

Mitchell Guttman

List of Publications by Year in descending order

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59
papers

42,395
citations

57681

46
h-index

139680

61
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70
all docs

70
docs citations

70
times ranked

67814
citing authors

#	ARTICLE	IF	CITATIONS
1	Essential Roles for RNA in Shaping Nuclear Organization. <i>Cold Spring Harbor Perspectives in Biology</i> , 2022, 14, a039719.	2.3	19
2	Single-cell measurement of higher-order 3D genome organization with scSPRITE. <i>Nature Biotechnology</i> , 2022, 40, 64-73.	9.4	63
3	SPRITE: a genome-wide method for mapping higher-order 3D interactions in the nucleus using combinatorial split-and-pool barcoding. <i>Nature Protocols</i> , 2022, 17, 36-75.	5.5	24
4	Xist spatially amplifies SHARP/SPEN recruitment to balance chromosome-wide silencing and specificity to the X chromosome. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 239-249.	3.6	46
5	Integrative genome modeling platform reveals essentiality of rare contact events in 3D genome organizations. <i>Nature Methods</i> , 2022, 19, 938-949.	9.0	20
6	Integrated spatial genomics reveals global architecture of single nuclei. <i>Nature</i> , 2021, 590, 344-350.	13.7	228
7	Nuclear compartmentalization as a mechanism of quantitative control of gene expression. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 653-670.	16.1	131
8	RNA promotes the formation of spatial compartments in the nucleus. <i>Cell</i> , 2021, 184, 5775-5790.e30.	13.5	192
9	Xist nucleates local protein gradients to propagate silencing across the X chromosome. <i>Cell</i> , 2021, 184, 6174-6192.e32.	13.5	62
10	High-Resolution Mapping of Multiway Enhancer-Promoter Interactions Regulating Pathogen Detection. <i>Molecular Cell</i> , 2020, 80, 359-373.e8.	4.5	21
11	SARS-CoV-2 Disrupts Splicing, Translation, and Protein Trafficking to Suppress Host Defenses. <i>Cell</i> , 2020, 183, 1325-1339.e21.	13.5	442
12	A protein assembly mediates Xist localization and gene silencing. <i>Nature</i> , 2020, 587, 145-151.	13.7	123
13	Xist drives spatial compartmentalization of DNA and protein to orchestrate initiation and maintenance of X inactivation. <i>Current Opinion in Cell Biology</i> , 2020, 64, 139-147.	2.6	38
14	The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. <i>Nature Genetics</i> , 2019, 51, 1024-1034.	9.4	60
15	Phase separation drives X-chromosome inactivation: a hypothesis. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 331-334.	3.6	98
16	Approaches for Understanding the Mechanisms of Long Noncoding RNA Regulation of Gene Expression. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032151.	2.3	58
17	RAP-MS: A Method to Identify Proteins that Interact Directly with a Specific RNA Molecule in Cells. <i>Methods in Molecular Biology</i> , 2018, 1649, 473-488.	0.4	68
18	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. <i>Nature</i> , 2018, 561, 132-136.	13.7	303

