

# Antonin Morillon

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2670227/publications.pdf>

Version: 2024-02-01

57  
papers

4,496  
citations

218592

26  
h-index

143943

57  
g-index

71  
all docs

71  
docs citations

71  
times ranked

6132  
citing authors

#	ARTICLE	IF	CITATIONS
1	History, Discovery, and Classification of lncRNAs. <i>Advances in Experimental Medicine and Biology</i> , 2017, 1008, 1-46.	0.8	659
2	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	2.6	380
3	XUTs are a class of Xrn1-sensitive antisense regulatory non-coding RNA in yeast. <i>Nature</i> , 2011, 475, 114-117.	13.7	329
4	Gene loops juxtapose promoters and terminators in yeast. <i>Nature Genetics</i> , 2004, 36, 1014-1018.	9.4	321
5	Methylation of Histone H3 K4 Mediates Association of the Isw1p ATPase with Chromatin. <i>Molecular Cell</i> , 2003, 12, 1325-1332.	4.5	248
6	Pervasive transcription constitutes a new level of eukaryotic genome regulation. <i>EMBO Reports</i> , 2009, 10, 973-982.	2.0	210
7	Dynamic Lysine Methylation on Histone H3 Defines the Regulatory Phase of Gene Transcription. <i>Molecular Cell</i> , 2005, 18, 723-734.	4.5	179
8	A cryptic unstable transcript mediates transcriptional <i>trans</i> -silencing of the Ty1 retrotransposon in <i>S. cerevisiae</i> . <i>Genes and Development</i> , 2008, 22, 615-626.	2.7	173
9	Isw1 Chromatin Remodeling ATPase Coordinates Transcription Elongation and Termination by RNA Polymerase II. <i>Cell</i> , 2003, 115, 425-435.	13.5	160
10	H3 lysine 4 di- and tri-methylation deposited by cryptic transcription attenuates promoter activation. <i>EMBO Journal</i> , 2009, 28, 1697-1707.	3.5	146
11	Long Noncoding RNAs as New Architects in Cancer Epigenetics, Prognostic Biomarkers, and Potential Therapeutic Targets. <i>BioMed Research International</i> , 2015, 2015, 1-14.	0.9	122
12	GC content shapes mRNA storage and decay in human cells. <i>ELife</i> , 2019, 8, .	2.8	121
13	Diversification of human plasmacytoid dendritic cells in response to a single stimulus. <i>Nature Immunology</i> , 2018, 19, 63-75.	7.0	106
14	Nonsense-Mediated Decay Restricts lncRNA Levels in Yeast Unless Blocked by Double-Stranded RNA Structure. <i>Molecular Cell</i> , 2016, 61, 379-392.	4.5	101
15	ISWI complexes in <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 2004, 1677, 100-112.	2.4	86
16	Activation of the Kss1 Invasive-Filamentous Growth Pathway Induces Ty1 Transcription and Retrotransposition in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2000, 20, 5766-5776.	1.1	75
17	Prognostic value of a newly identified MALAT1 alternatively spliced transcript in breast cancer. <i>British Journal of Cancer</i> , 2016, 114, 1395-1404.	2.9	75
18	Pervasive transcription – Lessons from yeast. <i>Biochimie</i> , 2011, 93, 1889-1896.	1.3	69

#	ARTICLE	IF	CITATIONS
19	Expression of Human Fibroblast Growth Factor 2 mRNA Is Post-transcriptionally Controlled by a Unique Destabilizing Element Present in the 3'â€²-Untranslated Region between Alternative Polyadenylation Sites. <i>Journal of Biological Chemistry</i> , 1999, 274, 21402-21408.	1.6	68
20	Noncoding RNAs in gene regulation. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 728-738.	6.6	68
21	Regulation of Elongating RNA Polymerase II by Forkhead Transcription Factors in Yeast. <i>Science</i> , 2003, 300, 492-495.	6.0	62
22	Differential Effects of Chromatin and Gcn4 on the 50-Fold Range of Expression among Individual Yeast Ty1 Retrotransposons. <i>Molecular and Cellular Biology</i> , 2002, 22, 2078-2088.	1.1	58
23	Severe Adenine Starvation Activates Ty1 Transcription and Retrotransposition in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2005, 25, 7459-7472.	1.1	54
24	Native elongating transcript sequencing reveals global anti-correlation between sense and antisense nascent transcription in fission yeast. <i>Rna</i> , 2018, 24, 196-208.	1.6	43
25	Bridging the gap between reference and real transcriptomes. <i>Genome Biology</i> , 2019, 20, 112.	3.8	38
26	Transcription-wide mapping of dihydrouridine reveals that mRNA dihydrouridylation is required for meiotic chromosome segregation. <i>Molecular Cell</i> , 2022, 82, 404-419.e9.	4.5	34
27	LncRNAs, lost in translation or licence to regulate?. <i>Current Genetics</i> , 2017, 63, 29-33.	0.8	33
28	<scp>RNA</scp> â€œprocessing proteins regulate Mec1/ <scp>ATR</scp> activation by promoting generation of <scp>RPA</scp> â€œcoated ss <scp>DNA</scp>. <i>EMBO Reports</i> , 2015, 16, 221-231.	2.0	32
29	Subtelomeric Transcription and its Regulation. <i>Journal of Molecular Biology</i> , 2020, 432, 4199-4219.	2.0	30
30	Nucleosome Remodeling and Transcriptional Repression Are Distinct Functions of Isw1 in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2009, 29, 2419-2430.	1.1	29
31	Cytoplasmic Control of Sense-Antisense mRNA Pairs. <i>Cell Reports</i> , 2015, 12, 1853-1864.	2.9	29
32	Histone deacetylation promotes transcriptional silencing at facultative heterochromatin. <i>Nucleic Acids Research</i> , 2018, 46, 5426-5440.	6.5	28
33	Zinc-mediated RNA fragmentation allows robust transcript reassembly upon whole transcriptome RNA-Seq. <i>Methods</i> , 2013, 63, 25-31.	1.9	27
34	Expanding heterochromatin reveals discrete subtelomeric domains delimited by chromatin landscape transitions. <i>Genome Research</i> , 2018, 28, 1867-1881.	2.4	27
35	HOTAIR lncRNA promotes epithelialâ€œmesenchymal transition by redistributing LSD1 at regulatory chromatin regions. <i>EMBO Reports</i> , 2021, 22, e50193.	2.0	27
36	Resection is responsible for loss of transcription around a double-strand break in <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2015, 4, .	2.8	26

