

List of Publications by Citations

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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.

100 papers	9,602 citations	43 h-index	97 g-index
123 ext. papers	12,739 ext. citations	10.7 avg, IF	5.2 L-index

#	Paper	IF	Citations
100	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
99	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
98	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013 , 45, 422-7, 427e1-2	36.3	624
97	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
96	Facing up to the global challenges of ageing. <i>Nature</i> , 2018 , 561, 45-56	50.4	342
95	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016 , 7, 11122	17.4	335
94	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
93	Meta-analysis of telomere length in 19,713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. <i>European Journal of Human Genetics</i> , 2013 , 21, 1163-8	5.3	291
92	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017 , 49, 131-138	36.3	252
91	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017 , 49, 139-145	36.3	240
90	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015 , 47, 589-97	36.3	229
89	Genome-wide association study identifies a single major locus contributing to survival into old age; the APOE locus revisited. <i>Aging Cell</i> , 2011 , 10, 686-98	9.9	218
88	GWAS of longevity in CHARGE consortium confirms APOE and FOXO3 candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015 , 70, 110-8	6.4	188
87	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014 , 23, 4420-32	5.6	188
86	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018 , 9, 260	17.4	174
85	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	11	151
84	A meta-analysis of thyroid-related traits reveals novel loci and gender-specific differences in the regulation of thyroid function. <i>PLoS Genetics</i> , 2013 , 9, e1003266	6	146

83	Variants near TERT and TERC influencing telomere length are associated with high-grade glioma risk. <i>Nature Genetics</i> , 2014 , 46, 731-5	36.3	141
82	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. <i>Aging Cell</i> , 2013 , 12, 184-93	9.9	140
81	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 398-409		119
80	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016 , 17, 138	18.3	118
79	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016 , 7, 10494	17.4	107
78	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016 , 6, 21243	4.9	105
77	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019 , 10, 3669	17.4	102
76	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2016 , 15, 695-707	24.1	100
75	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. <i>Nature Communications</i> , 2019 , 10, 3346	17.4	89
74	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. <i>Age</i> , 2013 , 35, 235-49		86
73	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
72	Gene expression analysis of mTOR pathway: association with human longevity. <i>Aging Cell</i> , 2013 , 12, 24-34	3.9	85
71	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
70	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
69	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. <i>International Journal of Epidemiology</i> , 2014 , 43, 878-86	7.8	83
68	A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1735-1742	4.3	80
67	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016 , 17, 191	18.3	80
66	WORLDWIDE GENOME-WIDE ASSOCIATION STUDY OF LONGEVITY. <i>Innovation in Aging</i> , 2017 , 1, 87-87	0.1	78

65	Identifying the genomic determinants of aging and longevity in human population studies: progress and challenges. <i>BioEssays</i> , 2013 , 35, 386-96	4.1	76
64	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. <i>Nature Communications</i> , 2018 , 9, 4455	17.4	75
63	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. <i>Diabetes</i> , 2017 , 66, 2296-2309	0.9	69
62	The CTRB1/2 locus affects diabetes susceptibility and treatment via the incretin pathway. <i>Diabetes</i> , 2013 , 62, 3275-81	0.9	63
61	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. <i>PLoS Genetics</i> , 2015 , 11, e1005230	6	59
60	Genomics of human longevity. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011 , 366, 35-42	5.8	59
59	Systemic Age-Associated DNA Hypermethylation of ELOVL2 Gene: In Vivo and In Vitro Evidences of a Cell Replication Process. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2017 , 72, 1015-1023	6.4	50
58	Correlation of the two most frequent HLA haplotypes in the Italian population to the differential regional incidence of Covid-19. <i>Journal of Translational Medicine</i> , 2020 , 18, 352	8.5	45
57	Fibroblast growth factor 21 reflects liver fat accumulation and dysregulation of signalling pathways in the liver of C57BL/6J mice. <i>Scientific Reports</i> , 2016 , 6, 30484	4.9	42
56	Genome-wide association and functional studies identify a role for matrix Gla protein in osteoarthritis of the hand. <i>Annals of the Rheumatic Diseases</i> , 2017 , 76, 2046-2053	2.4	42
55	The MC1R Gene and Youthful Looks. <i>Current Biology</i> , 2016 , 26, 1213-20	6.3	42
54	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020 , 106, 389-404	11	40
53	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018 , 1, e181670	10.4	40
52	Short telomere length is associated with impaired cognitive performance in European ancestry cohorts. <i>Translational Psychiatry</i> , 2017 , 7, e1100	8.6	38
51	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020 , 6, eaax0301	14.3	38
50	Genome-Wide Association Study on Immunoglobulin G Glycosylation Patterns. <i>Frontiers in Immunology</i> , 2018 , 9, 277	8.4	36
49	Transcriptional profiling of human familial longevity indicates a role for ASF1A and IL7R. <i>PLoS ONE</i> , 2012 , 7, e27759	3.7	34
48	Multivariate genomic scan implicates novel loci and haem metabolism in human ageing. <i>Nature Communications</i> , 2020 , 11, 3570	17.4	33

