Eirini Marouli

List of Publications by Year
in descending order

39 papers	5,481 citations	279798 23 h-index	265206 42 g-index
51 all docs	51 docs citations	51 times ranked	10957 citing authors

#	Article	IF	Citations
1	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
2	Thyroid function, pernicious anemia and erythropoiesis: a two-sample Mendelian randomization study. Human Molecular Genetics, 2022, 31, 2548-2559.	2.9	9
3	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
4	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	3.5	12
5	Variation in Normal Range Thyroid Function Affects Serum Cholesterol Levels, Blood Pressure, and Type 2 Diabetes Risk: A Mendelian Randomization Study. Thyroid, 2021, 31, 721-731.	4.5	31
6	No Clinically Relevant Effect of Heart Rate Increase and Heart Rate Recovery During Exercise on Cardiovascular Disease: A Mendelian Randomization Analysis. Frontiers in Genetics, 2021, 12, 569323.	2.3	15
7	Thyroid function, sex hormones and sexual function: a Mendelian randomization study. European Journal of Epidemiology, 2021, 36, 335-344.	5.7	43
8	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18
9	Thyroid Function and Mood Disorders: A Mendelian Randomization Study. Thyroid, 2021, 31, 1171-1181.	4.5	23
10	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	4.5	13
11	Composite trait Mendelian randomization reveals distinct metabolic and lifestyle consequences of differences in body shape. Communications Biology, 2021, 4, 1064.	4.4	13
12	COVID-19 susceptibility variants associate with blood clots, thrombophlebitis and circulatory diseases. PLoS ONE, 2021, 16, e0256988.	2.5	12
13	Thyroid Function and the Risk of Alzheimer's Disease: A Mendelian Randomization Study. Thyroid, 2021, 31, 1794-1799.	4.5	14
14	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
15	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
16	Thyroid Function Affects the Risk of Stroke via Atrial Fibrillation: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 2634-2641.	3.6	31
17	Potential Interplay between Dietary Saturated Fats and Genetic Variants of the NLRP3 Inflammasome to Modulate Insulin Resistance and Diabetes Risk: Insights from a Metaâ€Analysis of 19Â005 Individuals. Molecular Nutrition and Food Research, 2019, 63, e1900226.	3.3	12
18	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41

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19	Dairy Intake and Body Composition and Cardiometabolic Traits among Adults: Mendelian Randomization Analysis of 182041 Individuals from 18 Studies. Clinical Chemistry, 2019, 65, 751-760.	3.2	20
20	Epigenome-Wide Association Study (EWAS) of Blood Lipids in Healthy Population from STANISLAS Family Study (SFS). International Journal of Molecular Sciences, 2019, 20, 1014.	4.1	17
21	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	4.4	35
22	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
23	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
24	Meta-analysis of genome-wide association studies for body fat distribution in 694Â649 individuals of European ancestry. Human Molecular Genetics, 2019, 28, 166-174.	2.9	752
25	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
26	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. Translational Psychiatry, 2018, 8, 252.	4.8	73
27	Combination therapy as a potential risk factor for the development of type 2 diabetes in patients with schizophrenia: the GOMAP study. BMC Psychiatry, 2018, 18, 249.	2.6	5
28	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
29	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
30	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
31	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
32	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
33	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	21.4	571
34	Evaluating the glucose raising effect of established loci via a genetic risk score. PLoS ONE, 2017, 12, e0186669.	2.5	6
35	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
36	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261

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37	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
38	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
39	Gender Specificity of a Genetic Variant of Androgen Receptor and Risk of Coronary Artery Disease. Journal of Clinical Laboratory Analysis, 2016, 30, 204-207.	2.1	3