




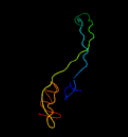

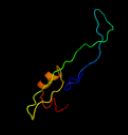

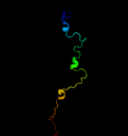

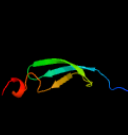

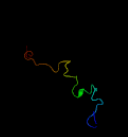

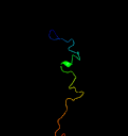

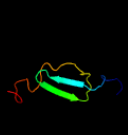

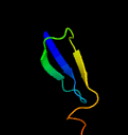


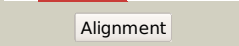

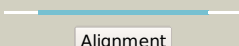
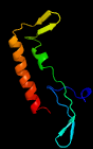

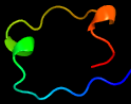



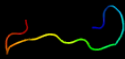


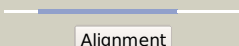

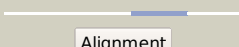

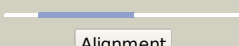

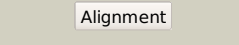
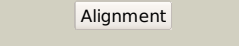


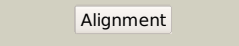
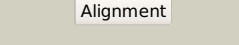




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1298_(rpmE)_1455169_1455411
 Date Wed Jul 31 22:05:39 BST 2019
 Unique Job ID 597ef6f3fa5b45a8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zet2_	 Alignment		100.0	82	PDB header: ribosome Chain: 2: PDB Molecule: 50s ribosomal protein l31; PDBTitle: m. smegmatis p/p state 50s ribosomal subunit
2	c2hgj3_	 Alignment		100.0	54	PDB header: ribosome Chain: 3: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of the 70s thermus thermophilus ribosome showing how2 the 16s 3'-end mimicks mrna e and p codons. this entry 2hgj contains3 50s ribosomal subunit. the 30s ribosomal subunit can be found in pdb4 entry 2hgi.
3	c2b664_	 Alignment		100.0	37	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
4	d1vs6z1	 Alignment		100.0	55	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
5	c3bbo1_	 Alignment		100.0	33	PDB header: ribosome Chain: 1: PDB Molecule: ribosomal protein l31; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
6	c5o60g_	 Alignment		99.9	75	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
7	d2j0141	 Alignment		99.9	59	Fold: L28p-like Superfamily: L28p-like Family: Ribosomal protein L31p
8	c2j034_	 Alignment		99.9	59	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
9	c6dzpg_	 Alignment		99.8	48	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: cryo-em structure of mycobacterium smegmatis c(minus) 50s ribosomal2 subunit
10	c1vw4V_	 Alignment		97.8	18	PDB header: ribosome Chain: V: PDB Molecule: 54s ribosomal protein l36, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
11	c3f1f4_	 Alignment		97.5	59	PDB header: ribosome Chain: 4: PDB Molecule: 50s ribosomal protein l31; PDBTitle: crystal structure of a translation termination complex formed with2 release factor rf2. this file contains the 50s subunit of one 70s3 ribosome. the entire crystal structure contains two 70s ribosomes as4 described in remark 400.

