

Marc Buehler

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

4,679
citations

117625

34
h-index

168389

53
g-index

61
all docs

61
docs citations

61
times ranked

6395
citing authors

#	ARTICLE	IF	CITATIONS
1	m6A RNA methylation of major satellite repeat transcripts facilitates chromatin association and RNA:DNA hybrid formation in mouse heterochromatin. <i>Nucleic Acids Research</i> , 2021, 49, 5568-5587.	14.5	21
2	An enhancer screen identifies new suppressors of small-RNA-mediated epigenetic gene silencing. <i>PLoS Genetics</i> , 2021, 17, e1009645.	3.5	2
3	Long Non-coding RNA Depletion Using Self-Cleaving Ribozymes. <i>Methods in Molecular Biology</i> , 2021, 2167, 287-301.	0.9	2
4	Scaling up dissection of functional RNA elements. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 771-773.	8.2	0
5	A fully automated deep learning pipeline for high-throughput colony segmentation and classification. <i>Biology Open</i> , 2020, 9, .	1.2	5
6	Mammalian RNA Decay Pathways Are Highly Specialized and Widely Linked to Translation. <i>Molecular Cell</i> , 2020, 77, 1222-1236.e13.	9.7	78
7	Small RNAs in the Transgenerational Inheritance of Epigenetic Information. <i>Trends in Genetics</i> , 2020, 36, 203-214.	6.7	65
8	The RNA hairpin binder TRIM71 modulates alternative splicing by repressing MBNL1. <i>Genes and Development</i> , 2019, 33, 1221-1235.	5.9	31
9	The ChAHP Complex Counteracts Chromatin Looping at CTCF Sites that Emerged from SINE Expansions in Mouse. <i>Cell</i> , 2019, 178, 1437-1451.e14.	28.9	118
10	Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. <i>Molecular Cell</i> , 2019, 74, 534-541.e4.	9.7	23
11	Zc3h13/Flacc is required for adenosine methylation by bridging the mRNA-binding factor Rbm15/Spenito to the m ⁶ A machinery component Wtap/Fl(2)d. <i>Genes and Development</i> , 2018, 32, 415-429.	5.9	416
12	Adenosine methylation as a molecular imprint defining the fate of RNA. <i>FEBS Letters</i> , 2018, 592, 2845-2859.	2.8	41
13	Activity-dependent neuroprotective protein recruits HP1 and CHD4 to control lineage-specifying genes. <i>Nature</i> , 2018, 557, 739-743.	27.8	169
14	Distinctive features of lincRNA gene expression suggest widespread RNA-independent functions. <i>Life Science Alliance</i> , 2018, 1, e201800124.	2.8	32
15	Disruption of an RNA-binding hinge region abolishes LHP1-mediated epigenetic repression. <i>Genes and Development</i> , 2017, 31, 2115-2120.	5.9	33
16	The Histone Acetyltransferase Mst2 Protects Active Chromatin from Epigenetic Silencing by Acetylating the Ubiquitin Ligase Brl1. <i>Molecular Cell</i> , 2017, 67, 294-307.e9.	9.7	41
17	RNA fate determination through cotranscriptional adenosine methylation and microprocessor binding. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 561-569.	8.2	117
18	The RNA-induced transcriptional silencing complex targets chromatin exclusively via interacting with nascent transcripts. <i>Genes and Development</i> , 2016, 30, 2571-2580.	5.9	60

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19	CGG Repeat-Induced FMR1 Silencing Depends on the Expansion Size in Human iPSCs and Neurons Carrying Unmethylated Full Mutations. <i>Stem Cell Reports</i> , 2016, 7, 1059-1071.	4.8	25
20	H3K9 methylation extends across natural boundaries of heterochromatin in the absence of an HP1 protein. <i>EMBO Journal</i> , 2015, 34, 2789-2803.	7.8	24
21	Genome-Engineering Tools to Establish Accurate Reporter Cell Lines That Enable Identification of Therapeutic Strategies to Treat Friedreich's Ataxia. <i>Journal of Biomolecular Screening</i> , 2015, 20, 760-767.	2.6	0
22	Single-Step Generation of Conditional Knockout Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2015, 12, 709-716.	6.4	76
23	Dicer and Hsp104 Function in a Negative Feedback Loop to Confer Robustness to Environmental Stress. <i>Cell Reports</i> , 2015, 10, 47-61.	6.4	15
24	The Paf1 complex represses small-RNA-mediated epigenetic gene silencing. <i>Nature</i> , 2015, 520, 248-252.	27.8	92
25	Single Cell RNA-Sequencing of Pluripotent States Unlocks Modular Transcriptional Variation. <i>Cell Stem Cell</i> , 2015, 17, 471-485.	11.1	505
26	miR455 is linked to hypoxia signaling and is deregulated in preeclampsia. <i>Cell Death and Disease</i> , 2014, 5, e1408-e1408.	6.3	38
27	Noncoding RNAs prevent spreading of a repressive histone mark. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 994-1000.	8.2	68
28	Regulation of Transcription through Acetylation of H3K122 on the Lateral Surface of the Histone Octamer. <i>Cell</i> , 2013, 152, 859-872.	28.9	209
29	Nuclear organisation and RNAi in fission yeast. <i>Current Opinion in Cell Biology</i> , 2013, 25, 372-377.	5.4	6
30	Chromatin-associated ncRNA activities. <i>Chromosome Research</i> , 2013, 21, 627-641.	2.2	35
31	Noncoding RNAs prevent spreading of a repressive histone mark. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1340-1340.	8.2	16
32	Dynamic nature of heterochromatin highlighted by a HP1 ^{Swi6} -dependent gene silencing mechanism. <i>Cell Cycle</i> , 2012, 11, 3907-3908.	2.6	4
33	RNAi keeps Atf1-bound stress response genes in check at nuclear pores. <i>Genes and Development</i> , 2012, 26, 683-692.	5.9	53
34	HP1 ^{Swi6} Mediates the Recognition and Destruction of Heterochromatic RNA Transcripts. <i>Molecular Cell</i> , 2012, 47, 215-227.	9.7	115
35	A Detour to Mature. <i>Molecular Cell</i> , 2012, 46, 719-721.	9.7	0
36	<i>Schizosaccharomyces pombe</i> reporter strains for relative quantitative assessment of heterochromatin silencing. <i>Yeast</i> , 2012, 29, 335-341.	1.7	3

