Mensur Dlakic

List of Publications by Year in descending order

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MENSUD DIAKIC

#	Article	IF	CITATIONS
1	Sulfur cycling and host-virus interactions in <i>Aquificales</i> -dominated biofilms from Yellowstone's hottest ecosystems. ISME Journal, 2022, 16, 842-855.	4.4	8
2	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. Science, 2021, 374, 57-65.	6.0	152
3	An ancient evolutionary connection between Ribonuclease A and EndoU families. Rna, 2020, 26, 803-813.	1.6	11
4	Co-occurring genomic capacity for anaerobic methane and dissimilatory sulfur metabolisms discovered in the Korarchaeota. Nature Microbiology, 2019, 4, 614-622.	5.9	91
5	Marsarchaeota are an aerobic archaeal lineage abundant in geothermal iron oxide microbial mats. Nature Microbiology, 2018, 3, 732-740.	5.9	53
6	A Journey of Cytolethal Distending Toxins through Cell Membranes. Frontiers in Cellular and Infection Microbiology, 2016, 6, 81.	1.8	32
7	The Cytolethal Distending Toxin Contributes to Microbial Virulence and Disease Pathogenesis by Acting As a Tri-Perditious Toxin. Frontiers in Cellular and Infection Microbiology, 2016, 6, 168.	1.8	63
8	The toxicity of the <i>Aggregatibacter actinomycetemcomitans</i> cytolethal distending toxin correlates with its phosphatidylinositol-3,4,5-triphosphate phosphatase activity. Cellular Microbiology, 2016, 18, 223-243.	1.1	34
9	Characterization of a Single b-type Heme, FAD, and Metal Binding Sites in the Transmembrane Domain of Six-transmembrane Epithelial Antigen of the Prostate (STEAP) Family Proteins. Journal of Biological Chemistry, 2015, 290, 22558-22569.	1.6	38
10	The Aggregatibacter actinomycetemcomitans Cytolethal Distending Toxin Active Subunit CdtB Contains a Cholesterol Recognition Sequence Required for Toxin Binding and Subunit Internalization. Infection and Immunity, 2015, 83, 4042-4055.	1.0	20
11	Blockade of the PI-3K signalling pathway by the <i>Aggregatibacter actinomycetemcomitans</i> cytolethal distending toxin induces macrophages to synthesize and secrete pro-inflammatory cytokines. Cellular Microbiology, 2014, 16, 1391-1404.	1.1	47
12	Odorant receptors of a primitive hymenopteran pest, the wheat stem sawfly. Insect Molecular Biology, 2013, 22, 659-667.	1.0	12
13	Structural Studies of E73 from a Hyperthermophilic Archaeal Virus Identify the "RH3―Domain, an Elaborated Ribbon–Helix–Helix Motif Involved in DNA Recognition. Biochemistry, 2012, 51, 2899-2910.	1.2	22
14	Terminal Oxidase Diversity and Function in " <i>Metallosphaera yellowstonensis</i> ― Gene Expression and Protein Modeling Suggest Mechanisms of Fe(II) Oxidation in the <i>Sulfolobales</i> . Applied and Environmental Microbiology, 2011, 77, 1844-1853.	1.4	59
15	Prp8, the pivotal protein of the spliceosomal catalytic center, evolved from a retroelement-encoded reverse transcriptase. Rna, 2011, 17, 799-808.	1.6	78
16	HHsvm: fast and accurate classification of profile–profile matches identified by HHsearch. Bioinformatics, 2009, 25, 3071-3076.	1.8	9
17	A Novel Mode of Action for a Microbial-Derived Immunotoxin: The Cytolethal Distending Toxin Subunit B Exhibits Phosphatidylinositol 3,4,5-Triphosphate Phosphatase Activity. Journal of Immunology, 2007, 178, 5099-5108.	0.4	94
18	Roles of the HEAT repeat proteins Utp10 and Utp20 in 40S ribosome maturation. Rna, 2007, 13, 1516-1527.	1.6	43