47	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , 2015 , 6, 6065	17.4	32
46	Aging as accelerated accumulation of somatic variants: whole-genome sequencing of centenarian and middle-aged monozygotic twin pairs. <i>Twin Research and Human Genetics</i> , 2013 , 16, 1026-32	2.2	30
45	IL7R gene expression network associates with human healthy ageing. <i>Immunity and Ageing</i> , 2015 , 12, 21	9.7	29
44	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016 , 53, 441-9	5.8	27
43	Uncompromised 10-year survival of oldest old carrying somatic mutations in DNMT3A and TET2. <i>Blood</i> , 2016 , 127, 1512-5	2.2	27
42	LDL cholesterol still a problem in old age? A Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2015 , 44, 604-12	7.8	26
41	Lack of consensus on an aging biology paradigm? A global survey reveals an agreement to disagree, and the need for an interdisciplinary framework. <i>Mechanisms of Ageing and Development</i> , 2020 , 191, 111316	5.6	26
40	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018 , 1862, 637-648	4	25
39	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. <i>Biological Psychiatry</i> , 2019 , 86, 599-607	7.9	24
38	How to deal with the early GWAS data when imputing and combining different arrays is necessary. <i>European Journal of Human Genetics</i> , 2012 , 20, 572-6	5.3	23
37	Distinguishing between longevity and buffered-deleterious genotypes for exceptional human longevity: the case of the MTP gene. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2012 , 67, 1153-60	6.4	22
36	Phenome and genome based studies into human ageing and longevity: An overview. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018 , 1864, 2742-2751	6.9	21
35	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , 2018 , 61, 117-129	10.3	21
34	Employing biomarkers of healthy ageing for leveraging genetic studies into human longevity. <i>Experimental Gerontology</i> , 2016 , 82, 166-74	4.5	21
33	Association of adiponectin and leptin with relative telomere length in seven independent cohorts including 11,448 participants. <i>European Journal of Epidemiology</i> , 2014 , 29, 629-38	12.1	18
32	Metabolic effects of a 13-weeks lifestyle intervention in older adults: The Growing Old Together Study. <i>Aging</i> , 2016 , 8, 111-26	5.6	17
31	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019 ,	6.5	17
30	The complex genetics of gait speed: genome-wide meta-analysis approach. <i>Aging</i> , 2017 , 9, 209-246	5.6	16

