Kyle J Gaulton

List of Publications by Year
in descending order

57	9,622	70961 41	133063 59
papers	citations	h-index	g-index

81	81	81	16661
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Characterizing cis-regulatory elements using single-cell epigenomics. Nature Reviews Genetics, 2023, 24, 21-43.	7.7	72
2	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
3	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	2.8	15
4	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
5	Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. PLoS Genetics, 2021, 17, e1009531.	1.5	13
6	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402.	13.7	170
7	Cardiac cell typeâ€“specific gene regulatory programs and disease risk association. Science Advances, 2021, 7, .	4.7	63
8	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	13.7	89
9	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	13.7	95
10	Mutations and variants of ONECUT1 in diabetes. Nature Medicine, 2021, 27, 1928-1940.	15.2	24
11	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. Nature Communications, 2021, 12, 6636.	5.8	31
12	A single-cell atlas of chromatin accessibility in the human genome. Cell, 2021, 184, 5985-6001.e19.	13.5	194
13	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	13.7	257
14	Single-cell multiomic profiling of human lungs reveals cell-type-specific and age-dynamic control of SARS-CoV2 host genes. ELife, 2020, 9, .	2.8	129
15	Neighborhoods to Nucleotidesâ€”Advances and Gaps for an Obesity Disparities Systems Epidemiology Model. Current Epidemiology Reports, 2019, 6, 476-485.	1.1	1
16	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	5.8	82
17	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
18	Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. Genome Medicine, 2019, 11, 19.	3.6	33

#	Article	IF	Citations
19	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	3.8	65
20	Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517.	9.4	35
21	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
22	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
23	Shared genetic risk contributes to type 1 and type 2 diabetes etiology. Human Molecular Genetics, 2018, , .	1.4	45
24	Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. PLoS Medicine, 2018, 15, e1002654.	3.9	373
25	Integration of human pancreatic islet genomic data refines regulatory mechanisms at Type 2 Diabetes susceptibility loci. ELife, 2018, 7, .	2.8	103
26	Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. American Journal of Human Genetics, 2017, 100, 238-256.	2.6	60
27	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
28	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
29	Mechanisms of Type 2 Diabetes Risk Loci. Current Diabetes Reports, 2017, 17, 72.	1.7	39
30	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	5.8	149
31	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	9.4	452
32	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
33	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
34	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
35	Trans-ethnic Fine Mapping Highlights Kidney-Function Genes Linked to Salt Sensitivity. American Journal of Human Genetics, 2016, 99, 636-646.	2.6	67
36	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406

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37	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
38	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
39	Transcript Expression Data from Human Islets Links Regulatory Signals from Genome-Wide Association Studies for Type 2 Diabetes and Glycemic Traits to Their Downstream Effectors. PLoS Genetics, 2015, 11, e1005694.	1.5	178
40	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2015, 97, 801-815.	2.6	49
41	Lipid-Induced Epigenomic Changes in Human Macrophages Identify a Coronary Artery Disease-Associated Variant that Regulates PPAP2B Expression through Altered C/EBP-Beta Binding. PLoS Genetics, 2015, 11, e1005061.	1.5	56
42	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	1.5	124
43	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	1.5	95
44	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	1.4	8
45	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
46	Identification of a Regulatory Variant That Binds FOXA1 and FOXA2 at the CDC123/CAMK1D Type 2 Diabetes GWAS Locus. PLoS Genetics, 2014, 10, e1004633.	1.5	80
47	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
48	Whole Genome and Exome Sequencing of Type 2 Diabetes. Frontiers in Diabetes, 2014, , 29-41.	0.4	0
49	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
50	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. Nature Genetics, 2014, 46, 136-143.	9.4	475
51	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
52	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	2.6	24
53	The South Asian Genome. PLoS ONE, 2014, 9, e102645.	1.1	43
54	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. PLoS ONE, 2013, 8, e55272.	1.1	178

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55	A map of open chromatin in human pancreatic islets. Nature Genetics, 2010, 42, 255-259.	9.4	515
56	Comprehensive Association Study of Type 2 Diabetes and Related Quantitative Traits With 222 Candidate Genes. Diabetes, 2008, 57, 3136-3144.	0.3	104
57	A computational system to select candidate genes for complex human traits. Bioinformatics, 2007, 23, 1132-1140.	1.8	79