#	ARTICLE	IF	CITATIONS
37	The Crohn's disease-related bacterial strain LF82 assembles biofilm-like communities to protect itself from phagolysosomal attack. <i>Communications Biology</i> , 2021, 4, 627.	2.0	21
38	VING: a software for visualization of deep sequencing signals. <i>BMC Research Notes</i> , 2015, 8, 419.	0.6	18
39	A Dual Model for Prioritizing Cancer Mutations in the Non-coding Genome Based on Germline and Somatic Events. <i>PLoS Computational Biology</i> , 2015, 11, e1004583.	1.5	17
40	A Role for the Mre11-Rad50-Xrs2 Complex in Gene Expression and Chromosome Organization. <i>Molecular Cell</i> , 2021, 81, 183-197.e6.	4.5	15
41	Dnmt3l-knockout donor cells improve somatic cell nuclear transfer reprogramming efficiency. <i>Reproduction</i> , 2015, 150, 245-256.	1.1	14
42	PHD and TFIIIS-Like Domains of the Bye1 Transcription Factor Determine Its Multivalent Genomic Distribution. <i>PLoS ONE</i> , 2014, 9, e102464.	1.1	14
43	Urinary extracellular vesicles contain mature transcriptome enriched in circular and long noncoding RNAs with functional significance in prostate cancer. <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12210.	5.5	14
44	From Yeast to Mammals, the Nonsense-Mediated mRNA Decay as a Master Regulator of Long Non-Coding RNAs Functional Trajectory. <i>Non-coding RNA</i> , 2021, 7, 44.	1.3	12
45	Reference-free transcriptome exploration reveals novel RNAs for prostate cancer diagnosis. <i>Life Science Alliance</i> , 2019, 2, e201900449.	1.3	12
46	Bases of antisense lncRNA-associated regulation of gene expression in fission yeast. <i>PLoS Genetics</i> , 2018, 14, e1007465.	1.5	11
47	The anti-cancer drug 5-fluorouracil affects cell cycle regulators and potential regulatory long non-coding RNAs in yeast. <i>RNA Biology</i> , 2019, 16, 727-741.	1.5	10
48	Expression of Subtelomeric lncRNAs Links Telomeres Dynamics to RNA Decay in <i>S. cerevisiae</i> . <i>Non-coding RNA</i> , 2015, 1, 94-126.	1.3	9
49	Endogenous RNAi pathway evolutionarily shapes the destiny of the antisense lncRNAs transcriptome. <i>Life Science Alliance</i> , 2019, 2, e201900407.	1.3	9
50	RNA polymerase II CTD S2P is dispensable for embryogenesis but mediates exit from developmental diapause in <i>C. elegans</i> . <i>Science Advances</i> , 2020, 6, .	4.7	9
51	Transcription-dependent spreading of the Dal80 yeast GATA factor across the body of highly expressed genes. <i>PLoS Genetics</i> , 2019, 15, e1007999.	1.5	8
52	A Viable Hypomorphic Allele of the Essential IMP3 Gene Reveals Novel Protein Functions in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2011, 6, e19500.	1.1	5
53	Is histone loss a common feature of DNA metabolism regulation? This paper is one of a selection of papers published in this Special Issue, entitled 27th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process.. <i>Biochemistry and Cell Biology</i> , 2006, 84, 450-452.	0.9	4
54	Strains isogenic to S288C used in the Yeast Genome Sequencing Programme carry a functional KSS1 gene. <i>Current Genetics</i> , 2001, 39, 291-296.	0.8	3

#	ARTICLE	IF	CITATIONS
55	Editorial for "Diversity of the non-coding transcriptomes revealed by RNA-seq technologies"; Methods, 2013, 63, 1-2.	1.9	2
56	Utilisation de longs ARN non codants vers un diagnostic urinaire du cancer de la prostate. Bulletin De L'Academie Nationale De Medecine, 2019, 203, 186-192.	0.0	0
57	Discussion suite à la communication: "Utilisation de longs ARN non codants pour le diagnostic urinaire du cancer de la prostate". Bulletin De L'Academie Nationale De Medecine, 2019, 203, 235-236.	0.0	0