12	c2wh44_	 Alignment		97.5	59	PDB header: ribosome Chain: 4; PDB Molecule: 50s ribosomal protein l31; PDBTitle: insights into translational termination from the structure2 of rf2 bound to the ribosome
13	c4qjty_	 Alignment		32.1	27	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: crystal structure of elongation factor 4 (ef4/lepa) bound to the2 thermus thermophilus 70s ribosome, 30s subunit of the 70s ribosome
14	c5ikkA_	 Alignment		28.8	12	PDB header: transcription Chain: A; PDB Molecule: histone deacetylase clr3; PDBTitle: structure of the histone deacetylase clr3
15	c2ketA_	 Alignment		26.1	46	PDB header: antibiotic Chain: A; PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27
16	c5xknF_	 Alignment		24.6	39	PDB header: transferase/signaling protein Chain: F; PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epf4
17	c5xknE_	 Alignment		24.6	39	PDB header: transferase/signaling protein Chain: E; PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complexe with epf4
18	d1tqza1	 Alignment		24.5	16	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Necap1 N-terminal domain-like
19	c4x2eA_	 Alignment		23.7	62	PDB header: transferase Chain: A; PDB Molecule: fic family protein putative filamentation induced by camp PDBTitle: clostridium difficile wild type fic protein
20	c1v0eB_	 Alignment		23.0	27	PDB header: hydrolase Chain: B; PDB Molecule: endo-alpha-sialidase; PDBTitle: endosialidase of bacteriophage k1f
21	c5oI5B_	 Alignment	not modelled	21.6	25	PDB header: splicing Chain: B; PDB Molecule: dna polymerase iii subunit alpha,dna polymerase iii subunit PDBTitle: crystal structure of an inactivated ssp siclopps intein with cfahpq2 extein
22	d1iufa2	 Alignment	not modelled	21.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
23	d1x6ha1	 Alignment	not modelled	20.8	44	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
24	c3cucB_	 Alignment	not modelled	19.4	62	PDB header: signaling protein Chain: B; PDB Molecule: protein of unknown function with a fic domain; PDBTitle: crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution
25	c6eu1Q_	 Alignment	not modelled	19.0	83	PDB header: transcription Chain: Q; PDB Molecule: dna-directed rna polymerase iii subunit rpc7; PDBTitle: rna polymerase iii - open dna complex (oc-pol3)
26	c3cngC_	 Alignment	not modelled	18.7	26	PDB header: hydrolase Chain: C; PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
27	c3pr6A_	 Alignment	not modelled	18.6	11	PDB header: transport protein Chain: A; PDB Molecule: trapp-associated protein tca17; PDBTitle: crystal structure analysis of yeast trapp associate protein tca17
28	c2keoA_	 Alignment	not modelled	18.1	25	PDB header: splicing Chain: A; PDB Molecule: dna polymerase iii alpha subunit, nucleic

28	c2keqA	Alignment	not modelled	18.1	23	acid PDBTitle: solution structure of dnae intein from nostoc punctiforme PDB header: transferase
29	c3ltiA	Alignment	not modelled	17.1	24	Chain: A; PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of the escherichia coli rna polymerase beta subunit2 beta2-beta4 domains
30	c1iufA	Alignment	not modelled	16.1	29	PDB header: dna binding protein Chain: A; PDB Molecule: centromere abp1 protein; PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
31	c1q69B	Alignment	not modelled	15.9	50	PDB header: membrane protein/transferase Chain: B; PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd8 alpha2 chain and proto-oncogene tyrosine-protein kinase lck3 fragments
32	c4u0zH	Alignment	not modelled	14.2	54	PDB header: transferase Chain: H; PDB Molecule: adenosine monophosphate-protein transferase ficd; PDBTitle: eukaryotic fic domain containing protein with bound apcpp
33	c1zd7B	Alignment	not modelled	14.2	25	PDB header: transferase Chain: B; PDB Molecule: dna polymerase iii alpha subunit; PDBTitle: 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
34	c4d7wA	Alignment	not modelled	14.2	32	PDB header: hydrolase Chain: A; PDB Molecule: sortase family protein; PDBTitle: crystal structure of sortase c1 (srta1) from streptococcus agalactiae
35	d1mi8a	Alignment	not modelled	12.0	25	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
36	d1eb7a2	Alignment	not modelled	11.9	42	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
37	c2lwyA	Alignment	not modelled	11.8	26	PDB header: unknown function Chain: A; PDB Molecule: bacterial intein-like domain; PDBTitle: solution structure of bacterial intein-like domain from clostridium2 thermocellum
38	c1q68B	Alignment	not modelled	11.8	50	PDB header: membrane protein/transferase Chain: B; PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
39	c4o1rA	Alignment	not modelled	11.6	25	PDB header: splicing Chain: A; PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of npudnab intein
40	c5k9aA	Alignment	not modelled	10.9	26	PDB header: hydrolase Chain: A; PDB Molecule: putative fimbrial associated sortase-like protein; PDBTitle: sortase a from corynebacterium diphtheriae
41	c4hizA	Alignment	not modelled	10.7	33	PDB header: hydrolase,viral protein Chain: A; PDB Molecule: endosialidase; PDBTitle: phage phi92 endosialidase
42	c3n3vA	Alignment	not modelled	10.6	54	PDB header: transferase Chain: A; PDB Molecule: adenosine monophosphate-protein transferase ibpa; PDBTitle: crystal structure of ibpafic2-h3717a in complex with adenylated2 cdc42
43	c2nb9A	Alignment	not modelled	10.5	24	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of zitp zinc finger
44	c3g66A	Alignment	not modelled	10.4	26	PDB header: transferase Chain: A; PDB Molecule: sortase c; PDBTitle: the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
45	d1nmla2	Alignment	not modelled	10.3	33	Fold: Cytochrome c Superfamily: Cytochrome c Family: Di-heme cytochrome c peroxidase
46	c2imzA	Alignment	not modelled	10.1	17	PDB header: hydrolase Chain: A; PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
47	c4rglA	Alignment	not modelled	10.1	54	PDB header: dna binding protein Chain: A; PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
48	c1mpxB	Alignment	not modelled	9.9	44	PDB header: hydrolase Chain: B; PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
49	c5jj6A	Alignment	not modelled	9.9	62	PDB header: transferase Chain: A; PDB Molecule: adenosine monophosphate-protein transferase ficd homolog; PDBTitle: fic-1 (aa134 - 508) from c. elegans
50	c3o0pA	Alignment	not modelled	9.8	26	PDB header: transferase , hydrolase Chain: A; PDB Molecule: sortase family protein; PDBTitle: pilus-related sortase c of group b streptococcus
51	c3dd7A	Alignment	not modelled	9.7	10	PDB header: ribosome inhibitor Chain: A; PDB Molecule: death on curing protein; PDBTitle: structure of doch66y in complex with the c-terminal domain of phd
52	d1e7la1	Alignment	not modelled	9.7	60	Fold: LEM/SAP HeH motif Superfamily: Recombination endonuclease VII, C-terminal and dimerization domains Family: Recombination endonuclease VII, C-terminal and dimerization domains

