

Giorgia Girotto

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

78
papers

4,534
citations

27
h-index

67
g-index

93
ext. papers

6,417
ext. citations

11
avg, IF

3.69
L-index

#	Paper	IF	Citations
78	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	12.7	2
77	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , 2022 ,	36.3	7
76	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
75	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
74	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
73	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. <i>Science Advances</i> , 2021 , 7,	14.3	11
72	Natural human knockouts and Mendelian disorders: deep phenotyping in Italian isolates. <i>European Journal of Human Genetics</i> , 2021 , 29, 1272-1281	5.3	1
71	Variants in USP48 encoding ubiquitin hydrolase are associated with autosomal dominant non-syndromic hereditary hearing loss. <i>Human Molecular Genetics</i> , 2021 , 30, 1785-1796	5.6	1
70	Hearing loss 2021 , 305-322		0
69	Non-Syndromic Sensorineural Prelingual and Postlingual Hearing Loss due to COL11A1 Gene Mutation. <i>Journal of International Advanced Otology</i> , 2021 , 17, 81-83	1.1	
68	Non-Syndromic Autosomal Dominant Hearing Loss: The First Italian Family Carrying a Mutation in the Gene. <i>Genes</i> , 2021 , 12,	4.2	2
67	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
66	Benefit of cochlear implantation in a patient with Myhre syndrome. <i>BMJ Case Reports</i> , 2021 , 14,	0.9	
65	Genetics, odor perception and food liking: The intriguing role of cinnamon. <i>Food Quality and Preference</i> , 2021 , 93, 104277	5.8	1
64	Functional analysis of candidate genes from genome-wide association studies of hearing. <i>Hearing Research</i> , 2020 , 387, 107879	3.9	4
63	A bird's-eye view of Italian genomic variation through whole-genome sequencing. <i>European Journal of Human Genetics</i> , 2020 , 28, 435-444	5.3	16
62	Lights and Shadows in the Genetics of Syndromic and Non-Syndromic Hearing Loss in the Italian Population. <i>Genes</i> , 2020 , 11,	4.2	7

61	Molecular testing for the study of non-syndromic hearing loss. <i>Hearing, Balance and Communication</i> , 2020 , 18, 270-277	0.7	3
60	Hearing loss and brain abnormalities due to pathogenic mutations in ADGRV1 gene: a case report. <i>Hearing, Balance and Communication</i> , 2020 , 18, 196-198	0.7	0
59	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
58	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
57	Next Generation Sequencing and Animal Models Reveal as a New Gene Involved in Human Age-Related Hearing Loss. <i>Frontiers in Genetics</i> , 2019 , 10, 142	4.5	6
56	Mutations in PLS1, encoding fimbrin, cause autosomal dominant nonsyndromic hearing loss. <i>Human Mutation</i> , 2019 , 40, 2286-2295	4.7	14
55	Next generation sequencing study in a cohort of Italian patients with syndromic hearing loss. <i>Hearing Research</i> , 2019 , 381, 107769	3.9	2
54	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 3118-3131	15.1	12
53	Genome-wide association meta-analysis identifies five novel loci for age-related hearing impairment. <i>Scientific Reports</i> , 2019 , 9, 15192	4.9	14
52	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
51	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
50	Next-generation sequencing identified SPATC1L as a possible candidate gene for both early-onset and age-related hearing loss. <i>European Journal of Human Genetics</i> , 2019 , 27, 70-79	5.3	14
49	TBL1Y: a new gene involved in syndromic hearing loss. <i>European Journal of Human Genetics</i> , 2019 , 27, 466-474	5.3	8
48	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	36.3	59
47	Mutations in L-type amino acid transporter-2 support as a novel gene involved in age-related hearing loss. <i>ELife</i> , 2018 , 7,	8.9	27
46	Whole-genome sequencing reveals new insights into age-related hearing loss: cumulative effects, pleiotropy and the role of selection. <i>European Journal of Human Genetics</i> , 2018 , 26, 1167-1179	5.3	14
45	Cx26 partial loss causes accelerated presbycusis by redox imbalance and dysregulation of Nfr2 pathway. <i>Redox Biology</i> , 2018 , 19, 301-317	11.3	28
44	Genomic Studies in a Large Cohort of Hearing Impaired Italian Patients Revealed Several New Alleles, a Rare Case of Uniparental Disomy (UPD) and the Importance to Search for Copy Number Variations. <i>Frontiers in Genetics</i> , 2018 , 9, 681	4.5	13