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19	Coupling of Double-Stranded RNA Synthesis and siRNA Generation in Fission Yeast RNAi. Molecular Cell, 2007, 27, 449-461.	4.5	134
20	DUF283 domain of Dicer proteins has a double-stranded RNA-binding fold. Bioinformatics, 2006, 22, 2711-2714.	1.8	59
21	Characterization of the Archaeal Thermophile Sulfolobus Turreted Icosahedral Virus Validates an Evolutionary Link among Double-Stranded DNA Viruses from All Domains of Life. Journal of Virology, 2006, 80, 7625-7635.	1.5	86
22	3D models of yeast RNase P/MRP proteins Rpp1p and Pop3p. Rna, 2005, 11, 123-127.	1.6	12
23	Functional Characterization of XendoU, the Endoribonuclease Involved in Small Nucleolar RNA Biosynthesis*. Journal of Biological Chemistry, 2005, 280, 18996-19002.	1.6	48
24	Epimerase Active Domain of Pseudomonas aeruginosa AlgG, a Protein That Contains a Right-Handed β-Helix. Journal of Bacteriology, 2005, 187, 4573-4583.	1.0	30
25	DNA Bendability and Nucleosome Positioning in Transcriptional Regulation. , 2005, , 189-202.		3
26	The ribosomal subunit assembly line. Genome Biology, 2005, 6, 234.	13.9	13
27	The Noc proteins involved in ribosome synthesis and export contain divergent HEAT repeats. Rna, 2004, 10, 351-354.	1.6	15
28	PIN domain of Nob1p is required for D-site cleavage in 20S pre-rRNA. Rna, 2004, 10, 1698-1701.	1.6	110
29	A pre-ribosome-associated HEAT-repeat protein is required for export of both ribosomal subunits. Genes and Development, 2004, 18, 196-209.	2.7	105
30	Nob1p Is Required for Cleavage of the 3′ End of 18S rRNA. Molecular and Cellular Biology, 2003, 23, 1798-1807.	1.1	144
31	Automated Identification of Putative Methyltransferases from Genomic Open Reading Frames. Molecular and Cellular Proteomics, 2003, 2, 525-540.	2.5	148
32	Ssf1p Prevents Premature Processing of an Early Pre-60S Ribosomal Particle. Molecular Cell, 2002, 9, 341-351.	4.5	167
33	A new family of putative insulin receptor-like proteins in C. elegans. Current Biology, 2002, 12, R155-R157.	1.8	28
34	A model of the replication fork blocking protein Fob1p based on the catalytic core domain of retroviral integrases. Protein Science, 2002, 11, 1274-1277.	3.1	14
35	Naf1p is a box H/ACA snoRNP assembly factor. Rna, 2002, 8, 1502-1514.	1.6	61
36	Naf1 p is a box H/ACA snoRNP assembly factor. Rna, 2002, 8, 1502-14.	1.6	65

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37	DNA sequence-dependent folding determines the divergence in binding specificities between Maf and other bZIP proteins. EMBO Journal, 2001, 20, 828-840.	3.5	44
38	Chromatin silencing protein and pachytene checkpoint regulator Dot1p has a methyltransferase fold. Trends in Biochemical Sciences, 2001, 26, 405-407.	3.7	32
39	Identification and cDNA Cloning of a Novel RNA-binding Protein That Interacts with the Cyclic Nucleotide-responsive Sequence in the Type-1 Plasminogen Activator Inhibitor mRNA. Journal of Biological Chemistry, 2001, 276, 3341-3347.	1.6	114
40	Is CdtB a Nuclease or a Phosphatase?. Science, 2001, 291, 547a-547.	6.0	34
41	Functionally unrelated signalling proteins contain a fold similar to Mg2+-dependent endonucleases. Trends in Biochemical Sciences, 2000, 25, 272-273.	3.7	155
42	Unconventional helical phasing of repetitive DNA motifs reveals their relative bending contributions. Nucleic Acids Research, 1998, 26, 4274-4279.	6.5	18
43	DIAMOD: display and modeling of DNA bending. Bioinformatics, 1998, 14, 326-331.	1.8	32
44	Strained DNA is kinked by low concentrations of Zn2+. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 10565-10570.	3.3	94
45	Kinked DNA. Nature, 1997, 386, 563-563.	13.7	172
46	The effects of sequence context on DNA curvature Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 3847-3852.	3.3	53
47	The Organic Crystallizing Agent 2-Methyl-2,4-pentanediol Reduces DNA Curvature by Means of Structural Changes in A-tracts. Journal of Biological Chemistry, 1996, 271, 17911-17919.	1.6	51
48	Bending and Torsional Flexibility of G/C-rich Sequences as Determined by Cyclization Assays. Journal of Biological Chemistry, 1995, 270, 29945-29952.	1.6	65
49	What is The Basis of Sequence-Directed Curvature in DNAs Containing A Tracts?. Journal of Biomolecular Structure and Dynamics, 1995, 13, 301-307.	2.0	40
50	Physiological Concentration of Magnesium Ions Induces a Strong Macroscopic Curvature in GGGCCC-containing DNA. Journal of Molecular Biology, 1994, 236, 26-32.	2.0	126
51	Evidence for opposite groove-directed curvature of GGGCCC and AAAAA sequence elements. Nucleic Acids Research, 1993, 21, 1025-1029.	6.5	79
52	Evidence for opposite groove-directed curvature of GGGCCC and AAAAA sequence elements. Nucleic Acids Research, 1993, 21, 1332-1332.	6.5	2