDB header: ribosome Chain: 5: PDB Molecule: ubiquitin-40s ribosomal protein s31; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
94	c2lk1A_	Alignment	not modelled	43.9	37	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
95	c2lk0A_	Alignment	not modelled	43.0	37	PDB header: rna binding protein Chain: A: PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
96	c1meyG_	Alignment	not modelled	42.8	55	PDB header: transferase/dna Chain: G: PDB Molecule: consensus zinc finger; PDBTitle: crystal structure of a designed zinc finger protein bound2 to dna
97	c6o3pA_	Alignment	not modelled	42.6	23	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
98	c2ctdA_	Alignment	not modelled	42.3	18	PDB header: metal binding protein Chain: A: PDB Molecule: zinc finger protein 512; PDBTitle: solution structure of two zf-c2h2 domains from human zinc2 finger protein 512
99	c5fywW_	Alignment	not modelled	42.0	42	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
100	c2jneA_	Alignment	not modelled	41.9	44	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.
101	d2jneA1	Alignment	not modelled	41.9	44	Fold: Rubredoxin-like Superfamily: Yfgj-like Family: Yfgj-like
102	d1x6ea2	Alignment	not modelled	41.7	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2

103	c2kwqA	Alignment	not modelled	41.2	24	PDB header: dna binding protein Chain: A; PDB Molecule: protein mcm10 homolog; PDBTitle: mcm10 c-terminal dna binding domain
104	c2lvuA	Alignment	not modelled	40.8	63	PDB header: transcription Chain: A; PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 10
105	d1a1ia2	Alignment	not modelled	40.6	40	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
106	c4cuyf	Alignment	not modelled	40.5	38	PDB header: ribosome Chain: F; PDB Molecule: us7; PDBTitle: kluyveromyces lactis 80s ribosome in complex with crpv-ires
107	d2cota1	Alignment	not modelled	40.5	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
108	c5fmrR	Alignment	not modelled	40.4	42	PDB header: transcription Chain: R; PDB Molecule: transcription initiation factor iie subunit alpha, tfa1; PDBTitle: the p-lobe of rna polymerase ii pre-initiation complex
109	c3u5gf	Alignment	not modelled	40.2	44	PDB header: ribosome Chain: F; PDB Molecule: 40s ribosomal protein s5; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome b
110	d1m2ka	Alignment	not modelled	40.1	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
111	c4esjA	Alignment	not modelled	40.1	21	PDB header: hydrolase/dna Chain: A; PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
112	c4pogC	Alignment	not modelled	40.0	19	PDB header: replication, dna binding protein/dna Chain: C; PDB Molecule: cell division control protein 21; PDBTitle: mcm-ssdna co-crystal structure
113	c2kaeA	Alignment	not modelled	40.0	19	PDB header: transcription/dna Chain: A; PDB Molecule: gata-type transcription factor; PDBTitle: data-driven model of med1:dna complex
114	c3hi2C	Alignment	not modelled	39.8	57	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)
115	c2js4A	Alignment	not modelled	39.8	13	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
116	c5aaqA	Alignment	not modelled	39.7	29	PDB header: calcium-binding protein Chain: A; PDB Molecule: calcium-binding and coiled-coil domain-containing protein PDBTitle: tbk1 recruitment to cytosol-invading salmonella induces2 anti-bacterial autophagy
117	d1llmc2	Alignment	not modelled	38.6	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
118	d2dula1	Alignment	not modelled	38.2	11	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
119	d2j0151	Alignment	not modelled	38.1	38	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
120	c1jocA	Alignment	not modelled	38.0	40	PDB header: membrane protein Chain: A; PDB Molecule: early endosomal autoantigen 1; PDBTitle: eea1 homodimer of c-terminal fyve domain bound to inositol2 1,3-diphosphate