Diane E Dickel

List of Publications by Year
in descending order

45	6,900	159525 30	214721 47
papers	citations	h-index	g-index

65	65	65	11871
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Perfect and imperfect views of ultraconserved sequences. Nature Reviews Genetics, 2022, 23, 182-194.	7.7	16
2	Characterization of Mammalian In Vivo Enhancers Using Mouse Transgenesis and CRISPR Genome Editing. Methods in Molecular Biology, 2022, 2403, 147-186.	0.4	20
3	Differential Etv2 threshold requirement for endothelial and erythropoietic development. Cell Reports, 2022, 39, 110881.	2.9	9
4	Ultraconserved enhancer function does not require perfect sequence conservation. Nature Genetics, 2021, 53, 521-528.	9.4	39
5	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
6	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
7	Plant single-cell solutions for energy and the environment. Communications Biology, 2021, 4, 962.	2.0	23
8	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
9	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
10	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
11	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
12	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
13	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
14	The changing mouse embryo transcriptome at whole tissue and single-cell resolution. Nature, 2020, 583, 760-767.	13.7	131
15	Supervised enhancer prediction with epigenetic pattern recognition and targeted validation. Nature Methods, 2020, 17, 807-814.	9.0	71
16	Comprehensive InÂVivo Interrogation Reveals Phenotypic Impact of Human Enhancer Variants. Cell, 2020, 180, 1262-1271.e15.	13.5	100
17	Genomic analyses implicate noncoding de novo variants in congenital heart disease. Nature Genetics, 2020, 52, 769-777.	9.4	97
18	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. Cell Reports, 2019, 28, 2048-2063.e8.	2.9	68

#	Article	IF	Citations
19	Molecular Mechanisms Driving Switch Behavior in Xylem Cell Differentiation. Cell Reports, 2019, 28, 342-351.e4.	2.9	61
20	Noncoding deletions reveal a gene that is critical for intestinal function. Nature, 2019, 571, 107-111.	13.7	24
21	Cardiac Reprogramming Factors Synergistically Activate Genome-wide Cardiogenic Stage-Specific Enhancers. Cell Stem Cell, 2019, 25, 69-86.e5.	5.2	72
22	High-Throughput Single-Cell Transcriptome Profiling of Plant Cell Types. Cell Reports, 2019, 27, 2241-2247.e4.	2.9	279
23	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
24	Enhancer redundancy provides phenotypic robustness in mammalian development. Nature, 2018, 554, 239-243.	13.7	514
25	Ultraconserved Enhancers Are Required for Normal Development. Cell, 2018, 172, 491-499.e15.	13.5	169
26	Relationship between genetic variation at PPP1R3B and levels of liver glycogen and triglyceride. Hepatology, 2018, 67, 2182-2195.	3.6	51
27	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
28	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
29	Genomic Patterns of De Novo Mutation in Simplex Autism. Cell, 2017, 171, 710-722.e12.	13.5	308
30	Germline Chd8 haploinsufficiency alters brain development in mouse. Nature Neuroscience, 2017, 20, 1062-1073.	7.1	210
31	Limb-Enhancer Genie: An accessible resource of accurate enhancer predictions in the developing limb. PLoS Computational Biology, 2017, 13, e1005720.	1.5	17
32	Fishing for Function in the Human Gene Pool. Trends in Genetics, 2016, 32, 392-394.	2.9	0
33	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. Cell, 2016, 167, 1163-1166.	13.5	27
34	Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923.	5.8	83
35	Progressive Loss of Function in a Limb Enhancer during Snake Evolution. Cell, 2016, 167, 633-642.e11.	13.5	275
36	Function-based identification of mammalian enhancers using site-specific integration. Nature Methods, 2014, 11, 566-571.	9.0	71

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37	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
38	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
39	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
40	A recurrent 16p12.1 microdeletion supports a two-hit model for severe developmental delay. Nature Genetics, 2010, 42, 203-209.	9.4	539
41	Microduplications of 16p11.2 are associated with schizophrenia. Nature Genetics, 2009, 41, 1223-1227.	9.4	646
42	Association Studies of Serotonin System Candidate Genes in Early-onset Obsessive-Compulsive Disorder. Biological Psychiatry, 2007, 61, 322-329.	0.7	81
43	Evidence for a Susceptibility Locus on Chromosome 10p15 in Early-Onset Obsessive-Compulsive Disorder. Biological Psychiatry, 2007, 62, 856-862.	0.7	72
44	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
45	Genomic Resolution of DLX-Orchestrated Transcriptional Circuits Driving Development of Forebrain GABAergic Neurons. SSRN Electronic Journal, 0, , .	0.4	0