

Manuel Garber

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

27,428
citations

76196

40
h-index

143772

57
g-index

65
all docs

65
docs citations

65
times ranked

40740
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
4	SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. <i>Cell</i> , 2020, 181, 1016-1035.e19.	13.5	1,956
5	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
6	lincRNAs act in the circuitry controlling pluripotency and differentiation. <i>Nature</i> , 2011, 477, 295-300.	13.7	1,749
7	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
8	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	13.7	1,016
9	Biogenesis and function of tRNA fragments during sperm maturation and fertilization in mammals. <i>Science</i> , 2016, 351, 391-396.	6.0	992
10	Computational methods for transcriptome annotation and quantification using RNA-seq. <i>Nature Methods</i> , 2011, 8, 469-477.	9.0	919
11	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
12	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	2.4	809
13	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
14	Higher-Order Inter-chromosomal Hubs Shape 3D Genome Organization in the Nucleus. <i>Cell</i> , 2018, 174, 744-757.e24.	13.5	649
15	Functional annotation of native enhancers with a Cas9-histone demethylase fusion. <i>Nature Methods</i> , 2015, 12, 401-403.	9.0	548
16	Metabolic labeling of RNA uncovers principles of RNA production and degradation dynamics in mammalian cells. <i>Nature Biotechnology</i> , 2011, 29, 436-442.	9.4	524
17	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	6.0	473
18	A Composite of Multiple Signals Distinguishes Causal Variants in Regions of Positive Selection. <i>Science</i> , 2010, 327, 883-886.	6.0	457

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19	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
20	Evolutionary dynamics and tissue specificity of human long noncoding RNAs in six mammals. <i>Genome Research</i> , 2014, 24, 616-628.	2.4	318
21	Gene Expression Is Circular: Factors for mRNA Degradation Also Foster mRNA Synthesis. <i>Cell</i> , 2013, 153, 1000-1011.	13.5	311
22	Simultaneous generation of many RNA-seq libraries in a single reaction. <i>Nature Methods</i> , 2015, 12, 323-325.	9.0	256
23	Quality scores and SNP detection in sequencing-by-synthesis systems. <i>Genome Research</i> , 2008, 18, 763-770.	2.4	232
24	DEBrowser: interactive differential expression analysis and visualization tool for count data. <i>BMC Genomics</i> , 2019, 20, 6.	1.2	186
25	Systematic Discovery of TLR Signaling Components Delineates Viral-Sensing Circuits. <i>Cell</i> , 2011, 147, 853-867.	13.5	177
26	Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013â€“2016 Epidemic. <i>Cell</i> , 2016, 167, 1088-1098.e6.	13.5	173
27	The PPAR α -FGF21 Hormone Axis Contributes to Metabolic Regulation by the Hepatic JNK Signaling Pathway. <i>Cell Metabolism</i> , 2014, 20, 512-525.	7.2	149
28	Evolutionary analysis across mammals reveals distinct classes of long non-coding RNAs. <i>Genome Biology</i> , 2016, 17, 19.	3.8	141
29	DNA sequence of human chromosome 17 and analysis of rearrangement in the human lineage. <i>Nature</i> , 2006, 440, 1045-1049.	13.7	130
30	Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. <i>Developmental Cell</i> , 2015, 35, 750-758.	3.1	130
31	Transcriptome-wide Analysis of Roles for tRNA Modifications in Translational Regulation. <i>Molecular Cell</i> , 2017, 68, 978-992.e4.	4.5	118
32	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
33	DNA-binding-domain fusions enhance the targeting range and precision of Cas9. <i>Nature Methods</i> , 2015, 12, 1150-1156.	9.0	107
34	Diverse repertoire of human adipocyte subtypes develops from transcriptionally distinct mesenchymal progenitor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17970-17979.	3.3	106
35	Analysis of the DNA sequence and duplication history of human chromosome 15. <i>Nature</i> , 2006, 440, 671-675.	13.7	67
36	DolphinNext: a distributed data processing platform for high throughput genomics. <i>BMC Genomics</i> , 2020, 21, 310.	1.2	66

