

Narisu Narisu

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

34,342
citations

29994

54
h-index

60497

81
g-index

86
all docs

86
docs citations

86
times ranked

36733
citing authors

#	ARTICLE	IF	CITATIONS
1	In vivo base editing rescues Hutchinsonâ€™Gilford progeria syndrome in mice. <i>Nature</i> , 2021, 589, 608-614.	13.7	275
2	A targeted antisense therapeutic approach for Hutchinsonâ€™Gilford progeria syndrome. <i>Nature Medicine</i> , 2021, 27, 536-545.	15.2	55
3	A Transcription Start Site Map in Human Pancreatic Islets Reveals Functional Regulatory Signatures. <i>Diabetes</i> , 2021, 70, 1581-1591.	0.3	7
4	Genetic effects on liver chromatin accessibility identify disease regulatory variants. <i>American Journal of Human Genetics</i> , 2021, 108, 1169-1189.	2.6	22
5	Single-cell ATAC-Seq in human pancreatic islets and deep learning upscaling of rare cells reveals cell-specific type 2 diabetes regulatory signatures. <i>Molecular Metabolism</i> , 2020, 32, 109-121.	3.0	103
6	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. <i>PLoS Genetics</i> , 2020, 16, e1009019.	1.5	11
7	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. <i>Nature Communications</i> , 2020, 11, 4912.	5.8	89
8	Analysis of somatic mutations identifies signs of selection during in vitro aging of primary dermal fibroblasts. <i>Aging Cell</i> , 2019, 18, e13010.	3.0	6
9	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. <i>Human Molecular Genetics</i> , 2019, 28, 4161-4172.	1.4	41
10	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 773-787.	2.6	45
11	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10883-10888.	3.3	114
12	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
13	Single-cell transcriptomics from human pancreatic islets: sample preparation matters. <i>Biology Methods and Protocols</i> , 2019, 4, bpz019.	1.0	15
14	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018, 27, 1664-1674.	1.4	30
15	Whole-genome sequencing of 175 Mongolians uncovers population-specific genetic architecture and gene flow throughout North and East Asia. <i>Nature Genetics</i> , 2018, 50, 1696-1704.	9.4	38
16	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. <i>PLoS ONE</i> , 2018, 13, e0195788.	1.1	18
17	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
18	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 428-443.	2.6	141

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19	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	3.3	189
20	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
21	A Low-Frequency Inactivating <i>AKT2</i> 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
22	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
23	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
24	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	1.5	49
25	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
26	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	5.8	114
27	Putative Prostate Cancer Risk SNP in an Androgen Receptor Binding Site of the Melanophilin Gene Illustrates Enrichment of Risk SNPs in Androgen Receptor Target Sites. Human Mutation, 2016, 37, 52-64.	1.1	35
28	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
29	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
30	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
31	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
32	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
33	Association Analysis of Genetic Variants with Type 2 Diabetes in a Mongolian Population in China. Journal of Diabetes Research, 2015, 2015, 1-7.	1.0	27
34	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
35	miR-22 and miR-29a Are Members of the Androgen Receptor Cistrome Modulating LAMC1 and Mcl-1 in Prostate Cancer. Molecular Endocrinology, 2015, 29, 1037-1054.	3.7	69
36	Profiling of miRNA expression in immune thrombocytopenia patients before and after Qishunbaolier (QSBLE) treatment. Biomedicine and Pharmacotherapy, 2015, 75, 196-204.	2.5	14

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37	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.3	297
38	The Genome of a Mongolian Individual Reveals the Genetic Imprints of Mongolians on Modern Human Populations. <i>Genome Biology and Evolution</i> , 2014, 6, 3122-3136.	1.1	24
39	Comprehensive Analysis of Pathogenic Deletion Variants in Fanconi Anemia Genes. <i>Human Mutation</i> , 2014, 35, n/a-n/a.	1.1	35
40	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. <i>PLoS Genetics</i> , 2014, 10, e1004147.	1.5	50
41	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	13.5	113
42	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
43	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	2.6	60
44	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
45	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	9.4	754
46	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
47	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. <i>PLoS Genetics</i> , 2013, 9, e1003379.	1.5	112
48	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
49	Use of microarray hybrid capture and next-generation sequencing to identify the anatomy of a transgene. <i>Nucleic Acids Research</i> , 2013, 41, e70-e70.	6.5	41
50	Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 17921-17926.	3.3	606
51	Autosomal Dominant Diabetes Arising From a Wolfram Syndrome 1 Mutation. <i>Diabetes</i> , 2013, 62, 3943-3950.	0.3	100
52	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
53	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
54	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855

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55	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.3	335
56	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
57	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. <i>Nature Genetics</i> , 2010, 42, 142-148.	9.4	591
58	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	9.4	1,631
59	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
60	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
61	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 535-544.	1.4	176
62	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. <i>Diabetes</i> , 2010, 59, 1266-1275.	0.3	237
63	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
64	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982
65	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. <i>PLoS Genetics</i> , 2009, 5, e1000508.	1.5	453
66	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	9.4	1,572
67	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. <i>Nature Genetics</i> , 2008, 40, 161-169.	9.4	1,488
68	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. <i>Nature Genetics</i> , 2008, 40, 638-645.	9.4	1,683
69	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
70	Screening of 134 Single Nucleotide Polymorphisms (SNPs) Previously Associated With Type 2 Diabetes Replicates Association With 12 SNPs in Nine Genes. <i>Diabetes</i> , 2007, 56, 256-264.	0.3	109
71	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. <i>Science</i> , 2007, 316, 1341-1345.	6.0	2,534
72	Common Variants in Maturity-Onset Diabetes of the Young Genes Contribute to Risk of Type 2 Diabetes in Finns. <i>Diabetes</i> , 2006, 55, 2534-2540.	0.3	69

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73	Association of Transcription Factor 7-Like 2 (TCF7L2) Variants With Type 2 Diabetes in a Finnish Sample. <i>Diabetes</i> , 2006, 55, 2649-2653.	0.3	224
74	Mitochondrial polymorphisms and susceptibility to type 2 diabetes-related traits in Finns. <i>Human Genetics</i> , 2005, 118, 245-254.	1.8	73
75	Genetic Variation Near the Hepatocyte Nuclear Factor-4 Gene Predicts Susceptibility to Type 2 Diabetes. <i>Diabetes</i> , 2004, 53, 1141-1149.	0.3	255
76	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. <i>Diabetes</i> , 2004, 53, 821-829.	0.3	73