Ilaria Gandin

List of Publications by Year
in descending order

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49 papers	11,245 citations	147801 31 h-index	168389 53 g-index
58 all docs	58 docs citations	58 times ranked	21521 citing authors

#	Article	IF	Citations
1	Machine learning in clinical and epidemiological research: isn't it time for biostatisticians to work on it?. , 2022, 16, .		8
2	Eating disinhibition and food liking are influenced by variants in CAV1 (caveolin 1) gene. Food Quality and Preference, 2022, 96, 104447.	4.6	1
3	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	6.1	14
4	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. PLoS Genetics, 2022, 18, e1010162.	3.5	12
5	Runs of homozygosity are associated with staging of periodontitis in isolated populations. Human Molecular Genetics, 2021, 30, 1154-1159.	2.9	3
6	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
7	Interpretability of time-series deep learning models: A study in cardiovascular patients admitted to Intensive care unit. Journal of Biomedical Informatics, 2021, 121, 103876.	4.3	22
8	A birdâ€™s-eye view of Italian genomic variation through whole-genome sequencing. European Journal of Human Genetics, 2020, 28, 435-444.	2.8	29
9	DKC1 Overexpression Induces a More Aggressive Cellular Behavior and Increases Intrinsic Ribosomal Activity in Immortalized Mammary Gland Cells. Cancers, 2020, 12, 3512.	3.7	21
10	Can we predict firmsâ€™ innovativeness? The identification of innovation performers in an Italian region through a supervised learning approach. PLoS ONE, 2019, 14, e0218175.	2.5	7
11	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
12	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
13	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
14	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
15	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
16	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
17	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
18	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89

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19	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature Genetics, 2019, 51, 245-257.	21.4	536
20	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. Nature Genetics, 2018, 50, 652-656.	21.4	86
21	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
22	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
23	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
24	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
25	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
26	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
27	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
28	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
29	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
30	Targeted sequencing identifies novel variants involved in autosomal recessive hereditary hearing loss in Qatari families. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2017, 800-802, 29-36.	1.0	23
31	Genetic variation within the Y chromosome is not associated with histological characteristics of the atherosclerotic carotid artery or aneurysmal wall. Atherosclerosis, 2017, 259, 114-119.	0.8	6
32	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
33	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
34	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
35	A semi-nested real-time PCR method to detect low chimerism percentage in small quantity of hematopoietic stem cell transplant DNA samples. Genome, 2017, 60, 183-192.	2.0	5
36	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204

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37	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
38	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
39	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
40	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
41	Excess of runs of homozygosity is associated with severe cognitive impairment in intellectual disability. Genetics in Medicine, 2015, 17, 396-399.	2.4	19
42	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
43	Target sequencing approach intended to discover new mutations in non-syndromic intellectual disability. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 781, 32-36.	1.0	10
44	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
45	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
46	Common Variants in UMOD Associate with Urinary Uromodulin Levels. Journal of the American Society of Nephrology: JASN, 2014, 25, 1869-1882.	6.1	85
47	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
48	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
49	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166