

# P Eline Slagboom

## List of Publications by Year in descending order

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Version: 2024-02-01

627  
papers

67,118  
citations

906

116  
h-index

1316

224  
g-index

663  
all docs

663  
docs citations

663  
times ranked

68190  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Cytogenetic analysis using quantitative, high-sensitivity, fluorescence hybridization.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1986, 83, 2934-2938.	7.1	3,003
3	Persistent epigenetic differences associated with prenatal exposure to famine in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17046-17049.	7.1	2,683
4	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
5	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
6	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
7	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. <i>Nature Genetics</i> , 2012, 44, 491-501.	21.4	1,100
8	DNA methylation differences after exposure to prenatal famine are common and timing- and sex-specific. <i>Human Molecular Genetics</i> , 2009, 18, 4046-4053.	2.9	1,042
9	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013, 45, 422-427.	21.4	808
10	Facing up to the global challenges of ageing. <i>Nature</i> , 2018, 561, 45-56.	27.8	760
11	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
12	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890.	12.8	706
13	L1 drives IFN in senescent cells and promotes age-associated inflammation. <i>Nature</i> , 2019, 566, 73-78.	27.8	701
14	Whole-genome sequence variation, population structure and demographic history of the Dutch population. <i>Nature Genetics</i> , 2014, 46, 818-825.	21.4	641
15	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	21.4	641
16	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
17	Telomere length and replicative aging in human vascular tissues.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 11190-11194.	7.1	587
18	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. <i>Nature Communications</i> , 2016, 7, 11122.	12.8	576

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19	Genetic determination of telomere size in humans: a twin study of three age groups. <i>American Journal of Human Genetics</i> , 1994, 55, 876-82.	6.2	572
20	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
21	DNA methylation signatures link prenatal famine exposure to growth and metabolism. <i>Nature Communications</i> , 2014, 5, 5592.	12.8	494
22	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
23	Accuracy of direct segmental multi-frequency bioimpedance analysis in the assessment of total body and segmental body composition in middle-aged adult population. <i>Clinical Nutrition</i> , 2011, 30, 610-615.	5.0	459
24	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	3.5	419
25	Periconceptional Maternal Folic Acid Use of 400 $\mu\text{g}$ per Day Is Related to Increased Methylation of the IGF2 Gene in the Very Young Child. <i>PLoS ONE</i> , 2009, 4, e7845.	2.5	410
26	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. <i>American Journal of Psychiatry</i> , 2017, 174, 850-858.	7.2	410
27	Human naive and memory T lymphocytes differ in telomeric length and replicative potential.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995, 92, 11091-11094.	7.1	394
28	Disease variants alter transcription factor levels and methylation of their binding sites. <i>Nature Genetics</i> , 2017, 49, 131-138.	21.4	390
29	Genome-wide patterns and properties of de novo mutations in humans. <i>Nature Genetics</i> , 2015, 47, 822-826.	21.4	384
30	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, 1163-1168.	2.8	380
31	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. <i>Lancet</i> , The, 2012, 380, 815-823.	13.7	373
32	Identification of context-dependent expression quantitative trait loci in whole blood. <i>Nature Genetics</i> , 2017, 49, 139-145.	21.4	363
33	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
34	Evidence of genetic enrichment for exceptional survival using a family approach: the Leiden Longevity Study. <i>European Journal of Human Genetics</i> , 2006, 14, 79-84.	2.8	339
35	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
36	A genomic scanning method for higher organisms using restriction sites as landmarks.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 9523-9527.	7.1	326

