

# Maximilian Haeussler

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

13,311  
citations

117625

34  
h-index

276875

41  
g-index

58  
all docs

58  
docs citations

58  
times ranked

26604  
citing authors

#	ARTICLE	IF	CITATIONS
1	The UCSC Genome Browser database: 2022 update. <i>Nucleic Acids Research</i> , 2022, 50, D1115-D1122.	14.5	175
2	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. <i>Developmental Cell</i> , 2021, 56, 292-309.e9.	7.0	63
3	The UCSC Genome Browser database: 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D1046-D1057.	14.5	354
4	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328.	19.0	26
5	Single-cell atlas of early human brain development highlights heterogeneity of human neuroepithelial cells and early radial glia. <i>Nature Neuroscience</i> , 2021, 24, 584-594.	14.8	244
6	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , 2021, 184, 2633-2648.e19.	28.9	94
7	UCSC Cell Browser: visualize your single-cell data. <i>Bioinformatics</i> , 2021, 37, 4578-4580.	4.1	105
8	Human microglia states are conserved across experimental models and regulate neural stem cell responses in chimeric organoids. <i>Cell Stem Cell</i> , 2021, 28, 2153-2166.e6.	11.1	98
9	Single-cell epigenomics reveals mechanisms of human cortical development. <i>Nature</i> , 2021, 598, 205-213.	27.8	154
10	UCSC Genome Browser enters 20th year. <i>Nucleic Acids Research</i> , 2020, 48, D756-D761.	14.5	138
11	AVADA: toward automated pathogenic variant evidence retrieval directly from the full-text literature. <i>Genetics in Medicine</i> , 2020, 22, 362-370.	2.4	24
12	CRISPR off-targets: a question of context. <i>Cell Biology and Toxicology</i> , 2020, 36, 5-9.	5.3	21
13	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	28.9	243
14	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , 2020, 369, 1318-1330.	12.6	2,385
15	The UCSC SARS-CoV-2 Genome Browser. <i>Nature Genetics</i> , 2020, 52, 991-998.	21.4	79
16	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	60
17	Cell stress in cortical organoids impairs molecular subtype specification. <i>Nature</i> , 2020, 578, 142-148.	27.8	387
18	The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. <i>Mobile DNA</i> , 2020, 11, 13.	3.6	31

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19	Neuronal vulnerability and multilineage diversity in multiple sclerosis. <i>Nature</i> , 2019, 573, 75-82.	27.8	385
20	Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair. <i>Nucleic Acids Research</i> , 2019, 47, 7989-8003.	14.5	135
21	Single-cell genomics identifies cell type-specific molecular changes in autism. <i>Science</i> , 2019, 364, 685-689.	12.6	600
22	Federated discovery and sharing of genomic data using Beacons. <i>Nature Biotechnology</i> , 2019, 37, 220-224.	17.5	75
23	The UCSC Genome Browser database: 2019 update. <i>Nucleic Acids Research</i> , 2019, 47, D853-D858.	14.5	699
24	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. <i>Nature Protocols</i> , 2018, 13, 946-986.	12.0	70
25	HNRNPA1 promotes recognition of splice site decoys by U2AF2 in vivo. <i>Genome Research</i> , 2018, 28, 689-698.	5.5	28
26	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. <i>Nucleic Acids Research</i> , 2018, 46, D718-D725.	14.5	90
27	The UCSC Genome Browser database: 2018 update. <i>Nucleic Acids Research</i> , 2018, 46, D762-D769.	14.5	476
28	CRISPR off-target analysis in genetically engineered rats and mice. <i>Nature Methods</i> , 2018, 15, 512-514.	19.0	176
29	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. <i>Cell</i> , 2018, 173, 1356-1369.e22.	28.9	366
30	CRISPOR: intuitive guide selection for CRISPR/Cas9 genome editing experiments and screens. <i>Nucleic Acids Research</i> , 2018, 46, W242-W245.	14.5	1,114
31	Registered access: authorizing data access. <i>European Journal of Human Genetics</i> , 2018, 26, 1721-1731.	2.8	33
32	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D626-D634.	14.5	308
33	Evaluation and rational design of guide RNAs for efficient CRISPR/Cas9-mediated mutagenesis in <i>Ciona</i> . <i>Developmental Biology</i> , 2017, 425, 8-20.	2.0	69
34	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	5.5	139
35	Spatiotemporal gene expression trajectories reveal developmental hierarchies of the human cortex. <i>Science</i> , 2017, 358, 1318-1323.	12.6	717
36	Evaluation of off-target and on-target scoring algorithms and integration into the guide RNA selection tool CRISPOR. <i>Genome Biology</i> , 2016, 17, 148.	8.8	1,334

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37	The UCSC Genome Browser database: 2016 update. <i>Nucleic Acids Research</i> , 2016, 44, D717-D725.	14.5	376
38	Ebola: an analysis of immunity at the molecular level. , 2015, , .		1
39	Navigating protected genomics data with UCSC Genome Browser in a Box. <i>Bioinformatics</i> , 2015, 31, 764-766.	4.1	49
40	The UCSC Genome Browser database: 2015 update. <i>Nucleic Acids Research</i> , 2015, 43, D670-D681.	14.5	891
41	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. <i>Nature</i> , 2014, 516, 242-245.	27.8	396
42	Structurally Conserved Primate lncRNAs Are Transiently Expressed During Human Cortical Differentiation and Influence Cell Type Specific Genes. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0