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37	End Sequence Analysis Toolkit (ESAT) expands the extractable information from single-cell RNA-seq data. <i>Genome Research</i> , 2016, 26, 1397-1410.	2.4	63
38	Frequent Loss of IRF2 in Cancers Leads to Immune Evasion through Decreased MHC Class I Antigen Presentation and Increased PD-L1 Expression. <i>Journal of Immunology</i> , 2019, 203, 1999-2010.	0.4	63
39	Simultaneous profiling of multiple chromatin proteins in the same cells. <i>Molecular Cell</i> , 2021, 81, 4736-4746.e5.	4.5	62
40	HIV-1-induced cytokines deplete homeostatic innate lymphoid cells and expand TCF7-dependent memory NK cells. <i>Nature Immunology</i> , 2020, 21, 274-286.	7.0	60
41	A Negative Feedback Loop of Transcription Factors Specifies Alternative Dendritic Cell Chromatin States. <i>Molecular Cell</i> , 2014, 56, 749-762.	4.5	58
42	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	53
43	An atlas of cell types in the mouse epididymis and vas deferens. <i>ELife</i> , 2020, 9, .	2.8	51
44	scRNA-seq of human vitiligo reveals complex networks of subclinical immune activation and a role for CCR5 in T reg function. <i>Science Translational Medicine</i> , 2021, 13, eabd8995.	5.8	50
45	GUIDEseq: a bioconductor package to analyze GUIDE-Seq datasets for CRISPR-Cas nucleases. <i>BMC Genomics</i> , 2017, 18, 379.	1.2	32
46	Early Epstein-Barr Virus Genomic Diversity and Convergence toward the B95.8 Genome in Primary Infection. <i>Journal of Virology</i> , 2018, 92, .	1.5	28
47	Spatial transcriptomic reconstruction of the mouse olfactory glomerular map suggests principles of odor processing. <i>Nature Neuroscience</i> , 2022, 25, 484-492.	7.1	27
48	High Epstein-Barr Virus Load and Genomic Diversity Are Associated with Generation of gp350-Specific Neutralizing Antibodies following Acute Infectious Mononucleosis. <i>Journal of Virology</i> , 2017, 91, .	1.5	23
49	High-Resolution Mapping of Multiway Enhancer-Promoter Interactions Regulating Pathogen Detection. <i>Molecular Cell</i> , 2020, 80, 359-373.e8.	4.5	21
50	Epstein-Barr Virus Latent Membrane Protein 1 Genetic Variability in Peripheral Blood B Cells and Oropharyngeal Fluids. <i>Journal of Virology</i> , 2014, 88, 3744-3755.	1.5	19
51	Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. <i>Cell Systems</i> , 2018, 6, 381-394.e7.	2.9	19
52	Hierarchy of signaling thresholds downstream of the T cell receptor and the Tec kinase ITK. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
53	Defining the 5' and 3' landscape of the <i>Drosophila</i> transcriptome with Exo-seq and RNaseH-seq. <i>Nucleic Acids Research</i> , 2017, 45, e95-e95.	6.5	11
54	Single cell transcriptomics reveals dysregulated cellular and molecular networks in a fragile X syndrome model. <i>PLoS Genetics</i> , 2022, 18, e1010221.	1.5	11

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55	Genome-wide assessment of post-transcriptional control in the fly brain. <i>Frontiers in Molecular Neuroscience</i> , 2013, 6, 49.	1.4	9
56	DNA sequence analysis of the conserved region around the SOD1 gene locus in recessively inherited ALS. <i>Neuroscience Letters</i> , 2009, 463, 64-69.	1.0	6
57	Gaining Insight into Vitiligo Genetics through the Lens of a Large Epidemiologic Study. <i>Journal of Investigative Dermatology</i> , 2021, 141, 718-721.	0.3	0