

Antonietta Robino

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

9,434
citations

94433

37
h-index

71685

76
g-index

82
all docs

82
docs citations

82
times ranked

17277
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
2	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
3	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
4	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
5	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
6	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
7	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412
8	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
9	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
10	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
11	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
12	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
13	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	21.4	215
14	<i>KLB</i> is associated with alcohol drinking, and its gene product β -Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	7.1	208
15	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
16	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
17	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
18	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	3.5	142

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19	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
20	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
21	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
22	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
23	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
24	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
25	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
26	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. <i>Nature Genetics</i> , 2018, 50, 652-656.	21.4	86
27	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.4	85
28	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
29	Evidence of Inbreeding Depression on Human Height. <i>PLoS Genetics</i> , 2012, 8, e1002655.	3.5	79
30	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	12.8	71
31	Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. <i>Scientific Reports</i> , 2016, 6, 25506.	3.3	69
32	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	2.9	64
33	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	12.8	64
34	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014, 23, 2490-2497.	2.9	56
35	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018, 19, 87.	8.8	47
36	Genetics of Food Preferences: A First View from Silk Road Populations. <i>Journal of Food Science</i> , 2012, 77, S413-8.	3.1	45

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37	Association Analysis of Bitter Receptor Genes in Five Isolated Populations Identifies a Significant Correlation between TAS2R43 Variants and Coffee Liking. PLoS ONE, 2014, 9, e92065.	2.5	41
38	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
39	Understanding the role of personality and alexithymia in food preferences and PROP taste perception. Physiology and Behavior, 2016, 157, 72-78.	2.1	37
40	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	10.3	36
41	A Population-Based Approach to Study the Impact of PROP Perception on Food Liking in Populations along the Silk Road. PLoS ONE, 2014, 9, e91716.	2.5	34
42	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
43	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	6.1	33
44	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
45	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
46	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. European Journal of Human Genetics, 2019, 27, 952-962.	2.8	29
47	A bird's-eye view of Italian genomic variation through whole-genome sequencing. European Journal of Human Genetics, 2020, 28, 435-444.	2.8	29
48	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
49	Polymorphisms in sweet taste genes (TAS1R2 and GLUT2), sweet liking, and dental caries prevalence in an adult Italian population. Genes and Nutrition, 2015, 10, 485.	2.5	25
50	Non-additive genome-wide association scan reveals a new gene associated with habitual coffee consumption. Scientific Reports, 2016, 6, 31590.	3.3	25
51	A Genome-Wide Association Study in isolated populations reveals new genes associated to common food likings. Reviews in Endocrine and Metabolic Disorders, 2016, 17, 209-219.	5.7	22
52	Polygenic Overlap Between Kidney Function and Large Artery Atherosclerotic Stroke. Stroke, 2014, 45, 3508-3513.	2.0	21
53	A Brief Review of Genetic Approaches to the Study of Food Preferences: Current Knowledge and Future Directions. Nutrients, 2019, 11, 1735.	4.1	20
54	Caries and Innate Immunity: <i>DEFB1</i> Gene Polymorphisms and Caries Susceptibility in Genetic Isolates from North-Eastern Italy. Caries Research, 2016, 50, 589-594.	2.0	19

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55	NLRC5 polymorphism is associated with susceptibility to chronic periodontitis. <i>Immunobiology</i> , 2017, 222, 704-708.	1.9	17
56	A genome-wide association study identifies an association between variants in <i>EFCAB4B</i> gene and periodontal disease in an Italian isolated population. <i>Journal of Periodontal Research</i> , 2018, 53, 992-998.	2.7	15
57	Combined influence of TAS2R38 genotype and PROP phenotype on the intensity of basic tastes, astringency and pungency in the Italian taste project. <i>Food Quality and Preference</i> , 2022, 95, 104361.	4.6	15
58	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 511-529.	6.1	14
59	Joint Data Analysis in Nutritional Epidemiology: Identification of Observational Studies and Minimal Requirements. <i>Journal of Nutrition</i> , 2018, 148, 285-297.	2.9	13
60	Analysis of functional variants reveals new candidate genes associated with alexithymia. <i>Psychiatry Research</i> , 2015, 227, 363-365.	3.3	12
61	Genome-wide association analysis on five isolated populations identifies variants of the HLA-DOA gene associated with white wine liking. <i>European Journal of Human Genetics</i> , 2015, 23, 1717-1722.	2.8	12
62	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , 2022, 18, e1010162.	3.5	12
63	TAS2R38 bitter taste genotype is associated with complementary feeding behavior in infants. <i>Genes and Nutrition</i> , 2019, 14, 13.	2.5	11
64	Factors associated with food liking and their relationship with metabolic traits in Italian cohorts. <i>Food Quality and Preference</i> , 2019, 75, 64-70.	4.6	9
65	Primary Ciliary Dyskinesia: The Impact of Taste Receptor (<i>TAS2R38</i>) Gene Polymorphisms on Disease Outcome and Severity. <i>International Archives of Allergy and Immunology</i> , 2020, 181, 727-731.	2.1	8
66	Dietary Macronutrient Composition in Relation to Circulating HDL and Non-HDL Cholesterol: A Federated Individual-Level Analysis of Cross-Sectional Data from Adolescents and Adults in 8 European Studies. <i>Journal of Nutrition</i> , 2021, 151, 2317-2329.	2.9	8
67	Investigation of the link between PROP taste perception and vegetables consumption using FAOSTAT data. <i>International Journal of Food Sciences and Nutrition</i> , 2019, 70, 484-490.	2.8	6
68	Association of <i>LTA</i> gene haploblock with periodontal disease in Italian adults. <i>Journal of Periodontal Research</i> , 2019, 54, 128-133.	2.7	3
69	Runs of homozygosity are associated with staging of periodontitis in isolated populations. <i>Human Molecular Genetics</i> , 2021, 30, 1154-1159.	2.9	3
70	Deleterious variants in genes associated with bone mineral density are linked to susceptibility to periodontitis development. <i>Meta Gene</i> , 2020, 24, 100670.	0.6	2
71	Eating disinhibition and food liking are influenced by variants in <i>CAV1</i> (caveolin 1) gene. <i>Food Quality and Preference</i> , 2022, 96, 104447.	4.6	1
72	Uncovering the genetic basis for food preferences: the key to personalized nutrition plans?. <i>Personalized Medicine</i> , 2015, 12, 315-317.	1.5	0

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73	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015, 70, 758-762.	0.4	0