

Kyle J Gaulton

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

9,622
citations

81434

41
h-index

150775

59
g-index

81
all docs

81
docs citations

81
times ranked

18410
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterizing cis-regulatory elements using single-cell epigenomics. <i>Nature Reviews Genetics</i> , 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. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
3	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. <i>ELife</i> , 2021, 10, .	2.8	15
4	Single-cell chromatin accessibility identifies pancreatic islet cell type-specific and state-specific regulatory programs of diabetes risk. <i>Nature Genetics</i> , 2021, 53, 455-466.	9.4	100
5	Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. <i>PLoS Genetics</i> , 2021, 17, e1009531.	1.5	13
6	Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. <i>Nature</i> , 2021, 594, 398-402.	13.7	170
7	Cardiac cell type-specific gene regulatory programs and disease risk association. <i>Science Advances</i> , 2021, 7, .	4.7	63
8	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	13.7	89
9	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	13.7	95
10	Mutations and variants of ONECUT1 in diabetes. <i>Nature Medicine</i> , 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. <i>Nature Communications</i> , 2021, 12, 6636.	5.8	31
12	A single-cell atlas of chromatin accessibility in the human genome. <i>Cell</i> , 2021, 184, 5985-6001.e19.	13.5	194
13	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 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. <i>ELife</i> , 2020, 9, .	2.8	129
15	Neighborhoods to Nucleotides—Advances and Gaps for an Obesity Disparities Systems Epidemiology Model. <i>Current Epidemiology Reports</i> , 2019, 6, 476-485.	1.1	1
16	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	5.8	82
17	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 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. <i>Genome Medicine</i> , 2019, 11, 19.	3.6	33

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

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37	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016, 99, 56-75.	2.6	55
38	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 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. <i>PLoS Genetics</i> , 2015, 11, e1005694.	1.5	178
40	Multiple Hepatic Regulatory Variants at the GALNT2 GWAS Locus Associated with High-Density Lipoprotein Cholesterol. <i>American Journal of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
44	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. <i>Human Molecular Genetics</i> , 2015, 24, 1504-1512.	1.4	8
45	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 2014, 10, e1004633.	1.5	80
47	Choice of transcripts and software has a large effect on variant annotation. <i>Genome Medicine</i> , 2014, 6, 26.	3.6	158
48	Whole Genome and Exome Sequencing of Type 2 Diabetes. <i>Frontiers in Diabetes</i> , 2014, , 29-41.	0.4	0
49	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
50	Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 2014, 94, 710-720.	2.6	24
53	The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645.	1.1	43
54	The miRNA Profile of Human Pancreatic Islets and Beta-Cells and Relationship to Type 2 Diabetes Pathogenesis. <i>PLoS ONE</i> , 2013, 8, e55272.	1.1	178

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