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19	Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. <i>Cell</i> , 2018, 174, 744-757.e24.	13.5	649
20	Linking Protein and RNA Function within the Same Gene. <i>Cell</i> , 2017, 168, 753-755.	13.5	2
21	Response to Comment on "Xist recruits the X chromosome to the nuclear lamina to enable chromosome-wide silencing" Science, 2017, 356, .	6.0	5
22	Re-evaluating the foundations of lnc RNA "Polycomb function. <i>EMBO Journal</i> , 2017, 36, 964-966.	3.5	11
23	Quantitative predictions of protein interactions with long noncoding RNAs. <i>Nature Methods</i> , 2017, 14, 5-6.	9.0	113
24	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	13.7	579
25	A Guide to Packing Your DNA. <i>Cell</i> , 2016, 165, 259-261.	13.5	2
26	m6A RNA methylation promotes XIST-mediated transcriptional repression. <i>Nature</i> , 2016, 537, 369-373.	13.7	1,250
27	Xist recruits the X chromosome to the nuclear lamina to enable chromosome-wide silencing. <i>Science</i> , 2016, 354, 468-472.	6.0	257
28	Long non-coding RNAs: spatial amplifiers that control nuclear structure and gene expression. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 756-770.	16.1	510
29	Local regulation of gene expression by lncRNA promoters, transcription and splicing. <i>Nature</i> , 2016, 539, 452-455.	13.7	1,056
30	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. <i>Genome Biology</i> , 2016, 17, 19.	3.8	141
31	Robust transcriptome-wide discovery of RNA-binding protein binding sites with enhanced CLIP (eCLIP). <i>Nature Methods</i> , 2016, 13, 508-514.	9.0	1,092
32	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	2.2	30
33	The Xist lncRNA interacts directly with SHARP to silence transcription through HDAC3. <i>Nature</i> , 2015, 521, 232-236.	13.7	946
34	Simultaneous generation of many RNA-seq libraries in a single reaction. <i>Nature Methods</i> , 2015, 12, 323-325.	9.0	256
35	Long noncoding RNAs: an emerging link between gene regulation and nuclear organization. <i>Trends in Cell Biology</i> , 2014, 24, 651-663.	3.6	286
36	Methods for comprehensive experimental identification of RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 203.	13.9	140

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37	RNA and dynamic nuclear organization. <i>Science</i> , 2014, 345, 1240-1241.	6.0	119
38	RNA-RNA Interactions Enable Specific Targeting of Noncoding RNAs to Nascent Pre-mRNAs and Chromatin Sites. <i>Cell</i> , 2014, 159, 188-199.	13.5	425
39	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	13.5	770
40	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. <i>Nature Genetics</i> , 2013, 45, 299-303.	9.4	237
41	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. <i>Cell</i> , 2013, 154, 240-251.	13.5	678
42	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	13.5	419
43	The Xist lncRNA Exploits Three-Dimensional Genome Architecture to Spread Across the X Chromosome. <i>Science</i> , 2013, 341, 1237-1243.	6.0	846
44	A High-Throughput Chromatin Immunoprecipitation Approach Reveals Principles of Dynamic Gene Regulation in Mammals. <i>Molecular Cell</i> , 2012, 47, 810-822.	4.5	375
45	Modular regulatory principles of large non-coding RNAs. <i>Nature</i> , 2012, 482, 339-346.	13.7	2,036
46	lincRNAs act in the circuitry controlling pluripotency and differentiation. <i>Nature</i> , 2011, 477, 295-300.	13.7	1,749
47	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
48	Integrative genomics viewer. <i>Nature Biotechnology</i> , 2011, 29, 24-26.	9.4	11,708
49	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
50	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	9.4	1,251
51	Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. <i>Nature Genetics</i> , 2010, 42, 1113-1117.	9.4	902
52	Digital transcriptome profiling from attomole-level RNA samples. <i>Genome Research</i> , 2010, 20, 519-525.	2.4	56
53	A Large Intergenic Noncoding RNA Induced by p53 Mediates Global Gene Repression in the p53 Response. <i>Cell</i> , 2010, 142, 409-419.	13.5	1,919
54	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	6.0	473

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55	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	13.7	3,801
56	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	3.3	2,709
57	Assessing the Significance of Conserved Genomic Aberrations Using High Resolution Genomic Microarrays. <i>PLoS Genetics</i> , 2007, 3, e143.	1.5	41
58	N-cadherin Expression in Breast Cancer: Correlation with an Aggressive Histologic Variant “ Invasive Micropapillary Carcinoma. <i>Breast Cancer Research and Treatment</i> , 2005, 94, 225-235.	1.1	78
59	A signaling pathway leading to metastasis is controlled by N-cadherin and the FGF receptor. <i>Cancer Cell</i> , 2002, 2, 301-314.	7.7	461