

# Jianâ€can Luan

## List of Publications by Year in descending order

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Version: 2024-02-01

91  
papers

39,974  
citations

17440

63  
h-index

34986

98  
g-index

107  
all docs

107  
docs citations

107  
times ranked

39789  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010, 466, 707-713.	27.8	3,249
3	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	21.4	2,641
4	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
5	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018, 50, 1112-1121.	21.4	1,835
6	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
8	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
9	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
10	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
11	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
12	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.	21.4	959
13	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.	21.4	836
14	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
15	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	21.4	754
16	Large-scale association analyses identify new loci influencing glycaemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	21.4	746
17	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
18	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544

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19	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	12.8	466
20	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. <i>Nature Genetics</i> , 2017, 49, 17-26.	21.4	452
21	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
22	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014, 9, 1192-1212.	12.0	398
23	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	27.8	383
24	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.	3.5	371
25	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
26	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
27	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
28	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
29	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	21.4	350
30	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341
31	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
32	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
33	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. <i>PLoS Medicine</i> , 2016, 13, e1002179.	8.4	324
34	Association Between Low-Density Lipoprotein Cholesterol and Lowering Genetic Variants and Risk of Type 2 Diabetes. <i>JAMA - Journal of the American Medical Association</i> , 2016, 316, 1383.	7.4	310
35	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2017, 5, 97-105.	11.4	298
36	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294

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37	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289
38	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
39	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
40	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
41	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
42	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
43	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
44	<i>KLB</i> is associated with alcohol drinking, and its gene product $\hat{I}^2$ -Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
45	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
46	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	12.6	192
47	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
48	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
49	Genome-wide physical activity interactions in adiposity $\hat{e}$ . A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
50	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
51	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. JAMA - Journal of the American Medical Association, 2018, 320, 2553.	7.4	152
52	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
53	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	21.4	117
54	Multi-ancestry genome-wide gene $\hat{e}$ smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112

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55	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	12.4	100
56	Effect of combined movement and heart rate monitor placement on physical activity estimates during treadmill locomotion and free-living. <i>European Journal of Applied Physiology</i> , 2006, 96, 517-524.	2.5	98
57	Synergistic insights into human health from aptamer- and antibody-based proteomic profiling. <i>Nature Communications</i> , 2021, 12, 6822.	12.8	95
58	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
59	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
60	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. <i>Scientific Reports</i> , 2017, 7, 11008.	3.3	88
61	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
62	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 321.	12.8	85
63	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
64	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
65	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
66	Novel Approach Identifies SNPs in <i>SLC2A10</i> and <i>KCNK9</i> with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	3.5	80
67	Liver Function and Risk of Type 2 Diabetes: Bidirectional Mendelian Randomization Study. <i>Diabetes</i> , 2019, 68, 1681-1691.	0.6	79
68	Genomic analysis of diet composition finds novel loci and associations with health and lifestyle. <i>Molecular Psychiatry</i> , 2021, 26, 2056-2069.	7.9	79
69	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	12.8	75
70	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
71	Genetic architecture of host proteins involved in SARS-CoV-2 infection. <i>Nature Communications</i> , 2020, 11, 6397.	12.8	71
72	Plasma Vitamin C and Type 2 Diabetes: Genome-Wide Association Study and Mendelian Randomization Analysis in European Populations. <i>Diabetes Care</i> , 2021, 44, 98-106.	8.6	68

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73	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	21.4	66
74	Meta-analysis investigating the role of interleukin-6 mediated inflammation in type 2 diabetes. <i>EBioMedicine</i> , 2020, 61, 103062.	6.1	46
75	The association between circulating 25-hydroxyvitamin D metabolites and type 2 diabetes in European populations: A meta-analysis and Mendelian randomisation analysis. <i>PLoS Medicine</i> , 2020, 17, e1003394.	8.4	45
76	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. <i>Molecular Psychiatry</i> , 2019, 24, 1920-1932.	7.9	44
77	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015, 6, 7756.	12.8	32
78	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. <i>Human Molecular Genetics</i> , 2017, 26, 2791-2802.	2.9	32
79	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. <i>BMJ: British Medical Journal</i> , 2019, 366, l4292.	2.3	28
80	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017, 13, e1006812.	3.5	24
81	MicroRNA-196a links human body fat distribution to adipose tissue extracellular matrix composition. <i>EBioMedicine</i> , 2019, 44, 467-475.	6.1	22
82	A multilevel linear mixed model of the association between candidate genes and weight and body mass index using the Framingham longitudinal family data. <i>BMC Proceedings</i> , 2009, 3, S115.	1.6	20
83	Genome-wide association analysis of type 2 diabetes in the EPIC-InterAct study. <i>Scientific Data</i> , 2020, 7, 393.	5.3	19
84	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 1065-1077.	3.6	12
85	Genome-wide association study of adipocyte lipolysis in the GENetics of adipocyte lipolysis (GENIAL) cohort. <i>Molecular Metabolism</i> , 2020, 34, 85-96.	6.5	11
86	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	3.1	11
87	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016, 25, 2082-2092.	2.9	10
88	Regional fat depot masses are influenced by protein-coding gene variants. <i>PLoS ONE</i> , 2019, 14, e0217644.	2.5	9
89	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein) Tj ETQq1_1 0.784314 rgBT /D e003288.	3.6	8
90	Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. <i>Nutrients</i> , 2021, 13, 1868.	4.1	6

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91	Utility of Genetically Predicted Lp(a) (Lipoprotein [a]) and ApoB Levels for Cardiovascular Risk Assessment. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003312.	3.6	6