

Elin Org

List of Publications by Year in descending order

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Version: 2024-02-01

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	Differences in microbial profile of endometrial fluid and tissue samples in women with in vitro fertilization failure are driven by <i>Lactobacillus</i> abundance. <i>Acta Obstetrica Et Gynecologica Scandinavica</i> , 2022, 101, 212-220.	2.8	11
2	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. <i>Nature Communications</i> , 2022, 13, 869.	12.8	12
3	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.	3.6	31
4	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
5	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. <i>MSystems</i> , 2021, 6, .	3.8	13
6	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.	3.3	9
7	The Nutritional Supplement L-Alpha Glycerolphosphorylcholine Promotes Atherosclerosis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13477.	4.1	16
8	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. <i>Frontiers in Immunology</i> , 2020, 11, 838.	4.8	14
9	Using the natural variation of mouse populations to understand host-gut microbiome interactions. <i>Drug Discovery Today: Disease Models</i> , 2018, 28, 61-71.	1.2	6
10	Interactions between <i>Roseburia intestinalis</i> and diet modulate atherogenesis in a murine model. <i>Nature Microbiology</i> , 2018, 3, 1461-1471.	13.3	310
11	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
12	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.	3.8	104
13	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	21.4	492
14	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. <i>Genome Biology</i> , 2017, 18, 70.	8.8	245
15	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	89
16	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, 70, .	2.7	123
17	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. <i>Genetics</i> , 2016, 204, 1379-1390.	2.9	26
18	Sex differences and hormonal effects on gut microbiota composition in mice. <i>Gut Microbes</i> , 2016, 7, 313-322.	9.8	564

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19	Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk. <i>Cell</i> , 2016, 165, 111-124.	28.9	1,358
20	Unraveling the environmental and genetic interactions in Atherosclerosis: Central role of the gut microbiota. <i>Atherosclerosis</i> , 2015, 241, 387-399.	0.8	67
21	Non-lethal Inhibition of Gut Microbial Trimethylamine Production for the Treatment of Atherosclerosis. <i>Cell</i> , 2015, 163, 1585-1595.	28.9	974
22	CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. <i>Human Genetics</i> , 2015, 134, 291-303.	3.8	32
23	Transmission of Atherosclerosis Susceptibility with Gut Microbial Transplantation. <i>Journal of Biological Chemistry</i> , 2015, 290, 5647-5660.	3.4	400
24	Genetic and environmental control of host-gut microbiota interactions. <i>Genome Research</i> , 2015, 25, 1558-1569.	5.5	288
25	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. <i>Lecture Notes in Computer Science</i> , 2015, , 136-153.	1.3	1
26	The genetic architecture of NAFLD among inbred strains of mice. <i>ELife</i> , 2015, 4, e05607.	6.0	96
27	β -Butyrobetaine Is a Proatherogenic Intermediate in Gut Microbial Metabolism of L-Carnitine to TMAO. <i>Cell Metabolism</i> , 2014, 20, 799-812.	16.2	416
28	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.	6.2	73
29	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014, 5, 4500.	12.8	464
30	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, 3403-3418.	4.2	60
31	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
32	Genetic Control of Obesity and Gut Microbiota Composition in Response to High-Fat, High-Sucrose Diet in Mice. <i>Cell Metabolism</i> , 2013, 17, 141-152.	16.2	464
33	Intestinal microbiota metabolism of l-carnitine, a nutrient in red meat, promotes atherosclerosis. <i>Nature Medicine</i> , 2013, 19, 576-585.	30.7	3,355
34	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
35	Blood Pressure Loci Identified with a Gene-Centric Array. <i>American Journal of Human Genetics</i> , 2011, 89, 688-700.	6.2	159
36	HYPEST study: profile of hypertensive patients in Estonia. <i>BMC Cardiovascular Disorders</i> , 2011, 11, 55.	1.7	9

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37	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. <i>Human Mutation</i> , 2011, 32, 806-814.	2.5	23
38	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.	2.9	168
39	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403
40	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, 1127-1135.	2.0	26
41	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
42	Polymorphisms in the WNK1 Gene Are Associated with Blood Pressure Variation and Urinary Potassium Excretion. <i>PLoS ONE</i> , 2009, 4, e5003.	2.5	43
43	Targeting 160 Candidate Genes for Blood Pressure Regulation with a Genome-Wide Genotyping Array. <i>PLoS ONE</i> , 2009, 4, e6034.	2.5	98
44	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, 2288-2296.	2.9	170
45	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
46	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	23
47	SLC2A9 Is a High-Capacity Urate Transporter in Humans. <i>PLoS Medicine</i> , 2008, 5, e197.	8.4	305