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37	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. <i>PLoS Genetics</i> , 2013, 9, e1003225.	3.5	323
38	The continuing value of twin studies in the omics era. <i>Nature Reviews Genetics</i> , 2012, 13, 640-653.	16.3	314
39	The impact of low-frequency and rare variants on lipid levels. <i>Nature Genetics</i> , 2015, 47, 589-597.	21.4	310
40	Genetic and environmental influences interact with age and sex in shaping the human methylome. <i>Nature Communications</i> , 2016, 7, 11115.	12.8	299
41	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.	12.8	295
42	Reduced insulin/IGF-1 signalling and human longevity. <i>Aging Cell</i> , 2005, 4, 79-85.	6.7	288
43	Variation, patterns, and temporal stability of DNA methylation: considerations for epigenetic epidemiology. <i>FASEB Journal</i> , 2010, 24, 3135-3144.	0.5	287
44	A genome-wide association study of anorexia nervosa. <i>Molecular Psychiatry</i> , 2014, 19, 1085-1094.	7.9	282
45	Telomere length predicts survival independent of genetic influences. <i>Aging Cell</i> , 2007, 6, 769-774.	6.7	271
46	Poly(ADP-ribose) polymerase activity in mononuclear leukocytes of 13 mammalian species correlates with species-specific life span.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 11759-11763.	7.1	262
47	Nonagenarian Siblings and Their Offspring Display Lower Risk of Mortality and Morbidity than Sporadic Nonagenarians: The Leiden Longevity Study. <i>Journal of the American Geriatrics Society</i> , 2009, 57, 1634-1637.	2.6	258
48	Epigenetic variation during the adult lifespan: cross-sectional and longitudinal data on monozygotic twin pairs. <i>Aging Cell</i> , 2012, 11, 694-703.	6.7	257
49	Rapid detection of human chromosome 21 aberrations by in situ hybridization.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 9664-9668.	7.1	254
50	Genome-wide association scan for five major dimensions of personality. <i>Molecular Psychiatry</i> , 2010, 15, 647-656.	7.9	250
51	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, 110-118.	3.6	250
52	A survey of the genomic distribution of alpha satellite DNA on all the human chromosomes, and derivation of a new consensus sequence. <i>Nucleic Acids Research</i> , 1991, 19, 1179-1182.	14.5	249
53	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, 686-698.	6.7	249
54	The Genome of the Netherlands: design, and project goals. <i>European Journal of Human Genetics</i> , 2014, 22, 221-227.	2.8	246

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55	Genomic organization of alpha satellite DNA on human chromosome 7: evidence for two distinct alphoid domains on a single chromosome.. <i>Molecular and Cellular Biology</i> , 1987, 7, 349-356.	2.3	227
56	Variation in plasminogen-activator-inhibitor-1 gene and risk of meningococcal septic shock. <i>Lancet</i> , The, 1999, 354, 561-563.	13.7	227
57	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, 4420-4432.	2.9	227
58	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222
59	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. <i>Science Advances</i> , 2018, 4, eaao4364.	10.3	219
60	Heritable rather than age-related environmental and stochastic factors dominate variation in DNA methylation of the human IGF2/H19 locus. <i>Human Molecular Genetics</i> , 2007, 16, 547-554.	2.9	218
61	The epigenome: Archive of the prenatal environment. <i>Epigenetics</i> , 2009, 4, 526-531.	2.7	218
62	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
63	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. <i>Nature Communications</i> , 2014, 5, 5068.	12.8	216
64	A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019, 10, 3669.	12.8	214
65	The number of p16INK4a positive cells in human skin reflects biological age. <i>Aging Cell</i> , 2012, 11, 722-725.	6.7	200
66	Nucleotide sequence heterogeneity of alpha satellite repetitive DNA: a survey of alphoid sequences from different human chromosomes. <i>Nucleic Acids Research</i> , 1987, 15, 7549-7569.	14.5	197
67	Variation in the human TP53 gene affects old age survival and cancer mortality. <i>Experimental Gerontology</i> , 2005, 40, 11-15.	2.8	196
68	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.	3.5	194
69	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. <i>Epigenetics and Chromatin</i> , 2013, 6, 26.	3.9	192
70	Identification of DIO2 as a new susceptibility locus for symptomatic osteoarthritis. <i>Human Molecular Genetics</i> , 2008, 17, 1867-1875.	2.9	190
71	Small nucleoli are a cellular hallmark of longevity. <i>Nature Communications</i> , 2017, 8, 16083.	12.8	190
72	N-glycomic biomarkers of biological aging and longevity: A link with inflammaging. <i>Ageing Research Reviews</i> , 2013, 12, 685-698.	10.9	189

