Giorgio Dieci

List of Publications by Year
in descending order

65 papers	3,284 citations	147801 31 h-index	155660 55 g-index
67 all docs	67 docs citations	67 times ranked	3889 citing authors

#	Article	IF	Citations
1	Epigenetic regulation of human non-coding RNA gene transcription. Biochemical Society Transactions, 2022, 50, 723-736.	3.4	11
2	Retrotransposons as Drivers of Mammalian Brain Evolution. Life, 2021, 11, 376.	2.4	24
3	Removing quote marks from the RNA polymerase II CTD â€˜codeâ€™. BioSystems, 2021, 207, 104468.	2.0	4
4	TFIIIC Binding to Alu Elements Controls Gene Expression via Chromatin Looping and Histone Acetylation. Molecular Cell, 2020, 77, 475-487.e11.	9.7	65
5	Alu RNA Modulates the Expression of Cell Cycle Genes in Human Fibroblasts. International Journal of Molecular Sciences, 2019, 20, 3315.	4.1	10
6	Interpreting and integrating big data in non-coding RNA research. Emerging Topics in Life Sciences, 2019, 3, 343-355.	2.6	2
7	The third (III) road to cell transformation. Cell Cycle, 2018, 17, 410-411.	2.6	0
8	Epigenetic and Transcriptional Modifications in Repetitive Elements in Petrol Station Workers Exposed to Benzene and MTBE. International Journal of Environmental Research and Public Health, 2018, 15, 735.	2.6	22
9	Multiple roles of the general regulatory factor Abf1 in yeast ribosome biogenesis. Current Genetics, 2017, 63, 65-68.	1.7	8
10	Abf1 and other general regulatory factors control ribosome biogenesis gene expression in budding yeast. Nucleic Acids Research, 2017, 45, 4493-4506.	14.5	41
11	Transcriptional control of yeast ribosome biogenesis: A multifaceted role for general regulatory factors. Transcription, 2017, 8, 254-260.	3.1	17
12	Identification of RNA Polymerase III-Transcribed SINEs at Single-Locus Resolution from RNA Sequencing Data. Non-coding RNA, 2017, 3, 15.	2.6	4
13	Whole-genome expression analysis of mammalian-wide interspersed repeat elements in human cell lines. DNA Research, 2016, 24, dsw048.	3.4	16
14	Promoter architecture and transcriptional regulation of Abf1-dependent ribosomal protein genes inSaccharomyces cerevisiae. Nucleic Acids Research, 2016, 44, 6113-6126.	14.5	28
15	Hydroquinone induces DNA hypomethylation-independent overexpression of retroelements in human leukemia and hematopoietic stem cells. Biochemical and Biophysical Research Communications, 2016, 474, 691-695.	2.1	15
16	Identification of RNA polymerase III-transcribed Alu loci by computational screening of RNA-Seq data. Nucleic Acids Research, 2015, 43, 817-835.	14.5	55
17	Abiotic ligation of DNA oligomers templated by their liquid crystal ordering. Nature Communications, 2015, 6, 6424.	12.8	42
18	Investigating transcription reinitiation through in vitro approaches. Transcription, 2014, 5, e27704.	3.1	9

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19	An intronic ncRNA-dependent regulation of SORL1 expression affecting AÎ² formation is upregulated in post-mortem Alzheimer's disease brain samples. DMM Disease Models and Mechanisms, 2013, 6, 424-33.	2.4	131
20	Identification of RNA polymerase III-transcribed genes in eukaryotic genomes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 296-305.	1.9	75
21	Transcription reinitiation by RNA polymerase III. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 331-341.	1.9	50
22	A novel snRNA-like transcript affects amyloidogenesis and cell cycle progression through perturbation of Fe65L1 (APBB2) alternative splicing. Biochimica Et Biophysica Acta - Molecular Cell Research, 2013, 1833, 1511-1526.	4.1	18
23	Neuroblastoma: Inhibition by Alu-Like RNA. Pediatric Cancer, 2013, , 57-66.	0.0	0
24	The Murine PSE/TATA-Dependent Transcriptome: Evidence of Functional Homologies with Its Human Counterpart. International Journal of Molecular Sciences, 2012, 13, 14813-14827.	4.1	2
25	RNA polymerase III transcription control elements: Themes and variations. Gene, 2012, 493, 185-194.	2.2	123
26	A common sequence motif involved in selection of transcription start sites of Arabidopsis and budding yeast tRNA genes. Genomics, 2011, 97, 166-172.	2.9	12
27	17A, a novel non-coding RNA, regulates GABA B alternative splicing and signaling in response to inflammatory stimuli and in Alzheimer disease. Neurobiology of Disease, 2011, 41, 308-317.	4.4	199
28	Promoter architectures in the yeast ribosomal expression program. Transcription, 2011, 2, 71-77.	3.1	31
29	RNA polymerase III drives alternative splicing of the potassium channelâ€“interacting protein contributing to brain complexity and neurodegeneration. Journal of Cell Biology, 2011, 193, 851-866.	5.2	35
30	Widespread occurrence of non-canonical transcription termination by human RNA polymerase III. Nucleic Acids Research, 2011, 39, 5499-5512.	14.5	64
31	An Aluâ€like RNA promotes cell differentiation and reduces malignancy of human neuroblastoma cells. FASEB Journal, 2010, 24, 4033-4046.	0.5	71
32	General transcription factors and subunits of RNA polymerase III. Transcription, 2010, 1, 130-135.	3.1	16
33	The Telomere-Binding Protein Tbf1 Demarcates snoRNA Gene Promoters in Saccharomyces cerevisiae. Molecular Cell, 2010, 38, 614-620.	9.7	58
34	Genome-wide location analysis reveals a role for Sub1 in RNA polymerase III transcription. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14265-14270.	7.1	47
35	Positive modulation of RNA polymerase III transcription by ribosomal proteins. Biochemical and Biophysical Research Communications, 2009, 379, 489-493.	2.1	24
36	Eukaryotic snoRNAs: A paradigm for gene expression flexibility. Genomics, 2009, 94, 83-88.	2.9	278

