

# Marina Ciullo

## List of Publications by Year in descending order

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75  
papers

9,505  
citations

81900

39  
h-index

74163

75  
g-index

79  
all docs

79  
docs citations

79  
times ranked

17360  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	21.4	675
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	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	21.4	492
5	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
6	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
7	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	27.8	401
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	Meta-analysis of genome-wide association studies for personality. <i>Molecular Psychiatry</i> , 2012, 17, 337-349.	7.9	340
10	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
11	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
12	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294
13	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	11.0	289
14	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
15	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
16	Age- And Sex-Related Variations in Platelet Count in Italy: A Proposal of Reference Ranges Based on 40987 Subjects' Data. <i>PLoS ONE</i> , 2013, 8, e54289.	2.5	190
17	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
18	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	2.1	178

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19	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
20	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
21	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
22	Initiation of the breakage-fusion-bridge mechanism through common fragile site activation in human breast cancer cells: the model of PIP gene duplication from a break at FRA7I. <i>Human Molecular Genetics</i> , 2002, 11, 2887-2894.	2.9	124
23	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
24	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	12.8	118
25	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	2.8	113
26	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	8.2	106
27	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	2.1	103
28	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
29	Meta-analysis of genome-wide association studies identifies common variants in CTNNA2 associated with excitement-seeking. <i>Translational Psychiatry</i> , 2011, 1, e49-e49.	4.8	97
30	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
31	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, 369-374.	3.2	71
32	Genetics of VEGF Serum Variation in Human Isolated Populations of Cilento: Importance of VEGF Polymorphisms. <i>PLoS ONE</i> , 2011, 6, e16982.	2.5	68
33	Body mass index is directly associated with biomarkers of angiogenesis and inflammation in children and adolescents. <i>Nutrition</i> , 2012, 28, 262-266.	2.4	67
34	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
35	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.5	64
36	Meta-Analysis of the INSIG2 Association with Obesity Including 74,345 Individuals: Does Heterogeneity of Estimates Relate to Study Design?. <i>PLoS Genetics</i> , 2009, 5, e1000694.	3.5	62

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37	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. <i>PLoS Genetics</i> , 2016, 12, e1005874.	3.5	56
38	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. <i>Nature Communications</i> , 2018, 9, 4228.	12.8	43
39	Angiogenesis and biomarkers of cardiovascular risk in adults with metabolic syndrome. <i>Journal of Internal Medicine</i> , 2010, 268, 338-347.	6.0	40
40	New susceptibility locus for hypertension on chromosome 8q by efficient pedigree-breaking in an Italian isolate. <i>Human Molecular Genetics</i> , 2006, 15, 1735-1743.	2.9	39
41	Expression and molecular characterization of alternative transcripts of the ARHGEF5/TIM oncogene specific for human breast cancer. <i>Human Molecular Genetics</i> , 2003, 13, 323-334.	2.9	37
42	Heritability and Demographic Analyses in the Large Isolated Population of Val Borbera Suggest Advantages in Mapping Complex Traits Genes. <i>PLoS ONE</i> , 2009, 4, e7554.	2.5	37
43	Genome-wide association analysis on normal hearing function identifies <i>PCDH20</i> and <i>SLC28A3</i> as candidates for hearing function and loss. <i>Human Molecular Genetics</i> , 2015, 24, 5655-5664.	2.9	37
44	Influence of age, sex and ethnicity on platelet count in five Italian geographic isolates: mild thrombocytopenia may be physiological. <i>British Journal of Haematology</i> , 2012, 157, 384-387.	2.5	33
45	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	6.1	33
46	Comparing population structure as inferred from genealogical versus genetic information. <i>European Journal of Human Genetics</i> , 2009, 17, 1635-1641.	2.8	31
47	Salt-inducible kinase 3, SIK3, is a new gene associated with hearing. <i>Human Molecular Genetics</i> , 2014, 23, 6407-6418.	2.9	30
48	Campora: A Young Genetic Isolate in South Italy. <i>Human Heredity</i> , 2007, 64, 123-135.	0.8	28
49	Strategies for phasing and imputation in a population isolate. <i>Genetic Epidemiology</i> , 2018, 42, 201-213.	1.3	27
50	Variation of hemoglobin levels in normal Italian populations from genetic isolates. <i>Haematologica</i> , 2008, 93, 1372-1375.	3.5	25
51	Biosynthesis and immunobiochemical characterization of gp17/GCDFP-15. A glycoprotein from seminal vesicles and from breast tumors, in HeLa cells and in <i>Pichia pastoris</i> yeast. <i>FEBS Journal</i> , 1999, 265, 664-670.	0.2	24
52	Intragenic amplification and formation of extrachromosomal small circular DNA molecules from the PIP gene on chromosome 7 in primary breast carcinomas. <i>International Journal of Cancer</i> , 2002, 99, 370-377.	5.1	21
53	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	5.2	18
54	Age-related hearing loss in four Italian genetic isolates: An epidemiological study. <i>International Journal of Audiology</i> , 2009, 48, 465-472.	1.7	17