53	c2lcjA_	Alignment	not modelled	9.3	20	PDB header: hydrolase Chain: A: PDB Molecule: pab polc intein; PDBTitle: solution nmr structure of pab polii intein
54	c2kw8A_	Alignment	not modelled	8.9	16	PDB header: protein binding Chain: A: PDB Molecule: lpxtg-site transpeptidase family protein; PDBTitle: solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
55	c1nmlA_	Alignment	not modelled	8.8	33	PDB header: oxidoreductase Chain: A: PDB Molecule: di-haem cytochrome c peroxidase; PDBTitle: di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
56	d1am2a_	Alignment	not modelled	8.7	20	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Intein (protein splicing domain)
57	c2v7sA_	Alignment	not modelled	8.7	19	PDB header: unknown function Chain: A: PDB Molecule: probable conserved lipoprotein lppa; PDBTitle: crystal structure of the putative lipoprotein lppa from2 mycobacterium tuberculosis
58	c4g1hA_	Alignment	not modelled	8.2	28	PDB header: transferase Chain: A: PDB Molecule: sortase family protein; PDBTitle: group b streptococcus pilus island 1 sortase c2
59	c4ultN_	Alignment	not modelled	8.0	19	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of verrucarin bound to the yeast 80s ribosome
60	c1vxvX_	Alignment	not modelled	8.0	19	PDB header: ribosome Chain: X: PDB Molecule: 60s ribosomal protein l24; PDBTitle: structures of yeast 80s ribosome-trna complexes in the rotated and2 non-rotated conformations (class ii - rotated ribosome with 1 trna,3 this entry contains the large ribosomal subunit proteins)
61	c5ldwe_	Alignment	not modelled	8.0	44	PDB header: oxidoreductase Chain: E: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 2, PDBTitle: structure of mammalian respiratory complex i, class1
62	d1g47a1	Alignment	not modelled	7.9	30	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
63	c4b6aW_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
64	c4ukeO_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cycloheximide bound to the yeast 80s ribosome
65	c4ukyO_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of edeine bound to the yeast 80s ribosome
66	c4byuW_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
67	c4bynW_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet eukaryotic2 translation initiation complex
68	c3u5iW_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 60s subunit, ribosome b
69	c4ukjN_	Alignment	not modelled	7.9	19	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of blasticidin s bound to the yeast 80s ribosome
70	c4uldO_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of nagilactone c bound to the yeast 80s ribosome
71	c4uk3O_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of anisomycin bound to the yeast 80s ribosome
72	c4ujjO_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of narclasine bound to the yeast 80s ribosome
73	c4ukoN_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cryptopleurine bound to the yeast 80s ribosome
74	c4ul3O_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of geneticin bound to the yeast 80s ribosome
75	c4uloO_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of phyllanthoside bound to the yeast 80s ribosome
76	c4ul8O_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of homoharringtonine bound to the yeast 80s ribosome
77	c4ujoO_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of lycorine bound to the yeast 80s ribosome
78	c4ulvN_	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: N: PDB Molecule: 60s ribosomal protein l24-a;