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73	MARK-AGE biomarkers of ageing. <i>Mechanisms of Ageing and Development</i> , 2015, 151, 2-12.	4.6	189
74	Efficacy and toxicity of methotrexate in early rheumatoid arthritis are associated with single-nucleotide polymorphisms in genes coding for folate pathway enzymes. <i>Arthritis and Rheumatism</i> , 2006, 54, 1087-1095.	6.7	188
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.	12.8	188
76	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	28.9	188
77	A genome-wide association study on common SNPs and rare CNVs in anorexia nervosa. <i>Molecular Psychiatry</i> , 2011, 16, 949-959.	7.9	186
78	The Adult Netherlands Twin Register: Twenty-Five Years of Survey and Biological Data Collection. <i>Twin Research and Human Genetics</i> , 2013, 16, 271-281.	0.6	186
79	Large-scale analysis of association between <i>GDF5</i> and <i>FRZB</i> variants and osteoarthritis of the hip, knee, and hand. <i>Arthritis and Rheumatism</i> , 2009, 60, 1710-1721.	6.7	181
80	Genome-wide analyses identify a role for <i>SLC17A4</i> and <i>AADAT</i> in thyroid hormone regulation. <i>Nature Communications</i> , 2018, 9, 4455.	12.8	181
81	A genome-wide association study identifies an osteoarthritis susceptibility locus on chromosome 7q22. <i>Arthritis and Rheumatism</i> , 2010, 62, 499-510.	6.7	178
82	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	12.8	178
83	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. <i>Aging Cell</i> , 2013, 12, 184-193.	6.7	170
84	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
85	Infection with cytomegalovirus but not herpes simplex virus induces the accumulation of late-differentiated CD4+ and CD8+ T-cells in humans. <i>Journal of General Virology</i> , 2011, 92, 2746-2756.	2.9	162
86	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
87	Variants near <i>TERT</i> and <i>TERC</i> influencing telomere length are associated with high-grade glioma risk. <i>Nature Genetics</i> , 2014, 46, 731-735.	21.4	161
88	Lipidomics of familial longevity. <i>Aging Cell</i> , 2013, 12, 426-434.	6.7	157
89	A meta-analysis of European and Asian cohorts reveals a global role of a functional SNP in the 5' UTR of <i>GDF5</i> with osteoarthritis susceptibility. <i>Human Molecular Genetics</i> , 2008, 17, 1497-1504.	2.9	156
90	MethylAid: visual and interactive quality control of large Illumina 450k datasets. <i>Bioinformatics</i> , 2014, 30, 3435-3437.	4.1	154

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91	Blood lipids influence DNA methylation in circulating cells. <i>Genome Biology</i> , 2016, 17, 138.	8.8	154
92	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	6.2	154
93	Relative validity of the food frequency questionnaire used to assess dietary intake in the Leiden Longevity Study. <i>Nutrition Journal</i> , 2013, 12, 75.	3.4	153
94	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
95	Dynamic changes in the higher-level chromatin organization of specific sequences revealed by in situ hybridization to nuclear halos. <i>Journal of Cell Biology</i> , 1994, 126, 289-304.	5.2	150
96	Hallmark Features of Immunosenescence Are Absent in Familial Longevity. <i>Journal of Immunology</i> , 2010, 185, 4618-4624.	0.8	147
97	A whole genome association study of neuroticism using DNA pooling. <i>Molecular Psychiatry</i> , 2008, 13, 302-312.	7.9	145
98	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016, 6, 21243.	3.3	145
99	Human beta satellite DNA: genomic organization and sequence definition of a class of highly repetitive tandem DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1989, 86, 6250-6254.	7.1	143
100	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. <i>Alzheimer's and Dementia</i> , 2018, 14, 707-722.	0.8	143
101	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. <i>PLoS ONE</i> , 2014, 9, e103056.	2.5	142
102	The Netherlands Twin Register Biobank: A Resource for Genetic Epidemiological Studies. <i>Twin Research and Human Genetics</i> , 2010, 13, 231-245.	0.6	141
103	Early gestation as the critical time-window for changes in the prenatal environment to affect the adult human blood methylome. <i>International Journal of Epidemiology</i> , 2015, 44, 1211-1223.	1.9	139
104	Genome-wide association study (GWAS)-identified disease risk alleles do not compromise human longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18046-18049.	7.1	138
105	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. <i>Circulation Research</i> , 2019, 124, 1808-1820.	4.5	137
106	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. <i>Nature Genetics</i> , 2014, 46, 498-502.	21.4	136
107	Senescent human melanocytes drive skin ageing via paracrine telomere dysfunction. <i>EMBO Journal</i> , 2019, 38, e101982.	7.8	136
108	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	7.9	134