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37	Dicer associates with chromatin to repress genome activity in <i>Schizosaccharomyces pombe</i> . <i>Nature Structural and Molecular Biology</i> , 2011, 18, 94-99.	8.2	80
38	An extended dsRBD with a novel zinc-binding motif mediates nuclear retention of fission yeast Dicer. <i>EMBO Journal</i> , 2011, 30, 4223-4235.	7.8	45
39	Long intronic GAA repeats causing Friedreich ataxia impede transcription elongation. <i>EMBO Molecular Medicine</i> , 2010, 2, 120-129.	6.9	113
40	Proteomic and functional analysis of the noncanonical poly(A) polymerase Cid14. <i>Rna</i> , 2010, 16, 1124-1129.	3.5	24
41	Nuclear Retention of Fission Yeast Dicer Is a Prerequisite for RNAi-Mediated Heterochromatin Assembly. <i>Developmental Cell</i> , 2010, 18, 102-113.	7.0	81
42	RNA brings chromatin into shape. <i>Biochemist</i> , 2010, 32, 8-10.	0.5	0
43	RNA turnover and chromatin-dependent gene silencing. <i>Chromosoma</i> , 2009, 118, 141-151.	2.2	43
44	Silent chromatin at the middle and ends: lessons from yeasts. <i>EMBO Journal</i> , 2009, 28, 2149-2161.	7.8	64
45	TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the <i>Schizosaccharomyces pombe</i> siRNA pathway. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1015-1023.	8.2	173
46	RNAi-Dependent and -Independent RNA Turnover Mechanisms Contribute to Heterochromatic Gene Silencing. <i>Cell</i> , 2007, 129, 707-721.	28.9	226
47	Coupling of Double-Stranded RNA Synthesis and siRNA Generation in Fission Yeast RNAi. <i>Molecular Cell</i> , 2007, 27, 449-461.	9.7	134
48	Two different Argonaute complexes are required for siRNA generation and heterochromatin assembly in fission yeast. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 200-207.	8.2	105
49	Transcription and RNAi in heterochromatic gene silencing. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1041-1048.	8.2	211
50	Tethering RITS to a Nascent Transcript Initiates RNAi- and Heterochromatin-Dependent Gene Silencing. <i>Cell</i> , 2006, 125, 873-886.	28.9	355
51	EJC-independent degradation of nonsense immunoglobulin mRNA depends on 3' UTR length. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 462-464.	8.2	225
52	Studies on the Mechanism of RNAi-dependent Heterochromatin Assembly. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2006, 71, 461-471.	1.1	40
53	Alternative splicing induced by nonsense mutations in the immunoglobulin VDJ exon is independent of truncation of the open reading frame. <i>Rna</i> , 2005, 11, 139-146.	3.5	19
54	Nonsense-associated alternative splicing of T-cell receptor genes: No evidence for frame dependence. <i>Rna</i> , 2005, 11, 147-156.	3.5	20

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55	Transcriptional Silencing of Nonsense Codon-Containing Immunoglobulin Minigenes. <i>Molecular Cell</i> , 2005, 18, 307-317.	9.7	64
56	Efficient downregulation of immunoglobulin λ mRNA with premature translation-termination codons requires the 5'-half of the VDJ exon. <i>Nucleic Acids Research</i> , 2004, 32, 3304-3315.	14.5	65
57	Intranuclear degradation of nonsense codon-containing mRNA. <i>EMBO Reports</i> , 2002, 3, 646-651.	4.5	54