Elin Org

List of Publications by Year
in descending order

47 papers	16,827 citations	147801 31 h-index	206112 48 g-index
53 all docs	53 docs citations	53 times ranked	23141 citing authors

#	Article	IF	Citations
1	Intestinal microbiota metabolism of l-carnitine, a nutrient in red meat, promotes atherosclerosis. Nature Medicine, 2013, 19, 576-585.	30.7	3,355
2	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
3	Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk. Cell, 2016, 165, 111-124.	28.9	1,358
4	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	21.4	1,104
5	Non-lethal Inhibition of Gut Microbial Trimethylamine Production for the Treatment of Atherosclerosis. Cell, 2015, 163, 1585-1595.	28.9	974
6	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
7	Large-scale association analyses identify host factors influencing human gut microbiome composition. Nature Genetics, 2021, 53, 156-165.	21.4	676
8	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
9	Sex differences and hormonal effects on gut microbiota composition in mice. Gut Microbes, 2016, 7, 313-322.	9.8	564
10	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
11	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. Cell Metabolism, 2013, 17, 141-152.	16.2	464
12	Individual diet has sex-dependent effects on vertebrate gut microbiota. Nature Communications, 2014, 5, 4500.	12.8	464
13	γ-Butyrobetaine Is a Proatherogenic Intermediate in Gut Microbial Metabolism of L-Carnitine to TMAO. Cell Metabolism, 2014, 20, 799-812.	16.2	416
14	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
15	Transmission of Atherosclerosis Susceptibility with Gut Microbial Transplantation. Journal of Biological Chemistry, 2015, 290, 5647-5660.	3.4	400
16	Interactions between Roseburia intestinalis and diet modulate atherogenesis in a murine model. Nature Microbiology, 2018, 3, 1461-1471.	13.3	310
17	SLC2A9 Is a High-Capacity Urate Transporter in Humans. PLoS Medicine, 2008, 5, e197.	8.4	305
18	Genetic and environmental control of host-gut microbiota interactions. Genome Research, 2015, 25, 1558-1569.	5.5	288

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19	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. Genome Biology, 2017, 18, 70.	8.8	245
20	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. Human Molecular Genetics, 2009, 18, 2288-2296.	2.9	170
21	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
22	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	6.2	159
23	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
24	Flavin monooxygenase 3, the host hepatic enzyme in the metaorganismal trimethylamine Nâ€oxideâ€generating pathway, modulates platelet responsiveness and thrombosis risk. Journal of Thrombosis and Haemostasis, 2018, 16, 1857-1872.	3.8	104
25	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. PLoS ONE, 2009, 4, e6034.	2.5	98
26	The genetic architecture of NAFLD among inbred strains of mice. ELife, 2015, 4, e05607.	6.0	96
27	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
28	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
29	Unraveling the environmental and genetic interactions inÂatherosclerosis: Central role of the gut microbiota. Atherosclerosis, 2015, 241, 387-399.	0.8	67
30	Transgenic 6F tomatoes act on the small intestine to prevent systemic inflammation and dyslipidemia caused by Western diet and intestinally derived lysophosphatidic acid. Journal of Lipid Research, 2013, 54, 3403-3418.	4.2	60
31	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. PLoS ONE, 2009, 4, e5003.	2.5	43
32	CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. Human Genetics, 2015, 134, 291-303.	3.8	32
33	The Gut Microbiome in Polycystic Ovary Syndrome and Its Association with Metabolic Traits. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 858-871.	3.6	31
34	Age-Dependent Association of the Polymorphisms in the Mitochondria-Shaping Gene, OPA1, With Blood Pressure and Hypertension in Korean Population. American Journal of Hypertension, 2011, 24, 1127-1135.	2.0	26
35	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. Genetics, 2016, 204, 1379-1390.	2.9	26
36	N-acetyltransferase 8, a positional candidate for blood pressure and renal regulation: resequencing, association and in silico study. BMC Medical Genetics, 2008, 9, 25.	2.1	23

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37	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. Human Mutation, 2011, 32, 806-814.	2.5	23
38	The Nutritional Supplement L-Alpha Glycerylphosphorylcholine Promotes Atherosclerosis. International Journal of Molecular Sciences, 2021, 22, 13477.	4.1	16
39	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. Frontiers in Immunology, 2020, 11, 838.	4.8	14
40	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. MSystems, 2021, 6, .	3.8	13
41	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. Nature Communications, 2022, 13, 869.	12.8	12
42	Differences in microbial profile of endometrial fluid and tissue samples in women with in vitro fertilization failure are driven by <i>Lactobacillus</i> abundance. Acta Obstetricia Et Gynecologica Scandinavica, 2022, 101, 212-220.	2.8	11
43	HYPEST study: profile of hypertensive patients in Estonia. BMC Cardiovascular Disorders, 2011, 11, 55.	1.7	9
44	Using fecal immunochemical tubes for the analysis of the gut microbiome has the potential to improve colorectal cancer screening. Scientific Reports, 2021, 11, 19603.	3.3	9
45	Hypervariable intronic region in NCX1 is enriched in short insertion-deletion polymorphisms and showed association with cardiovascular traits. BMC Medical Genetics, 2010, 11, 15.	2.1	8
46	Using the natural variation of mouse populations to understand host-gut microbiome interactions. Drug Discovery Today: Disease Models, 2018, 28, 61-71.	1.2	6
47	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. Lecture Notes in Computer Science, 2015, , 136-153.	1.3	1