Ruifang Li-Gao

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68 papers	3,950 citations	25 h-index	62 g-index
81 ext. papers	5,795 ext. citations	13.9 avg, IF	3.33 L-index

#	Paper	IF	Citations
68	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
67	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
66	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
65	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. *Nature Genetics*, **2017**, 49, 403-415	36.3	313
64	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
63	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
62	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
61	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
60	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
59	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
58	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. *American Journal of Human Genetics*, **2018**, 102, 88-102	11	119
57	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
56	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
55	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
54	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
53	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
52	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. *Circulation: Cardiovascular Genetics*, **2016**, 9, 511-520		34

51	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. *American Journal of Human Genetics*, **2016**, 99, 481-8	11	31
50	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
49	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
48	CETP (Cholesteryl Ester Transfer Protein) Concentration: A Genome-Wide Association Study Followed by Mendelian Randomization on Coronary Artery Disease. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002034	5.2	30
47	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. *Molecular Psychiatry*, **2019**, 24, 1920-1932	15.1	30
46	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
45	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
44	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
43	Development of a method to consistently quantify the structural distance between scaffolds and to assess scaffold hopping potential. *Journal of Chemical Information and Modeling*, **2011**, 51, 2507-14	6.1	23
42	Genome-wide association study of breakfast skipping links clock regulation with food timing. *American Journal of Clinical Nutrition*, **2019**, 110, 473-484	7	22
41	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug-metabolite atlas. *Nature Medicine*, **2020**, 26, 110-117	50.5	19
40	Assessment of reproducibility and biological variability of fasting and postprandial plasma metabolite concentrations using 1H NMR spectroscopy. *PLoS ONE*, **2019**, 14, e0218549	3.7	18
39	Mendelian randomization reveals unexpected effects of CETP on the lipoprotein profile. *European Journal of Human Genetics*, **2019**, 27, 422-431	5.3	18
38	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
37	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. *Diabetologia*, **2018**, 61, 317-330	10.3	17
36	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
35	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
34	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. *American Journal of Human Genetics*, **2019**, 105, 15-28	11	12

33	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
32	Postprandial metabolite profiles associated with type 2 diabetes clearly stratify individuals with impaired fasting glucose. *Metabolomics*, **2018**, 14, 13	4.7	10
31	Trans-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation		10
30	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. *Diabetes*, **2020**, 69, 2806-2818	0.9	10
29	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. *Pharmacogenomics Journal*, **2018**, 18, 127-135	3.5	9
28	Depression and Inflammatory Bowel Disease: A Bidirectional two-sample Mendelian Randomization Study. *Journal of Crohns and Colitis*, **2021**,	1.5	8
27	Factor V levels and risk of venous thrombosis: The MEGA case-control study. *Research and Practice in Thrombosis and Haemostasis*, **2018**, 2, 320-326	5.1	7
26	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. *Drug and Alcohol Dependence*, **2018**, 188, 94-101	4.9	7
25	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
24	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	6
23	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. *Journal of Medical Genetics*, **2017**, 54, 313-323	5.8	5
22	Systematic assessment of scaffold distances in ChEMBL: prioritization of compound data sets for scaffold hopping analysis in virtual screening. *Journal of Computer-Aided Molecular Design*, **2012**, 26, 1101-9	4.3	4
21	Genetic Studies of Metabolomics Change After a Liquid Meal Illuminate Novel Pathways for Glucose and Lipid Metabolism. *Diabetes*, **2021**, 70, 2932-2946	0.9	4
20	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
19	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
18	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2020**, 13, 387-395	5.2	4
17	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. *Blood*, **2021**, 137, 2394-2402	2.2	4
16	Glucose levels and diabetes are not associated with the risk of venous thrombosis: results from the MEGA case-control study. *British Journal of Haematology*, **2019**, 184, 431-435	4.5	4

15	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
14	Genome-Wide Association Study on the Early-Phase Insulin Response to a Liquid Mixed Meal: Results From the NEO Study. *Diabetes*, **2019**, 68, 2327-2336	0.9	3
13	Higher thyrotropin leads to unfavorable lipid profile and somewhat higher cardiovascular disease risk: evidence from multi-cohort Mendelian randomization and metabolomic profiling. *BMC Medicine*, **2021**, 19, 266	11.4	3
12	Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. *Pharmacogenomics Journal*, **2018**, 18, 215-226	3.5	2
11	Replication of Type 2 diabetes-associated variants in a Saudi Arabian population. *Physiological Genomics*, **2018**, 50, 296-297	3.6	2
10	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. *Atherosclerosis*, **2017**, 266, 196-204	3.1	2
9	The Heritability of Type D Personality by an Extended Twin-Pedigree Analysis in the Netherlands Twin Register. *Behavior Genetics*, **2021**, 51, 1-11	3.2	2
8	Genome-Wide Association Study of the Postprandial Triglyceride Response Yields Common Genetic Variation in LIPC (Hepatic Lipase). *Circulation Genomic and Precision Medicine*, **2020**, 13, e002693	5.2	1
7	Genetics of fasting and postprandial metabolite levels are overlapping. *Physiological Genomics*, **2018**, 50, 235-236	3.6	1
6	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*,3, 4	4.8	1
5	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
4	Investigating the relationships between unfavourable habitual sleep and metabolomic traits: evidence from multi-cohort multivariable regression and Mendelian randomization analyses. *BMC Medicine*, **2021**, 19, 69	11.4	1
3	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 Cholesterol) and Triglyceride Concentrations. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003288	5.2	1
2	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. *Scientific Reports*, **2021**, 11, 19365	4.9	0
1	The association of genetic variants in the cholesteryl ester transfer protein gene with hemostatic factors and a first venous thrombosis. *Journal of Thrombosis and Haemostasis*, **2019**, 17, 1535-1543	15.4	