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109	Prenatal Famine and Genetic Variation Are Independently and Additively Associated with DNA Methylation at Regulatory Loci within IGF2/H19. <i>PLoS ONE</i> , 2012, 7, e37933.	2.5	132
110	High-yield noninvasive human genomic DNA isolation method for genetic studies in geographically dispersed families and populations. <i>American Journal of Human Genetics</i> , 1995, 57, 1252-4.	6.2	131
111	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. <i>Epigenetics and Chromatin</i> , 2018, 11, 25.	3.9	130
112	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 270-277.	0.9	130
113	Effects of a Web-Based Intervention on Physical Activity and Metabolism in Older Adults: Randomized Controlled Trial. <i>Journal of Medical Internet Research</i> , 2013, 15, e233.	4.3	130
114	Evidence for familial aggregation of hand, hip, and spine but not knee osteoarthritis in siblings with multiple joint involvement: the GARP study. <i>Annals of the Rheumatic Diseases</i> , 2004, 64, 438-443.	0.9	129
115	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. <i>Biological Psychiatry</i> , 2020, 87, 409-418.	1.3	129
116	Heritabilities of radiologic osteoarthritis in peripheral joints and of disc degeneration of the spine. <i>Arthritis and Rheumatism</i> , 1999, 42, 1729-1735.	6.7	127
117	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 349-355.	0.9	126
118	DNA methylation of <i>IGF2</i> , <i>GNASAS</i> , <i>INSIGF</i> and <i>LEP</i> and being born small for gestational age. <i>Epigenetics</i> , 2011, 6, 171-176.	2.7	126
119	Genome-wide Association Study of Smoking Initiation and Current Smoking. <i>American Journal of Human Genetics</i> , 2009, 84, 367-379.	6.2	125
120	Gene Variants in the Novel Type 2 Diabetes Loci <i>CDC123/CAMK1D</i> , <i>THADA</i> , <i>ADAMTS9</i> , <i>BCL11A</i> , and <i>MTNR1B</i> Affect Different Aspects of Pancreatic $\beta$ -Cell Function. <i>Diabetes</i> , 2010, 59, 293-301.	0.6	125
121	Detection of restriction fragment length polymorphisms at the centromeres of human chromosomes by using chromosome-specific alpha satellite DNA probes: implications for development of centromere-based genetic linkage maps.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> . 1986. 83, 5611-5615.	7.1	123
122	Subclass-specific IgG glycosylation is associated with markers of inflammation and metabolic health. <i>Scientific Reports</i> , 2017, 7, 12325.	3.3	123
123	Association between leptin, adiponectin and resistin and long-term progression of hand osteoarthritis. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 1282-1284.	0.9	120
124	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. <i>Genome Biology</i> , 2016, 17, 191.	8.8	120
125	Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 864-867.	0.9	119
126	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. <i>Diabetologia</i> , 2013, 56, 298-310.	6.3	119