43	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
42	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
41	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
40	Targeted sequencing identifies novel variants involved in autosomal recessive hereditary hearing loss in Qatari Families. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2017 , 800-802, 29-36	3.3	13
39	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017 , 7, 45040	4.9	70
38	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 ,	8.5	85
37	A novel founder MYO15A frameshift duplication is the major cause of genetic hearing loss in Oman. <i>Journal of Human Genetics</i> , 2017 , 62, 259-264	4.3	18
36	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016 , 48, 1462-1472	36.3	198
35	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	11.5	90
34	Pharmacogenetics driving personalized medicine: analysis of genetic polymorphisms related to breast cancer medications in Italian isolated populations. <i>Journal of Translational Medicine</i> , 2016 , 14, 22	8.5	3
33	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
32	Increased rate of deleterious variants in long runs of homozygosity of an inbred population from Qatar. <i>Human Heredity</i> , 2015 , 79, 14-9	1.1	22
31	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-462	50.4	119
30	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	36.3	226
29	Genome-wide association analysis on normal hearing function identifies PCDH20 and SLC28A3 as candidates for hearing function and loss. <i>Human Molecular Genetics</i> , 2015 , 24, 5655-64	5.6	24
28	PSIP1/LEDGF: a new gene likely involved in sensorineural progressive hearing loss. <i>Scientific Reports</i> , 2015 , 5, 18568	4.9	4
27	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 ²⁻⁴		
26	Association of SNPs in LCP1 and CTIF with hearing in 11 year old children: findings from the Avon Longitudinal Study of Parents and Children (ALSPAC) birth cohort and the G-EAR consortium. <i>BMC Medical Genomics</i> , 2015 , 8, 48	3.7	2

25	The p.Cys169Tyr variant of connexin 26 is not a polymorphism. <i>Human Molecular Genetics</i> , 2015 , 24, 2641-8	3.8	9
24	Usher syndrome: an effective sequencing approach to establish a genetic and clinical diagnosis. <i>Hearing Research</i> , 2015 , 320, 18-23	3.9	22
23	Common variants in UMOD associate with urinary uromodulin levels: a meta-analysis. <i>Journal of the American Society of Nephrology: JASN</i> , 2014 , 25, 1869-82	12.7	71
22	A novel P2RX2 mutation in an Italian family affected by autosomal dominant nonsyndromic hearing loss. <i>Gene</i> , 2014 , 534, 236-9	3.8	25
21	Salt-inducible kinase 3, SIK3, is a new gene associated with hearing. <i>Human Molecular Genetics</i> , 2014 , 23, 6407-18	5.6	23
20	Age related hearing loss and level of education: An epidemiological study on a large cohort of isolated populations. <i>Hearing, Balance and Communication</i> , 2014 , 12, 94-98	0.7	3
19	Consanguinity and hereditary hearing loss in Qatar. <i>Human Heredity</i> , 2014 , 77, 175-82	1.1	13
18	Genetic landscape of populations along the Silk Road: admixture and migration patterns. <i>BMC Genetics</i> , 2014 , 15, 131	2.6	15
17	Hereditary hearing loss: a 96 gene targeted sequencing protocol reveals novel alleles in a series of Italian and Qatari patients. <i>Gene</i> , 2014 , 542, 209-16	3.8	45
16	Expression and replication studies to identify new candidate genes involved in normal hearing function. <i>PLoS ONE</i> , 2014 , 9, e85352	3.7	30
15	Estrogen-related receptor gamma and hearing function: evidence of a role in humans and mice. <i>Neurobiology of Aging</i> , 2013 , 34, 2077.e1-9	5.6	42
14	Maps of open chromatin highlight cell type-restricted patterns of regulatory sequence variation at hematological trait loci. <i>Genome Research</i> , 2013 , 23, 1130-41	9.7	31
13	Meta-analysis of genome-wide association studies identifies six new Loci for serum calcium concentrations. <i>PLoS Genetics</i> , 2013 , 9, e1003796	6	100
12	Lifestyle and normal hearing function in Italy and Central Asia: The potential role of coffee. <i>Hearing, Balance and Communication</i> , 2013 , 11, 218-223	0.7	5
11	Linkage study and exome sequencing identify a BDP1 mutation associated with hereditary hearing loss. <i>PLoS ONE</i> , 2013 , 8, e80323	3.7	43
10	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257
9	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012 , 21, 4805-15	5.6	24
8	GJB2 and GJB6 genes and the A1555G mitochondrial mutation are only minor causes of nonsyndromic hearing loss in the Qatari population. <i>International Journal of Audiology</i> , 2012 , 51, 181-5	2.6	25

7	Evidence of inbreeding depression on human height. <i>PLoS Genetics</i> , 2012 , 8, e1002655	6	62
6	Frequency of hearing loss in a series of rural communities of five developing countries located along the Silk Road. <i>Audiological Medicine</i> , 2011 , 9, 135-140		12
5	Hearing function and thresholds: a genome-wide association study in European isolated populations identifies new loci and pathways. <i>Journal of Medical Genetics</i> , 2011 , 48, 369-74	5.8	59
4	MYH9 related disease: four novel mutations of the tail domain of myosin-9 correlating with a mild clinical phenotype. <i>European Journal of Haematology</i> , 2010 , 84, 291-7	3.8	27
3	MYH9 related disease: a novel missense Ala95Asp mutation of the MYH9 gene. <i>Platelets</i> , 2009 , 20, 598-602	3.0	10
2	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
1	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1