Elin Org

List of Publications by Year in Descending Order

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	Differences in microbial profile of endometrial fluid and tissue samples in women with in vitro fertilization failure are driven by Lactobacillus abundance.. *Acta Obstetricia Et Gynecologica Scandinavica*, **2022**, 101, 212-220	3.8	0
49	Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort.. *Nature Communications*, **2022**, 13, 869	17.4	0
48	The Nutritional Supplement -Alpha Glycerylphosphorylcholine Promotes Atherosclerosis.. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	1
47	The Gut Microbiome in Polycystic Ovary Syndrome and Its Association with Metabolic Traits. *Journal of Clinical Endocrinology and Metabolism*, **2021**, 106, 858-871	5.6	6
46	Large-scale association analyses identify host factors influencing human gut microbiome composition. *Nature Genetics*, **2021**, 53, 156-165	36.3	80
45	Machine Learning Reveals Time-Varying Microbial Predictors with Complex Effects on Glucose Regulation. *MSystems*, **2021**, 6,	7.6	4
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	4.9	2
43	IL-22 Paucity in APECED Is Associated With Mucosal and Microbial Alterations in Oral Cavity. *Frontiers in Immunology*, **2020**, 11, 838	8.4	11
42	Flavin monooxygenase 3, the host hepatic enzyme in the metaorganismal trimethylamine N-oxide-generating pathway, modulates platelet responsiveness and thrombosis risk. *Journal of Thrombosis and Haemostasis*, **2018**, 16, 1857-1872	15.4	63
41	Using the natural variation of mouse populations to understand host-gut microbiome interactions. *Drug Discovery Today: Disease Models*, **2018**, 28, 61-71	1.3	1
40	Interactions between Roseburia intestinalis and diet modulate atherogenesis in a murine model. *Nature Microbiology*, **2018**, 3, 1461-1471	26.6	170
39	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
38	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
37	Relationships between gut microbiota, plasma metabolites, and metabolic syndrome traits in the METSIM cohort. *Genome Biology*, **2017**, 18, 70	18.3	167
36	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
35	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
34	Sex differences and hormonal effects on gut microbiota composition in mice. *Gut Microbes*, **2016**, 7, 313-322	8.2	329

33	Gut Microbial Metabolite TMAO Enhances Platelet Hyperreactivity and Thrombosis Risk. *Cell*, **2016**, 165, 111-124	56.2	872
32	Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure. *Genetics*, **2016**, 204, 1379-1390	4	14
31	CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. *Human Genetics*, **2015**, 134, 291-303	6.3	28
30	Transmission of atherosclerosis susceptibility with gut microbial transplantation. *Journal of Biological Chemistry*, **2015**, 290, 5647-60	5.4	294
29	Genetic and environmental control of host-gut microbiota interactions. *Genome Research*, **2015**, 25, 1558-69	9.7	199
28	Unraveling the environmental and genetic interactions in atherosclerosis: Central role of the gut microbiota. *Atherosclerosis*, **2015**, 241, 387-99	3.1	55
27	Non-lethal Inhibition of Gut Microbial Trimethylamine Production for the Treatment of Atherosclerosis. *Cell*, **2015**, 163, 1585-95	56.2	688
26	The genetic architecture of NAFLD among inbred strains of mice. *ELife*, **2015**, 4, e05607	8.9	61
25	Efficient and Accurate Multiple-Phenotypes Regression Method for High Dimensional Data Considering Population Structure. *Lecture Notes in Computer Science*, **2015**, 136-153	0.9	1
24	Butyrobetaine is a proatherogenic intermediate in gut microbial metabolism of L-carnitine to TMAO. *Cell Metabolism*, **2014**, 20, 799-812	24.6	313
23	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	11	52
22	Individual diet has sex-dependent effects on vertebrate gut microbiota. *Nature Communications*, **2014**, 5, 4500	17.4	330
21	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, 3403-18	6.3	51
20	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
19	Genetic control of obesity and gut microbiota composition in response to high-fat, high-sucrose diet in mice. *Cell Metabolism*, **2013**, 17, 141-52	24.6	383
18	Intestinal microbiota metabolism of L-carnitine, a nutrient in red meat, promotes atherosclerosis. *Nature Medicine*, **2013**, 19, 576-85	50.5	2528
17	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
16	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137

15	HYPEST study: profile of hypertensive patients in Estonia. *BMC Cardiovascular Disorders*, **2011**, 11, 55	2.3	7
14	Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. *Human Mutation*, **2011**, 32, 806-14	4.7	19
13	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146
12	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
11	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, 1127-35	2.3	23
10	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
9	Polymorphisms in the WNK1 gene are associated with blood pressure variation and urinary potassium excretion. *PLoS ONE*, **2009**, 4, e5003	3.7	36
8	Targeting 160 candidate genes for blood pressure regulation with a genome-wide genotyping array. *PLoS ONE*, **2009**, 4, e6034	3.7	89
7	Genome-wide scan identifies CDH13 as a novel susceptibility locus contributing to blood pressure determination in two European populations. *Human Molecular Genetics*, **2009**, 18, 2288-96	5.6	154
6	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
5	SLC2A9 is a high-capacity urate transporter in humans. *PLoS Medicine*, **2008**, 5, e197	11.6	254
4	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	17
3	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
2	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
1	Large-scale association analyses identify host factors influencing human gut microbiome composition		9