78	c4ujyv	Alignment	not modelled	7.8	19	PDBTitle: crystal structure of t-2 toxin bound to the yeast 80s ribosome PDB header: ribosome
79	c4uliO	Alignment	not modelled	7.8	19	Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of pactamycin bound to the yeast 80s ribosome
80	c4ujtO	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of lactimidomycin bound to the yeast 80s ribosome
81	c4uk8O	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of cca trinucleotide bound to the yeast 80s ribosome
82	d1at0a	Alignment	not modelled	7.7	10	Fold: Hedgehog/intein (Hint) domain Superfamily: Hedgehog/intein (Hint) domain Family: Hedgehog C-terminal (Hog) autoprocessing domain
83	d3bzka2	Alignment	not modelled	7.6	50	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Tex HhH-containing domain-like
84	c4uktO	Alignment	not modelled	7.6	19	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l24-a; PDBTitle: crystal structure of deoxynivalenol bound to the yeast 80s ribosome
85	c4v194	Alignment	not modelled	7.6	17	PDB header: ribosome Chain: 4: PDB Molecule: mitoribosomal protein bl31m, mrp155; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
86	d1oa8a	Alignment	not modelled	7.5	14	Fold: AXH domain Superfamily: AXH domain Family: AXH domain
87	c3hq7A	Alignment	not modelled	7.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome c551 peroxidase; PDBTitle: ccpa from g. sulfurreducens, g94k/k97q/r100i variant
88	c3izcZ	Alignment	not modelled	7.4	19	PDB header: ribosome Chain: Z: PDB Molecule: 60s ribosomal protein rpl24 (l24e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
89	c4a1eT	Alignment	not modelled	7.3	31	PDB header: ribosome Chain: T: PDB Molecule: rpl24; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
90	c5j8jA	Alignment	not modelled	7.2	14	PDB header: hydrolase Chain: A: PDB Molecule: histone deacetylase hda1; PDBTitle: a histone deacetylase from saccharomyces cerevisiae
91	c1x0gA	Alignment	not modelled	7.0	50	PDB header: metal binding protein Chain: A: PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
92	c2in0A	Alignment	not modelled	7.0	17	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease pi-mtui; PDBTitle: crystal structure of mtu reca intein splicing domain
93	c3j39W	Alignment	not modelled	6.9	15	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l24; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
94	c2yiuE	Alignment	not modelled	6.9	63	PDB header: oxidoreductase Chain: E: PDB Molecule: cytochrome c1, heme protein; PDBTitle: x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
95	c2jmzA	Alignment	not modelled	6.8	30	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein mj0781; PDBTitle: solution structure of a kba intein precursor from2 methanococcus jannaschii
96	d2j3wa1	Alignment	not modelled	6.8	28	Fold: Profilin-like Superfamily: SNARE-like Family: Sedlin (SEDL)
97	c2w1jB	Alignment	not modelled	6.7	26	PDB header: transferase Chain: B: PDB Molecule: putative sortase; PDBTitle: crystal structure of sortase c-1 (src1) from streptococcus2 pneumoniae
98	c2g9pA	Alignment	not modelled	6.7	20	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide latarcin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
99	c5ionA	Alignment	not modelled	6.6	36	PDB header: transcription Chain: A: PDB Molecule: zinc finger and btb domain-containing protein 17; PDBTitle: solution structure of miz-1 zinc finger 13