David Schlessinger

List of Publications by Year
in descending order

74 papers	23,461 citations	66343 42 h-index	76900 74 g-index
77 all docs	77 docs citations	77 times ranked	34805 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	21.4	2,828
3	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
6	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
7	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
8	The putative forkhead transcription factor FOXL2 is mutated in blepharophimosis/ptosis/epicanthus inversus syndrome. Nature Genetics, 2001, 27, 159-166.	21.4	886
9	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
10	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
11	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
12	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
13	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
14	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
15	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
16	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	21.4	193
17	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
18	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	2.1	178

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19	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
20	Homeostatic Control of Sebaceous Glands by Innate Lymphoid Cells Regulates Commensal Bacteria Equilibrium. Cell, 2019, 176, 982-997.e16.	28.9	159
21	Complex genetic signatures in immune cells underlie autoimmunity and inform therapy. Nature Genetics, 2020, 52, 1036-1045.	21.4	153
22	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	3.5	150
23	Eccrine sweat gland development and sweat secretion. Experimental Dermatology, 2015, 24, 644-650.	2.9	149
24	Genes and translocations involved in POF. American Journal of Medical Genetics Part A, 2002, 111, 328-333.	2.4	146
25	Assessing Mitochondrial DNA Variation and Copy Number in Lymphocytes of ~2,000 Sardinians Using Tailored Sequencing Analysis Tools. PLoS Genetics, 2015, 11, e1005306.	3.5	123
26	Arterial stiffness and influences of the metabolic syndrome: A cross-countries study. Atherosclerosis, 2014, 233, 654-660.	0.8	116
27	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
28	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
29	Gpc3 expression correlates with the phenotype of the Simpson-Golabi-Behmel syndrome. Developmental Dynamics, 1998, 213, 431-439.	1.8	104
30	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	21.4	96
31	Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia. Nature Communications, 2020, 11, 939.	12.8	96
32	PLAC1, an Xq26 Gene with Placenta-Specific Expression. Genomics, 2000, 68, 305-312.	2.9	95
33	Rare variant genotype imputation with thousands of study-specific whole-genome sequences: implications for cost-effective study designs. European Journal of Human Genetics, 2015, 23, 975-983.	2.8	92
34	Identification of Transcription Factors for Lineage-Specific ESC Differentiation. Stem Cell Reports, 2013, 1, 545-559.	4.8	76
35	Genomic history of the Sardinian population. Nature Genetics, 2018, 50, 1426-1434.	21.4	71
36	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

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37	Genome-wide association analyses based on whole-genome sequencing in Sardinia provide insights into regulation of hemoglobin levels. Nature Genetics, 2015, 47, 1264-1271.	21.4	66
38	Mitogenome Diversity in Sardinians: A Genetic Window onto an Island's Past. Molecular Biology and Evolution, 2017, 34, 1230-1239.	8.9	61
39	Variation in human chromosome 21 ribosomal RNA genes characterized by TAR cloning and long-read sequencing. Nucleic Acids Research, 2018, 46, 6712-6725.	14.5	61
40	ExAtlas: An interactive online tool for meta-analysis of gene expression data. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550019.	0.8	58
41	Involvement of Wnt, Eda and Shh at defined stages of sweat gland development. Development (Cambridge), 2014, 141, 3752-3760.	2.5	57
42	Genetic regulation of gene expression and splicing during a 10-year period of human aging. Genome Biology, 2019, 20, 230.	8.8	57
43	Determination and Stability of Gonadal Sex. Journal of Andrology, 2010, 31, 16-25.	2.0	46
44	Genetic-Driven Druggable Target Identification and Validation. Trends in Genetics, 2018, 34, 558-570.	6.7	44
45	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
46	Population- and individual-specific regulatory variation in Sardinia. Nature Genetics, 2017, 49, 700-707.	21.4	38
47	Prevalence of CKD and Its Relationship to eGFR-Related Genetic Loci and Clinical Risk Factors in the SardiNIA Study Cohort. Journal of the American Society of Nephrology: JASN, 2014, 25, 1533-1544.	6.1	36
48	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. Human Molecular Genetics, 2020, 29, 1292-1309.	2.9	36
49	Kidney size in relation to ageing, gender, renal function, birthweight and chronic kidney disease risk factors in a general population. Nephrology Dialysis Transplantation, 2020, 35, 640-647.	0.7	33
50	FOXL2 modulates cartilage, skeletal development and IGF1-dependent growth in mice. BMC Developmental Biology, 2015, 15, 27.	2.1	27
51	fastMitoCalc: an ultra-fast program to estimate mitochondrial DNA copy number from whole-genome sequences. Bioinformatics, 2017, 33, 1399-1401.	4.1	27
52	SOX9 accelerates ESC differentiation to three germ layer lineages by repressing SOX2 expression through P21 (WAF1/CIP1). Development (Cambridge), 2014, 141, 4254-4266.	2.5	22
53	Age-related changes of the retinal microvasculature. PLoS ONE, 2019, 14, e0215916.	2.5	20
54	Generation and gene expression profiling of 48 transcription-factor-inducible mouse embryonic stem cell lines. Scientific Reports, 2016, 6, 25667.	3.3	19

