

# Samuel Marguerat

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

6,474  
citations

109321  
35  
h-index

144013  
57  
g-index

74  
all docs

74  
docs citations

74  
times ranked

10044  
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. <i>Nature</i> , 2008, 453, 1239-1243.	27.8	888
2	Tuning gene expression to changing environments: from rapid responses to evolutionary adaptation. <i>Nature Reviews Genetics</i> , 2008, 9, 583-593.	16.3	857
3	Quantitative Analysis of Fission Yeast Transcriptomes and Proteomes in Proliferating and Quiescent Cells. <i>Cell</i> , 2012, 151, 671-683.	28.9	513
4	RNA-seq: from technology to biology. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 569-579.	5.4	423
5	Post-transcriptional control of gene expression: a genome-wide perspective. <i>Trends in Biochemical Sciences</i> , 2005, 30, 506-514.	7.5	247
6	The Wound Microenvironment Reprograms Schwann Cells to Invasive Mesenchymal-like Cells to Drive Peripheral Nerve Regeneration. <i>Neuron</i> , 2017, 96, 98-114.e7.	8.1	245
7	Proportionality: A Valid Alternative to Correlation for Relative Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004075.	3.2	232
8	Coordinating genome expression with cell size. <i>Trends in Genetics</i> , 2012, 28, 560-565.	6.7	188
9	A Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast. <i>Molecular Cell</i> , 2007, 26, 145-155.	9.7	184
10	Quantitative Impact of Thymic Clonal Deletion on the T Cell Repertoire. <i>Journal of Experimental Medicine</i> , 1997, 185, 377-384.	8.5	178
11	Interferon- $\gamma$ -Induced Endogenous Superantigen. <i>Immunity</i> , 2001, 15, 591-601.	14.3	133
12	A Coordinated Global Control over Cellular Transcription. <i>Current Biology</i> , 2010, 20, 2010-2015.	3.9	129
13	Next-generation sequencing: applications beyond genomes. <i>Biochemical Society Transactions</i> , 2008, 36, 1091-1096.	3.4	111
14	Exploring long non-coding RNAs through sequencing. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 200-205.	5.0	108
15	Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 873-880.	8.2	97
16	A Pre-mRNA Degradation Pathway that Selectively Targets Intron-Containing Genes Requires the Nuclear Poly(A)-Binding Protein. <i>Molecular Cell</i> , 2011, 44, 108-119.	9.7	93
17	Spt6 Regulates Intragenic and Antisense Transcription, Nucleosome Positioning, and Histone Modifications Genome-Wide in Fission Yeast. <i>Molecular and Cellular Biology</i> , 2013, 33, 4779-4792.	2.3	93
18	A simple method for directional transcriptome sequencing using Illumina technology. <i>Nucleic Acids Research</i> , 2009, 37, e148-e148.	14.5	88

#	ARTICLE	IF	CITATIONS
19	Size-Dependent Increase in RNA Polymerase II Initiation Rates Mediates Gene Expression Scaling with Cell Size. <i>Current Biology</i> , 2020, 30, 1217-1230.e7.	3.9	87
20	The RNA exosome promotes transcription termination of backtracked RNA polymerase II. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 919-926.	8.2	86
21	Size-Dependent Expression of the Mitotic Activator Cdc25 Suggests a Mechanism of Size Control in Fission Yeast. <i>Current Biology</i> , 2017, 27, 1491-1497.e4.	3.9	84
22	The <i>S. pombe</i> SAGA complex controls the switch from proliferation to sexual differentiation through the opposing roles of its subunits Gcn5 and Spt8. <i>Genes and Development</i> , 2008, 22, 3184-3195.	5.9	81
23	bayNorm: Bayesian gene expression recovery, imputation and normalization for single-cell RNA-sequencing data. <i>Bioinformatics</i> , 2020, 36, 1174-1181.	4.1	79
24	Defining transcribed regions using RNA-seq. <i>Nature Protocols</i> , 2010, 5, 255-266.	12.0	70
25	Natural genetic variation impacts expression levels of coding, non-coding, and antisense transcripts in fission yeast. <i>Molecular Systems Biology</i> , 2014, 10, 764.	7.2	65
26	LaSSO, a strategy for genome-wide mapping of intronic lariats and branch points using RNA-seq. <i>Genome Research</i> , 2014, 24, 1169-1179.	5.5	64
27	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. <i>EMBO Journal</i> , 2011, 30, 2843-2852.	7.8	63
28	The more the merrier: comparative analysis of microarray studies on cell cycle-regulated genes in fission yeast. <i>Yeast</i> , 2006, 23, 261-277.	1.7	61
29	Connecting growth with gene expression: of noise and numbers. <i>Current Opinion in Microbiology</i> , 2015, 25, 127-135.	5.1	58
30	Association of Human Endogenous Retrovirus K-18 Polymorphisms With Type 1 Diabetes. <i>Diabetes</i> , 2004, 53, 852-854.	0.6	56
31	Elimination of a specific histone H3K14 acetyltransferase complex bypasses the RNAi pathway to regulate pericentric heterochromatin functions. <i>Genes and Development</i> , 2011, 25, 214-219.	5.9	55
32	urg1: A Uracil-Regulatable Promoter System for Fission Yeast with Short Induction and Repression Times. <i>PLoS ONE</i> , 2008, 3, e1428.	2.5	55
33	Single-cell imaging and RNA sequencing reveal patterns of gene expression heterogeneity during fission yeast growth and adaptation. <i>Nature Microbiology</i> , 2019, 4, 480-491.	13.3	51
34	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. <i>EMBO Journal</i> , 2009, 28, 3400-3412.	7.8	46
35	The Nrd1-like protein Seb1 coordinates cotranscriptional 3' end processing and polyadenylation site selection. <i>Genes and Development</i> , 2016, 30, 1558-1572.	5.9	46
36	Long noncoding RNA repertoire and targeting by nuclear exosome, cytoplasmic exonuclease, and RNAi in fission yeast. <i>Rna</i> , 2018, 24, 1195-1213.	3.5	45

