Diane E Dickel

List of Publications by Year
in descending order

45 papers	6,900 citations	159358 30 h-index	214527 47 g-index
65 all docs	65 docs citations	65 times ranked	11871 citing authors

#	Article	IF	Citations
1	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
2	Microduplications of 16p11.2 are associated with schizophrenia. Nature Genetics, 2009, 41, 1223-1227.	9.4	646
3	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	9.4	539
4	Enhancer redundancy provides phenotypic robustness in mammalian development. Nature, 2018, 554, 239-243.	13.7	514
5	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	13.5	308
6	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	7.1	290
7	High-Throughput Single-Cell Transcriptome Profiling of Plant Cell Types. Cell Reports, 2019, 27, 2241-2247.e4.	2.9	279
8	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. Cell, 2016, 167, 633-642.e11.	13.5	275
9	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
10	Association Testing of the Positional and Functional Candidate Gene SLC1A1/EAAC1 in Early-Onset Obsessive-compulsive Disorder. Archives of General Psychiatry, 2006, 63, 778.	13.8	252
11	Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073.	7.1	210
12	Ultraconserved Enhancers Are Required for Normal Development. Cell, 2018, 172, 491-499.e15.	13.5	169
13	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767.	13.7	131
14	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
15	Reduced transcript expression of genes affected by inherited and de novo CNVs in autism. European Journal of Human Genetics, 2011, 19, 727-731.	1.4	109
16	Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. Cell Stem Cell, 2020, 27, 765-783.e14.	5.2	101
17	Comprehensive InÂVivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. Cell, 2020, 180, 1262-1271.e15.	13.5	100
18	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	9.4	97

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19	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
20	Five novel loci for inherited hearing loss mapped by SNP-based homozygosity profiles in Palestinian families. European Journal of Human Genetics, 2010, 18, 407-413.	1.4	83
21	Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923.	5.8	83
22	Association Studies of Serotonin System Candidate Genes in Early-onset Obsessive-Compulsive Disorder. Biological Psychiatry, 2007, 61, 322-329.	0.7	81
23	Improved regulatory element prediction based on tissue-specific local epigenomic signatures. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1633-E1640.	3.3	78
24	Evidence for a Susceptibility Locus on Chromosome 10p15 in Early-Onset Obsessive-Compulsive Disorder. Biological Psychiatry, 2007, 62, 856-862.	0.7	72
25	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. Cell Stem Cell, 2019, 25, 69-86.e5.	5.2	72
26	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	9.0	71
27	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	9.0	71
28	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68
29	Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Reports, 2019, 28, 342-351.e4.	2.9	61
30	Relationship between genetic variation at PPP1R3B and levels of liver glycogen and triglyceride. Hepatology, 2018, 67, 2182-2195.	3.6	51
31	Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528.	9.4	39
32	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	2.6	30
33	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. Cell, 2016, 167, 1163-1166.	13.5	27
34	Transcriptional network orchestrating regional patterning of cortical progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
35	Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111.	13.7	24
36	Plant single-cell solutions for energy and the environment. Communications Biology, 2021, 4, 962.	2.0	23

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37	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in Molecular Biology, 2022, 2403, 147-186.	0.4	20
38	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720.	1.5	17
39	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
40	Perfect and imperfect views of ultraconserved sequences. Nature Reviews Genetics, 2022, 23, 182-194.	7.7	16
41	Deletion of a non-canonical regulatory sequence causes loss of Scn1a expression and epileptic phenotypes in mice. Genome Medicine, 2021, 13, 69.	3.6	15
42	Single site-specific integration targeting coupled with embryonic stem cell differentiation provides a high-throughput alternative to in vivo enhancer analyses. Biology Open, 2013, 2, 1229-1238.	0.6	11
43	Differential Etv2 threshold requirement for endothelial and erythropoietic development. Cell Reports, 2022, 39, 110881.	2.9	9
44	Fishing for Function in the Human Gene Pool. Trends in Genetics, 2016, 32, 392-394.	2.9	0
45	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0