

Daniela Ruggiero

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9047633/publications.pdf>

Version: 2024-02-01

44
papers

8,474
citations

126708

33
h-index

233125

45
g-index

50
all docs

50
docs citations

50
times ranked

15655
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.	9.4	924
2	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	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.	9.4	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.	9.4	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.	9.4	426
6	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
7	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	13.7	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.	9.4	357
9	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
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.	2.6	326
11	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	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.	9.4	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.	6.0	289
14	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
15	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
16	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
17	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178
18	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173

#	ARTICLE	IF	CITATIONS
19	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	1.5	166
20	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	1.5	142
21	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, .	1.3	123
22	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	5.8	118
23	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
24	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.	1.4	103
25	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	1.6	98
26	Meta-analysis of genome-wide association studies identifies common variants in CTNNA2 associated with excitement-seeking. <i>Translational Psychiatry</i> , 2011, 1, e49-e49.	2.4	97
27	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
28	Genetics of VEGF Serum Variation in Human Isolated Populations of Cilento: Importance of VEGF Polymorphisms. <i>PLoS ONE</i> , 2011, 6, e16982.	1.1	68
29	Body mass index is directly associated with biomarkers of angiogenesis and inflammation in children and adolescents. <i>Nutrition</i> , 2012, 28, 262-266.	1.1	67
30	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.	1.4	64
31	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
32	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.	1.5	56
33	Identification of sixteen novel candidate genes for late onset Parkinson's disease. <i>Molecular Neurodegeneration</i> , 2021, 16, 35.	4.4	41
34	Angiogenesis and biomarkers of cardiovascular risk in adults with metabolic syndrome. <i>Journal of Internal Medicine</i> , 2010, 268, 338-347.	2.7	40
35	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.	3.0	33
36	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.	2.6	18

#	ARTICLE	IF	CITATIONS
37	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	2.0	17
38	Genetic Variants Modulating CRIPTO Serum Levels Identified by Genome-Wide Association Study in Cilento Isolates. <i>PLoS Genetics</i> , 2015, 11, e1004976.	1.5	13
39	Genetic and Environmental Factors Influencing the Placental Growth Factor (PGF) Variation in Two Populations. <i>PLoS ONE</i> , 2012, 7, e42537.	1.1	11
40	Whole-Exome Sequencing in the Isolated Populations of Cilento from South Italy. <i>Scientific Reports</i> , 2019, 9, 4059.	1.6	7
41	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.	1.6	6
42	Detecting the dominance component of heritability in isolated and outbred human populations. <i>Scientific Reports</i> , 2018, 8, 18048.	1.6	3
43	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.	1.4	1
44	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.	0.2	0