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37	The Fission Yeast Homeodomain Protein Yox1p Binds to MBF and Confines MBF-Dependent Cell-Cycle Transcription to G1-S via Negative Feedback. <i>PLoS Genetics</i> , 2009, 5, e1000626.	3.5	39
38	Differential patterns of intronic and exonic DNA regions with respect to RNA polymerase II occupancy, nucleosome density and H3K36me3 marking in fission yeast. <i>Genome Biology</i> , 2011, 12, R82.	9.6	39
39	Spt6 Is Required for Heterochromatic Silencing in the Fission Yeast <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 2011, 31, 4193-4204.	2.3	37
40	Genome-wide analysis of poly(A) site selection in <i>Schizosaccharomyces pombe</i> . <i>Rna</i> , 2013, 19, 1617-1631.	3.5	37
41	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. <i>Genome Research</i> , 2015, 25, 884-896.	5.5	37
42	Division rate, cell size and proteome allocation: impact on gene expression noise and implications for the dynamics of genetic circuits. <i>Royal Society Open Science</i> , 2018, 5, 172234.	2.4	37
43	The white matter is a pro-differentiative niche for glioblastoma. <i>Nature Communications</i> , 2021, 12, 2184.	12.8	37
44	Negative thymocyte selection to HERV-K18 superantigens in humans. <i>Blood</i> , 2005, 105, 4377-4382.	1.4	34
45	The DNA damage checkpoint pathway promotes extensive resection and nucleotide synthesis to facilitate homologous recombination repair and genome stability in fission yeast. <i>Nucleic Acids Research</i> , 2014, 42, 5644-5656.	14.5	27
46	Contributions of transcription and mRNA decay to gene expression dynamics of fission yeast in response to oxidative stress. <i>RNA Biology</i> , 2014, 11, 702-714.	3.1	26
47	A bacterial size law revealed by a coarse-grained model of cell physiology. <i>PLoS Computational Biology</i> , 2020, 16, e1008245.	3.2	25
48	Condensin controls cellular RNA levels through the accurate segregation of chromosomes instead of directly regulating transcription. <i>ELife</i> , 2018, 7, .	6.0	24
49	The fission yeast Rpb4 subunit of RNA polymerase II plays a specialized role in cell separation. <i>Molecular Genetics and Genomics</i> , 2006, 276, 545-554.	2.1	22
50	Transcriptional activation by bidirectional RNA polymerase II elongation over a silent promoter. <i>EMBO Reports</i> , 2005, 6, 956-960.	4.5	16
51	Growth-rate-dependent and nutrient-specific gene expression resource allocation in fission yeast. <i>Life Science Alliance</i> , 2022, 5, e202101223.	2.8	9
52	Functional profiling of long intergenic non-coding RNAs in fission yeast. <i>ELife</i> , 2022, 11, .	6.0	7
53	Transcriptional Activation of the General Amino Acid Permease Gene <i>per1</i> by the Histone Deacetylase <i>Clr6</i> Is Regulated by <i>Oca2</i> Kinase. <i>Molecular and Cellular Biology</i> , 2010, 30, 3396-3410.	2.3	6
54	Editorial: Determinants of Cell Size. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 115.	3.7	6

#	ARTICLE	IF	CITATIONS
55	Exploiting the multiplexing capabilities of tandem mass tags for high-throughput estimation of cellular protein abundances by mass spectrometry. <i>Methods</i> , 2015, 85, 100-107.	3.8	5
56	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. <i>PLoS Genetics</i> , 2021, 17, e1009784.	3.5	2
57	RNA-seq. , 2013, , 1877-1877.		0