Maximilian Haeussler

List of Publications by Year
in descending order

42	13,311	117625	276875
papers	citations	34	41
		h-index	g-index

58	58	58	26604
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
2	Evaluation of off-target and on-target scoring algorithms and integration into the guide RNA selection tool CRISPOR. Genome Biology, 2016, 17, 148.	8.8	1,334
3	CRISPOR: intuitive guide selection for CRISPR/Cas9 genome editing experiments and screens. Nucleic Acids Research, 2018, 46, W242-W245.	14.5	1,114
4	The UCSC Genome Browser database: 2015 update. Nucleic Acids Research, 2015, 43, D670-D681.	14.5	891
5	Spatiotemporal gene expression trajectories reveal developmental hierarchies of the human cortex. Science, 2017, 358, 1318-1323.	12.6	717
6	The UCSC Genome Browser database: 2019 update. Nucleic Acids Research, 2019, 47, D853-D858.	14.5	699
7	Single-cell genomics identifies cell type–specific molecular changes in autism. Science, 2019, 364, 685-689.	12.6	600
8	The UCSC Genome Browser database: 2018 update. Nucleic Acids Research, 2018, 46, D762-D769.	14.5	476
9	An evolutionary arms race between KRAB zinc-finger genes ZNF91/93 and SVA/L1 retrotransposons. Nature, 2014, 516, 242-245.	27.8	396
10	Cell stress in cortical organoids impairs molecular subtype specification. Nature, 2020, 578, 142-148.	27.8	387
11	Neuronal vulnerability and multilineage diversity in multiple sclerosis. Nature, 2019, 573, 75-82.	27.8	385
12	The UCSC Genome Browser database: 2016 update. Nucleic Acids Research, 2016, 44, D717-D725.	14.5	376
13	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. Cell, 2018, 173, 1356-1369.e22.	28.9	366
14	The UCSC Genome Browser database: 2021 update. Nucleic Acids Research, 2021, 49, D1046-D1057.	14.5	354
15	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D626-D634.	14.5	308
16	Single-cell atlas of early human brain development highlights heterogeneity of human neuroepithelial cells and early radial glia. Nature Neuroscience, 2021, 24, 584-594.	14.8	244
17	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
18	CRISPR off-target analysis in genetically engineered rats and mice. Nature Methods, 2018, 15, 512-514.	19.0	176

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19	The UCSC Genome Browser database: 2022 update. Nucleic Acids Research, 2022, 50, D1115-D1122.	14.5	175
20	Single-cell epigenomics reveals mechanisms of human cortical development. Nature, 2021, 598, 205-213.	27.8	154
21	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. Genome Research, 2017, 27, 1843-1858.	5.5	139
22	UCSC Genome Browser enters 20th year. Nucleic Acids Research, 2020, 48, D756-D761.	14.5	138
23	Massively parallel profiling and predictive modeling of the outcomes of CRISPR/Cas9-mediated double-strand break repair. Nucleic Acids Research, 2019, 47, 7989-8003.	14.5	135
24	UCSC Cell Browser: visualize your single-cell data. Bioinformatics, 2021, 37, 4578-4580.	4.1	105
25	Human microglia states are conserved across experimental models and regulate neural stem cell responses in chimeric organoids. Cell Stem Cell, 2021, 28, 2153-2166.e6.	11.1	98
26	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
27	ANISEED 2017: extending the integrated ascidian database to the exploration and evolutionary comparison of genome-scale datasets. Nucleic Acids Research, 2018, 46, D718-D725.	14.5	90
28	The UCSC SARS-CoV-2 Genome Browser. Nature Genetics, 2020, 52, 991-998.	21.4	79
29	Federated discovery and sharing of genomic data using Beacons. Nature Biotechnology, 2019, 37, 220-224.	17.5	75
30	Integrated design, execution, and analysis of arrayed and pooled CRISPR genome-editing experiments. Nature Protocols, 2018, 13, 946-986.	12.0	70
31	Evaluation and rational design of guide RNAs for efficient CRISPR/Cas9-mediated mutagenesis in Ciona. Developmental Biology, 2017, 425, 8-20.	2.0	69
32	Modeling Human TBX5 Haploinsufficiency Predicts Regulatory Networks for Congenital Heart Disease. Developmental Cell, 2021, 56, 292-309.e9.	7.0	63
33	AMELIE speeds Mendelian diagnosis by matching patient phenotype and genotype to primary literature. Science Translational Medicine, 2020, 12, .	12.4	60
34	Navigating protected genomics data with UCSC Genome Browser in a Box. Bioinformatics, 2015, 31, 764-766.	4.1	49
35	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	2.8	33
36	The UCSC repeat browser allows discovery and visualization of evolutionary conflict across repeat families. Mobile DNA, 2020, 11, 13.	3.6	31

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37	HNRNPA1 promotes recognition of splice site decoys by U2AF2 in vivo. Genome Research, 2018, 28, 689-698.	5.5	28
38	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. Nature Methods, 2021, 18, 327-328.	19.0	26
39	AVADA: toward automated pathogenic variant evidence retrieval directly from the full-text literature. Genetics in Medicine, 2020, 22, 362-370.	2.4	24
40	CRISPR off-targets: a question of context. Cell Biology and Toxicology, 2020, 36, 5-9.	5.3	21
41	Ebola: an analysis of immunity at the molecular level. , 2015, , .		1
42	Structurally Conserved Primate lncRNAs Are Transiently Expressed During Human Cortical Differentiation and Influence Cell Type Specific Genes. SSRN Electronic Journal, 0, , .	0.4	0