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55	Body composition, leg length and blood pressure in a rural Italian population: A test of the capacity-load model. <i>Nutrition, Metabolism and Cardiovascular Diseases</i> , 2014, 24, 1204-1212.	2.6	17
56	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	17
57	Identification and Replication of a Novel Obesity Locus on Chromosome 1q24 in Isolated Populations of Cilento. <i>Diabetes</i> , 2008, 57, 783-790.	0.6	16
58	Differential expression of insulin-dependent diabetes mellitus-associated HLA-DQA1 alleles in vivo. <i>European Journal of Immunology</i> , 1997, 27, 1549-1556.	2.9	15
59	Association of a variant in the CHRNA5-A3-B4 gene cluster region to heavy smoking in the Italian population. <i>European Journal of Human Genetics</i> , 2011, 19, 593-596.	2.8	13
60	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. <i>PLoS Genetics</i> , 2015, 11, e1004976.	3.5	13
61	Longevity candidate genes and their association with personality traits in the elderly. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 192-200.	1.7	12
62	Genetic and Environmental Factors Influencing the Placental Growth Factor (PGF) Variation in Two Populations. <i>PLoS ONE</i> , 2012, 7, e42537.	2.5	11
63	Control of Nucleo-cytoplasmic HLA-DRA mRNA Partitioning by Interaction of a Retention Signal with Compartmentalized Proteins. <i>Journal of Molecular Biology</i> , 1994, 240, 193-204.	4.2	10
64	Unbalanced expression of HLA-A and -B antigens: A specific feature of cutaneous melanoma and other non-hemopoietic malignancies reverted by IFN- $\gamma$ . <i>International Journal of Cancer</i> , 2001, 91, 500-507.	5.1	10
65	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. <i>Scientific Reports</i> , 2019, 9, 4059.	3.3	7
66	Genetics of PlGF plasma levels highlights a role of its receptors and supports the link between angiogenesis and immunity. <i>Scientific Reports</i> , 2021, 11, 16821.	3.3	6
67	Detecting the dominance component of heritability in isolated and outbred human populations. <i>Scientific Reports</i> , 2018, 8, 18048.	3.3	3
68	Polymorphism in the 5' terminal region of the mRNA of HLA-DQA1 gene: Identification of four groups of transcripts and their association with polymorphism in the a 1 domain. <i>Human Immunology</i> , 1997, 53, 167-173.	2.4	2
69	Regulation of HLA class II gene expression: the case for posttranscriptional control levels. <i>Microbes and Infection</i> , 1999, 1, 943-948.	1.9	2
70	Downstream Sequence Adjacent to AUG Affects Translation of Chloramphenicol Acetyl Transferase in Eukaryotic Cells. <i>DNA and Cell Biology</i> , 2000, 19, 39-46.	1.9	2
71	SNP-Based Linkage Analysis in Extended Pedigrees: Comparison between Two Alternative Approaches. <i>Human Heredity</i> , 2014, 78, 27-37.	0.8	1
72	A transnational collaborative network dedicated to the study and applications of the vascular endothelial growth factor-A in medical practice: the VEGF Consortium. <i>Clinical Chemistry and Laboratory Medicine</i> , 2018, 56, 83-86.	2.3	1

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73	Unbalanced expression of HLAâ€A and â€B antigens: A specific feature of cutaneous melanoma and other nonâ€hemopoietic malignancies reverted by IFNâ€³. International Journal of Cancer, 2001, 91, 500-507.	5.1	1
74	Moment estimators of relatedness from low-depth whole-genome sequencing data. BMC Bioinformatics, 2022, 23, .	2.6	1
75	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