David U Gorkin

List of Publications by Year in descending order

29 papers	6,827 citations	236833 25 h-index	434063 31 g-index
43 all docs	43 docs citations	43 times ranked	11831 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	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. Cell, 2015, 162, 900-910.	13.5	846
3	Chromatin Domains: The Unit of Chromosome Organization. Molecular Cell, 2016, 62, 668-680.	4.5	653
4	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
5	A method to predict the impact of regulatory variants from DNA sequence. Nature Genetics, 2015, 47, 955-961.	9.4	416
6	The 3D Genome in Transcriptional Regulation and Pluripotency. Cell Stem Cell, 2014, 14, 762-775.	5.2	353
7	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
8	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
9	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
10	N-methyladenine DNA Modification in Glioblastoma. Cell, 2018, 175, 1228-1243.e20.	13.5	236
11	A Polymorphism in IRF4 Affects Human Pigmentation through a Tyrosinase-Dependent MITF/TFAP2A Pathway. Cell, 2013, 155, 1022-1033.	13.5	184
12	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	3.6	172
13	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402.	13.7	170
14	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
15	Single-cell chromatin accessibility identifies pancreatic islet cell typeâ€“ and state-specific regulatory programs of diabetes risk. Nature Genetics, 2021, 53, 455-466.	9.4	100
16	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
17	Spatiotemporal DNA methylome dynamics of the developing mouse fetus. Nature, 2020, 583, 752-759.	13.7	84
18	Genome-wide compendium and functional assessment of in vivo heart enhancers. Nature Communications, 2016, 7, 12923.	5.8	83

#	Article	IF	Citations
19	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	5.8	82
20	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
21	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	3.8	65
22	Integration of ChIP-seq and machine learning reveals enhancers and a predictive regulatory sequence vocabulary in melanocytes. Genome Research, 2012, 22, 2290-2301.	2.4	64
23	SOX10 directly modulates ERBB3 transcription via an intronic neural crest enhancer. BMC Developmental Biology, 2011, 11, 40.	2.1	51
24	Knock in of the AKT1 E17K mutation in human breast epithelial cells does not recapitulate oncogenic PIK3CA mutations. Oncogene, 2010, 29, 2337-2345.	2.6	50
25	Genomic analysis reveals distinct mechanisms and functional classes of SOX10-regulated genes in melanocytes. Human Molecular Genetics, 2015, 24, 5433-5450.	1.4	34
26	Oligodendroglial and panâ€neural crest expression of Cre recombinase directed by Sox10 enhancer. Genesis, 2009, 47, 765-770.	0.8	21
27	Coding and noncoding variants in EBF3 are involved in HADDS and simplex autism. Human Genomics, 2021, 15, 44.	1.4	16
28	Closing the distance on obesity culprits. Nature, 2014, 507, 309-310.	13.7	11
29	Rapid changes in chromatin structure during dedifferentiation of primary hepatocytes in vitro. Genomics, 2022, 114, 110330.	1.3	4