

Jesse M Engreitz

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

10,456
citations

201385

27
h-index

276539

41
g-index

56
all docs

56
docs citations

56
times ranked

19102
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational estimates of annular diameter reveal genetic determinants of mitral valve function and disease. <i>JCI Insight</i> , 2022, 7, .	2.3	9
2	Systematic identification of genomic elements that regulate <i>FCGR2A</i> expression and harbor variants linked with autoimmune disease. <i>Human Molecular Genetics</i> , 2022, 31, 1946-1961.	1.4	7
3	Compatibility rules of human enhancer and promoter sequences. <i>Nature</i> , 2022, 607, 176-184.	13.7	67
4	Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity. <i>Nature Genetics</i> , 2022, 54, 827-836.	9.4	61
5	SNP-to-gene linking strategies reveal contributions of enhancer-related and candidate master-regulator genes to autoimmune disease. <i>Cell Genomics</i> , 2022, 2, 100145.	3.0	19
6	Activity-dependent regulome of human GABAergic neurons reveals new patterns of gene regulation and neurological disease heritability. <i>Nature Neuroscience</i> , 2021, 24, 437-448.	7.1	33
7	Genome-wide enhancer maps link risk variants to disease genes. <i>Nature</i> , 2021, 593, 238-243.	13.7	332
8	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	13.7	537
9	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.	13.7	376
10	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	5.8	38
11	HyPR-seq: Single-cell quantification of chosen RNAs via hybridization and sequencing of DNA probes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33404-33413.	3.3	21
12	CRISPR Tools for Systematic Studies of RNA Regulation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a035386.	2.3	22
13	Functional disease architectures reveal unique biological role of transposable elements. <i>Nature Communications</i> , 2019, 10, 4054.	5.8	14
14	Discovering metabolic disease gene interactions by correlated effects on cellular morphology. <i>Molecular Metabolism</i> , 2019, 24, 108-119.	3.0	13
15	Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. <i>Nature Genetics</i> , 2019, 51, 1664-1669.	9.4	631
16	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. <i>ELife</i> , 2019, 8, .	2.8	14
17	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	13.5	296
18	CRISPR-SURF: discovering regulatory elements by deconvolution of CRISPR tiling screen data. <i>Nature Methods</i> , 2018, 15, 992-993.	9.0	33

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19	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	5.8	79
20	Positional specificity of different transcription factor classes within enhancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7222-E7230.	3.3	72
21	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.	5.8	140
22	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. <i>Nature</i> , 2018, 561, 132-136.	13.7	303
23	Systematic dissection of genomic features determining transcription factor binding and enhancer function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1291-E1300.	3.3	150
24	A Genetic Variant Associated with Five Vascular Diseases Is a Distal Regulator of Endothelin-1 Gene Expression. <i>Cell</i> , 2017, 170, 522-533.e15.	13.5	356
25	Genome-scale activation screen identifies a lncRNA locus regulating a gene neighbourhood. <i>Nature</i> , 2017, 548, 343-346.	13.7	336
26	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017, 547, 55-60.	13.7	269
27	Systematic mapping of functional enhancer-promoter connections with CRISPR interference. <i>Science</i> , 2016, 354, 769-773.	6.0	512
28	Eradication of large established tumors in mice by combination immunotherapy that engages innate and adaptive immune responses. <i>Nature Medicine</i> , 2016, 22, 1402-1410.	15.2	437
29	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
30	Local regulation of gene expression by lncRNA promoters, transcription and splicing. <i>Nature</i> , 2016, 539, 452-455.	13.7	1,056
31	Neuregulin Autocrine Signaling Promotes Self-Renewal of Breast Tumor-Initiating Cells by Triggering HER2/HER3 Activation. <i>Cancer Research</i> , 2014, 74, 341-352.	0.4	30
32	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 198-206.	3.6	565
33	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
34	Transcriptome-wide Mapping Reveals Widespread Dynamic-Regulated Pseudouridylation of ncRNA and mRNA. <i>Cell</i> , 2014, 159, 148-162.	13.5	770
35	The Xist lncRNA Exploits Three-Dimensional Genome Architecture to Spread Across the X Chromosome. <i>Science</i> , 2013, 341, 1237-1243.	6.0	846
36	The Lin28/let-7 Axis Regulates Glucose Metabolism. <i>Cell</i> , 2011, 147, 81-94.	13.5	812

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37	ProfileChaser: searching microarray repositories based on genome-wide patterns of differential expression. <i>Bioinformatics</i> , 2011, 27, 3317-3318.	1.8	47
38	Content-based microarray search using differential expression profiles. <i>BMC Bioinformatics</i> , 2010, 11, 603.	1.2	36