29	Low mitochondrial DNA content associates with familial longevity: the Leiden Longevity Study. <i>Age</i> , 2014 , 36, 9629		15
28	Copy number variation associates with mortality in long-lived individuals: a genome-wide assessment. <i>Aging Cell</i> , 2016 , 15, 49-55	9.9	15
27	Non-homologous end-joining pathway associated with occurrence of myocardial infarction: gene set analysis of genome-wide association study data. <i>PLoS ONE</i> , 2013 , 8, e56262	3.7	13
26	A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention. <i>Human Molecular Genetics</i> , 2011 , 20, 4748-57	5.6	13
25	Sex-specific effects of naturally occurring variants in the dopamine receptor D2 locus on insulin secretion and type 2 diabetes susceptibility. <i>Diabetic Medicine</i> , 2014 , 31, 1001-8	3.5	10
24	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. <i>Genome Biology</i> , 2020 , 21, 220	18.3	10
23	The effect of standardized food intake on the association between BMI and H-NMR metabolites. <i>Scientific Reports</i> , 2016 , 6, 38980	4.9	9
22	Maternal and child cytokine relationship in early life is not altered by cytokine gene polymorphisms. <i>Genes and Immunity</i> , 2016 , 17, 380-385	4.4	9
21	Association between the rs7903146 Polymorphism in the TCF7L2 Gene and Parameters Derived with Continuous Glucose Monitoring in Individuals without Diabetes. <i>PLoS ONE</i> , 2016 , 11, e0149992	3.7	8
20	Hypothesis-free identification of modulators of genetic risk factors		7
19	Metabolic Age Based on the BBMRI-NL H-NMR Metabolomics Repository as Biomarker of Age-related Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 541-547	5.2	7
18	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. <i>Molecular Psychiatry</i> , 2021 , 26, 2148-2162	15.1	7
17	Disease variants alter transcription factor levels and methylation of their binding sites		6
16	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. <i>Human Molecular Genetics</i> , 2021 , 30, 393-409	5.6	6
15	Exome and whole genome sequencing in aging and longevity. <i>Advances in Experimental Medicine and Biology</i> , 2015 , 847, 127-39	3.6	5
14	Survival analysis with delayed entry in selected families with application to human longevity. <i>Statistical Methods in Medical Research</i> , 2018 , 27, 933-954	2.3	5
13	Fine mapping the region reveals a common intronic insertion associated to HDL-C. <i>Npj Aging and Mechanisms of Disease</i> , 2015 , 1, 15011	5.5	5
12	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. <i>PLoS ONE</i> , 2018 , 13, e0189886	3.7	5

11	Facial Wrinkles in Europeans: A Genome-Wide Association Study. <i>Journal of Investigative Dermatology</i> , 2018 , 138, 1877-1880	4.3	4
10	Assessment of the contribution of APOE gene variants to metabolic phenotypes associated with familial longevity at middle age. <i>Aging</i> , 2016 , 8, 1790-801	5.6	4
9	Genome-wide association study of plasma triglycerides, phospholipids and relation to cardio-metabolic risk factors		4
8	Lifestyle-Intervention-Induced Reduction of Abdominal Fat Is Reflected by a Decreased Circulating Glycerol Level and an Increased HDL Diameter. <i>Molecular Nutrition and Food Research</i> , 2020 , 64, e1900818	5.9	3
7	Estimation of metabolite networks with regard to a specific covariable: applications to plant and human data. <i>Metabolomics</i> , 2017 , 13, 129	4.7	3
6	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022 , 2, 19-30		3
5	Similar burden of pathogenic coding variants in exceptionally long-lived individuals and individuals without exceptional longevity. <i>Aging Cell</i> , 2020 , 19, e13216	9.9	3
4	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. <i>Scientific Reports</i> , 2019 , 9, 11623	4.9	2
3	Searching for the genetic key to a long and healthy life. <i>ELife</i> , 2020 , 9,	8.9	2
2	From mutation to mechanism: deciphering the molecular function of genetic variants linked to human ageing. <i>Briefings in Functional Genomics</i> , 2021 ,	4.9	1
1	Targeting multimorbidity: Using healthspan and lifespan to identify biomarkers of ageing that pinpoint shared disease mechanisms. <i>EBioMedicine</i> , 2021 , 67, 103364	8.8	0