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37	The transcription reinitiation properties of RNA polymerase III in the absence of transcription factors. Cellular and Molecular Biology Letters, 2008, 13, 112-8.	7.0	9
38	Requirement of Nhp6 Proteins for Transcription of a Subset of tRNA Genes and Heterochromatin Barrier Function in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2007, 27, 1545-1557.	2.3	40
39	New Small Nuclear RNA Gene-Like Transcriptional Units as Sources of Regulatory Transcripts. PLoS Genetics, 2007, 3, e1.	3.5	82
40	The expanding RNA polymerase III transcriptome. Trends in Genetics, 2007, 23, 614-622.	6.7	447
41	Distinct modes of TATA box utilization by the RNA polymerase III transcription machineries from budding yeast and higher plants. Gene, 2006, 379, 12-25.	2.2	14
42	Assembly into snoRNP controls 5â€²-end maturation of a box C/D snoRNA in Saccharomyces cerevisiae. Biochemical and Biophysical Research Communications, 2006, 351, 468-473.	2.1	8
43	Nucleosome Depletion Activates Poised RNA Polymerase III at Unconventional Transcription Sites in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2006, 281, 29155-29164.	3.4	34
44	A Minimal Promoter for TFIIIC-dependent in Vitro Transcription of snoRNA and tRNA Genes by RNA Polymerase III. Journal of Biological Chemistry, 2006, 281, 23945-23957.	3.4	26
45	A General Procedure for the Production of Antibody Reagents Against Eukaryotic Ribosomal Proteins. Protein and Peptide Letters, 2005, 12, 555-560.	0.9	13
46	Sequence Context Effects on Oligo(dT) Termination Signal Recognition by Saccharomyces cerevisiae RNA Polymerase III. Journal of Biological Chemistry, 2005, 280, 19551-19562.	3.4	97
47	Modulation of Yeast Genome Expression in Response to Defective RNA Polymerase III-Dependent Transcription. Molecular and Cellular Biology, 2005, 25, 8631-8642.	2.3	36
48	Distinct roles of transcription factors TFIIIB and TFIIIC in RNA polymerase III transcription reinitiation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13442-13447.	7.1	60
49	Functional Dissection of RNA Polymerase III Termination Using a Peptide Nucleic Acid as a Transcriptional Roadblock. Journal of Biological Chemistry, 2004, 279, 20708-20716.	3.4	11
50	Transcription reinitiation properties of bacteriophage T7 RNA polymerase. Biochemical and Biophysical Research Communications, 2004, 315, 376-380.	2.1	13
51	Detours and shortcuts to transcription reinitiation. Trends in Biochemical Sciences, 2003, 28, 202-209.	7.5	71
52	A Composite Upstream Sequence Motif Potentiates tRNA Gene Transcription in Yeast. Journal of Molecular Biology, 2003, 333, 1-20.	4.2	54
53	Visualizing RNA Extrusion and DNA Wrapping in Transcription Elongation Complexes of Bacterial and Eukaryotic RNA Polymerases. Journal of Molecular Biology, 2003, 326, 1413-1426.	4.2	62
54	Intragenic Promoter Adaptation and Facilitated RNA Polymerase III Recycling in the Transcription of SCR1, the 7SL RNA Gene ofSaccharomyces cerevisiae. Journal of Biological Chemistry, 2002, 277, 6903-6914.	3.4	43

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55	Inhibition of RNA Polymerase III Elongation by a T10 Peptide Nucleic Acid. Journal of Biological Chemistry, 2001, 276, 5720-5725.	3.4	16
56	A Plant 3â€²-Phosphoesterase Involved in the Repair of DNA Strand Breaks Generated by Oxidative Damage. Journal of Biological Chemistry, 2001, 276, 18038-18045.	3.4	27
57	TFIIIC-independent in vitro transcription of yeast tRNA genes 1 1Edited by M. Yaniv. Journal of Molecular Biology, 2000, 299, 601-613.	4.2	60
58	tRNA-Assisted Overproduction of Eukaryotic Ribosomal Proteins. Protein Expression and Purification, 2000, 18, 346-354.	1.3	34
59	Domain Organization and Functional Properties of Yeast Transcription Factor IIIA Species with Different Zinc Stoichiometries. Journal of Biological Chemistry, 1999, 274, 2539-2548.	3.4	7
60	Functional interchangeability of TFIIIB components from yeast and human cells invitro. EMBO Journal, 1997, 16, 4708-4716.	7.8	27
61	Facilitated Recycling Pathway for RNA Polymerase III. Cell, 1996, 84, 245-252.	28.9	175
62	[22] RNA polymerase III and class III transcription factors from Saccharomyces cerevisiae. Methods in Enzymology, 1996, 273, 249-267.	1.0	47
63	Selective Inactivation of Two Components of the Multiprotein Transcription Factor TFIIIB in Cycloheximide Growth-arrested Yeast Cells. Journal of Biological Chemistry, 1995, 270, 13476-13482.	3.4	32
64	Identification of new eukaryotic tRNA genes in genomic DNA databases by a multistep weight matrix anaylsis of transcriptional control regions. Nucleic Acids Research, 1994, 22, 1247-1256.	14.5	114
65	High-Level Expression in Escherichia coli and Purification of Yeast Transcription Factor IIIA. Biochemical and Biophysical Research Communications, 1994, 203, 1217-1223.	2.1	12