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127	Association of the frizzled-related protein gene with symptomatic osteoarthritis at multiple sites. <i>Arthritis and Rheumatism</i> , 2005, 52, 1077-1080.	6.7	118
128	VDR gene variants associate with cognitive function and depressive symptoms in old age. <i>Neurobiology of Aging</i> , 2009, 30, 466-473.	3.1	118
129	Novel genetic variants associated with lumbar disc degeneration in northern Europeans: a meta-analysis of 4600 subjects. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 1141-1148.	0.9	118
130	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
131	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.2	118
132	A Meta-analysis of Four Genome-Wide Association Studies of Survival to Age 90 Years or Older: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010, 65A, 478-487.	3.6	117
133	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.	0.7	117
134	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	6.2	116
135	Quantitative comparison of mRNA levels in mammalian tissues: 28S ribosomal RNA level as an accurate internal control. <i>Nucleic Acids Research</i> , 1989, 17, 10137-10138.	14.5	115
136	Mental Performance in Old Age Dependent on Cortisol and Genetic Variance in the Mineralocorticoid and Glucocorticoid Receptors. <i>Neuropsychopharmacology</i> , 2007, 32, 1295-1301.	5.4	115
137	Characteristics of de novo structural changes in the human genome. <i>Genome Research</i> , 2015, 25, 792-801.	5.5	115
138	Familial Longevity Is Associated with Decreased Thyroid Function. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 4979-4984.	3.6	112
139	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 427-436.	0.9	112
140	Metabolic biomarker profiling for identification of susceptibility to severe pneumonia and COVID-19 in the general population. <i>ELife</i> , 2021, 10, .	6.0	112
141	Heritabilities of Apolipoprotein and Lipid Levels in Three Countries. <i>Twin Research and Human Genetics</i> , 2002, 5, 87-97.	1.0	111
142	A Genomewide Scan for Intelligence Identifies Quantitative Trait Loci on 2q and 6p. <i>American Journal of Human Genetics</i> , 2005, 77, 318-326.	6.2	110
143	What evidence is there for the existence of individual genes with antagonistic pleiotropic effects?. <i>Mechanisms of Ageing and Development</i> , 2005, 126, 421-429.	4.6	109
144	Assessment of Osteoarthritis Candidate Genes in a Meta-analysis of Nine Genome-wide Association Studies. <i>Arthritis and Rheumatology</i> , 2014, 66, 940-949.	5.6	108

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145	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2130-2136.	0.9	108
146	Reduced Response to Activated Protein C Is Associated with Increased Risk for Cerebrovascular Disease. <i>Annals of Internal Medicine</i> , 1996, 125, 265.	3.9	107
147	Genes encoding longevity: from model organisms to humans. <i>Aging Cell</i> , 2008, 7, 270-280.	6.7	107
148	A gene variant near ATM is significantly associated with metformin treatment response in type 2 diabetes: a replication and meta-analysis of five cohorts. <i>Diabetologia</i> , 2012, 55, 1971-1977.	6.3	107
149	ApoE Plasma Levels and Risk of Cardiovascular Mortality in Old Age. <i>PLoS Medicine</i> , 2006, 3, e176.	8.4	107
150	Familial longevity is marked by enhanced insulin sensitivity. <i>Aging Cell</i> , 2011, 10, 114-121.	6.7	106
151	Associations between age and gray matter volume in anatomical brain networks in middle-aged to older adults. <i>Aging Cell</i> , 2014, 13, 1068-1074.	6.7	106
152	A common variant of the methylenetetrahydrofolate reductase gene (1p36) is associated with an increased risk of cancer. <i>Cancer Research</i> , 2003, 63, 1249-53.	0.9	106
153	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, 235-249.	3.0	105
154	Decreased Levels of Bisecting GlcNAc Glycoforms of IgG Are Associated with Human Longevity. <i>PLoS ONE</i> , 2010, 5, e12566.	2.5	104
155	Gene expression analysis of mTOR pathway: association with human longevity. <i>Aging Cell</i> , 2013, 12, 24-31.	6.7	104
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599	Hematopoietic Capacity and Exceptional Survival: The Leiden Longevity Study. <i>Journal of the American Geriatrics Society</i> , 2008, 56, 2009-2013.	2.6	3
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