

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.

50 papers	11,845 citations	31 h-index	53 g-index
53 ext. papers	14,586 ext. citations	15.3 avg, IF	5.18 L-index

#	Paper	IF	Citations
50	Intestinal microbiota metabolism of L-carnitine, a nutrient in red meat, promotes atherosclerosis. <i>Nature Medicine</i> , 2013 , 19, 576-85	50.5	2528
49	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
48	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009 , 41, 666-76	36.3	970
47	Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk. <i>Cell</i> , 2016 , 165, 111-124	56.2	872
46	Non-lethal Inhibition of Gut Microbial Trimethylamine Production for the Treatment of Atherosclerosis. <i>Cell</i> , 2015 , 163, 1585-95	56.2	688
45	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013 , 45, 145-54	36.3	505
44	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
43	Genetic control of obesity and gut microbiota composition in response to high-fat, high-sucrose diet in mice. <i>Cell Metabolism</i> , 2013 , 17, 141-52	24.6	383
42	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
41	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014 , 5, 4500	17.4	330
40	Sex differences and hormonal effects on gut microbiota composition in mice. <i>Gut Microbes</i> , 2016 , 7, 313-322	33.2	329
39	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
38	β-Butyrobetaine is a proatherogenic intermediate in gut microbial metabolism of L-carnitine to TMAO. <i>Cell Metabolism</i> , 2014 , 20, 799-812	24.6	313
37	Transmission of atherosclerosis susceptibility with gut microbial transplantation. <i>Journal of Biological Chemistry</i> , 2015 , 290, 5647-60	5.4	294
36	SLC2A9 is a high-capacity urate transporter in humans. <i>PLoS Medicine</i> , 2008 , 5, e197	11.6	254
35	Genetic and environmental control of host-gut microbiota interactions. <i>Genome Research</i> , 2015 , 25, 1558-69	9.7	199
34	Interactions between <i>Roseburia intestinalis</i> and diet modulate atherogenesis in a murine model. <i>Nature Microbiology</i> , 2018 , 3, 1461-1471	26.6	170

33	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. <i>Genome Biology</i> , 2017 , 18, 70	18.3	167
32	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. <i>Human Molecular Genetics</i> , 2009 , 18, 2288-96	5.6	154
31	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, 2273-84	5.6	146
30	Blood pressure loci identified with a gene-centric array. <i>American Journal of Human Genetics</i> , 2011 , 89, 688-700	11	137
29	Targeting 160 candidate genes for blood pressure regulation with a genome-wide genotyping array. <i>PLoS ONE</i> , 2009 , 4, e6034	3.7	89
28	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017 ,	8.5	85
27	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021 , 53, 156-165	36.3	80
26	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017 , 6,	6	65
25	Flavin monooxygenase 3, the host hepatic enzyme in the metaorganismal trimethylamine N-oxide-generating pathway, modulates platelet responsiveness and thrombosis risk. <i>Journal of Thrombosis and Haemostasis</i> , 2018 , 16, 1857-1872	15.4	63
24	The genetic architecture of NAFLD among inbred strains of mice. <i>ELife</i> , 2015 , 4, e05607	8.9	61
23	Unraveling the environmental and genetic interactions in atherosclerosis: Central role of the gut microbiota. <i>Atherosclerosis</i> , 2015 , 241, 387-99	3.1	55
22	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. <i>American Journal of Human Genetics</i> , 2014 , 95, 49-65	11	52
21	Transgenic 6F tomatoes act on the small intestine to prevent systemic inflammation and dyslipidemia caused by Western diet and intestinally derived lysophosphatidic acid. <i>Journal of Lipid Research</i> , 2013 , 54, 3403-18	6.3	51
20	Polymorphisms in the WNK1 gene are associated with blood pressure variation and urinary potassium excretion. <i>PLoS ONE</i> , 2009 , 4, e5003	3.7	36
19	CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. <i>Human Genetics</i> , 2015 , 134, 291-303	6.3	28
18	Age-dependent association of the polymorphisms in the mitochondria-shaping gene, OPA1, with blood pressure and hypertension in Korean population. <i>American Journal of Hypertension</i> , 2011 , 24, 1127-35	2.3	23
17	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. <i>Human Mutation</i> , 2011 , 32, 806-14	4.7	19
16	N-acetyltransferase 8, a positional candidate for blood pressure and renal regulation: resequencing, association and in silico study. <i>BMC Medical Genetics</i> , 2008 , 9, 25	2.1	17

15	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. <i>Genetics</i> , 2016 , 204, 1379-1390	4	14
14	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. <i>Frontiers in Immunology</i> , 2020 , 11, 838	8.4	11
13	Large-scale association analyses identify host factors influencing human gut microbiome composition		9
12	Hypervariable intronic region in NCX1 is enriched in short insertion-deletion polymorphisms and showed association with cardiovascular traits. <i>BMC Medical Genetics</i> , 2010 , 11, 15	2.1	8
11	HYPEST study: profile of hypertensive patients in Estonia. <i>BMC Cardiovascular Disorders</i> , 2011 , 11, 55	2.3	7
10	The Gut Microbiome in Polycystic Ovary Syndrome and Its Association with Metabolic Traits. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 858-871	5.6	6
9	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
8	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. <i>MSystems</i> , 2021 , 6,	7.6	4
7	Using fecal immunochemical tubes for the analysis of the gut microbiome has the potential to improve colorectal cancer screening. <i>Scientific Reports</i> , 2021 , 11, 19603	4.9	2
6	The Nutritional Supplement -Alpha Glycerylphosphorylcholine Promotes Atherosclerosis.. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
5	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. <i>Lecture Notes in Computer Science</i> , 2015 , 136-153	0.9	1
4	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
3	Using the natural variation of mouse populations to understand host-gut microbiome interactions. <i>Drug Discovery Today: Disease Models</i> , 2018 , 28, 61-71	1.3	1
2	Differences in microbial profile of endometrial fluid and tissue samples in women with in vitro fertilization failure are driven by Lactobacillus abundance.. <i>Acta Obstetricia Et Gynecologica Scandinavica</i> , 2022 , 101, 212-220	3.8	0
1	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort.. <i>Nature Communications</i> , 2022 , 13, 869	17.4	0