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55	Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan. American Journal of Human Genetics, 2020, 107, 60-71.	6.2	18
56	Arterial stiffness and multiple organ damage: a longitudinal study in population. Aging Clinical and Experimental Research, 2020, 32, 781-788.	2.9	17
57	Induction of specific neuron types by overexpression of single transcription factors. In Vitro Cellular and Developmental Biology - Animal, 2016, 52, 961-973.	1.5	15
58	PRF1 mutation alters immune system activation, inflammation, and risk of autoimmunity. Multiple Sclerosis Journal, 2021, 27, 1332-1340.	3.0	13
59	The genomic structure of a human chromosome 22 nucleolar organizer region determined by TAR cloning. Scientific Reports, 2021, 11, 2997.	3.3	13
60	Genome-wide association study of susceptibility loci for breast cancer in Sardinian population. BMC Cancer, 2015, 15, 383.	2.6	12
61	Identification of potassium and chloride channels in eccrine sweat glands. Journal of Dermatological Science, 2016, 81, 129-131.	1.9	12
62	Impact of Stiffer Arteries on the Response to Antihypertensive Treatment: A Longitudinal Study of the SardiNIA Cohort. Journal of the American Medical Directors Association, 2020, 21, 720-725.	2.5	11
63	Eda-activated RelB recruits an SWI/SNF (BAF) chromatin-remodeling complex and initiates gene transcription in skin appendage formation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8173-8178.	7.1	10
64	Novel action of FOXL2 as mediator of Col1a2 gene autoregulation. Developmental Biology, 2016, 416, 200-211.	2.0	9
65	Metaâ€MultiSKAT: Multiple phenotype metaâ€analysis for regionâ€based association test. Genetic Epidemiology, 2019, 43, 800-814.	1.3	9
66	Relative impact of indels versus SNPs on complex disease. Genetic Epidemiology, 2019, 43, 112-117.	1.3	9
67	Foxc1 Ablated Mice Are Anhidrotic and Recapitulate Features of Human Miliaria Sweat Retention Disorder. Journal of Investigative Dermatology, 2017, 137, 38-45.	0.7	7
68	Peptidyl arginine deiminase 2 (Padi2) is expressed in Sertoli cells in a specific manner and regulated by SOX9 during testicular development. Scientific Reports, 2018, 8, 13263.	3.3	7
69	Predicting physiological aging rates from a range of quantitative traits using machine learning. Aging, 2021, 13, 23471-23516.	3.1	6
70	STIM1, but not STIM2, Is the Calcium Sensor Critical for Sweat Secretion. Journal of Investigative Dermatology, 2018, 138, 704-707.	0.7	4
71	PLAC1 affects cell to cell communication by interacting with the desmosome complex. Placenta, 2021, 110, 39-45.	1.5	4
72	A Sardinian founder mutation in glycoprotein Ib platelet subunit beta (GP1BB) that impacts thrombocytopenia. British Journal of Haematology, 2020, 191, e124-e128.	2.5	2

#	Article	IF	Citations
73	The GLUT9 Gene is Associated with Serum Uric Acid Levels in Sardinia and Chianti Cohorts. PLoS Genetics, 2005, preprint, e194.	3.5	1
74	miRNAs Are Required for Postinduction Stage Sweat Gland Development. Journal of Investigative Dermatology, 2017, 137, 1571-1574.	0.7	0