P Eline Slagboom

List of Publications by Year
in descending order

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624	67,118	905 116	1314 224
papers	citations	h-index	g-index

663	663	663	68190
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Cytogenetic analysis using quantitative, high-sensitivity, fluorescence hybridization.. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 2934-2938.	3.3	3,003
3	Persistent epigenetic differences associated with prenatal exposure to famine in humans. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17046-17049.	3.3	2,683
4	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
5	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
6	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
7	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	9.4	1,100
8	DNA methylation differences after exposure to prenatal famine are common and timing- and sex-specific. Human Molecular Genetics, 2009, 18, 4046-4053.	1.4	1,042
9	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	9.4	808
10	Facing up to the global challenges of ageing. Nature, 2018, 561, 45-56.	13.7	760
11	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	13.7	743
12	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
13	L1 drives IFN in senescent cells and promotes age-associated inflammation. Nature, 2019, 566, 73-78.	13.7	701
14	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	9.4	641
15	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	9.4	641
16	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	9.4	590
17	Telomere length and replicative aging in human vascular tissues.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 11190-11194.	3.3	587
18	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	5.8	576

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19	Genetic determination of telomere size in humans: a twin study of three age groups. American Journal of Human Genetics, 1994, 55, 876-82.	2.6	572
20	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	5.8	533
21	DNA methylation signatures link prenatal famine exposure to growth and metabolism. Nature Communications, 2014, 5, 5592.	5.8	494
22	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	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. Clinical Nutrition, 2011, 30, 610-615.	2.3	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. PLoS Genetics, 2012, 8, e1002607.	1.5	419
25	Periconceptional Maternal Folic Acid Use of 400 Âµg per Day Is Related to Increased Methylation of the IGF2 Gene in the Very Young Child. PLoS ONE, 2009, 4, e7845.	1.1	410
26	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	4.0	410
27	Human naive and memory T lymphocytes differ in telomeric length and replicative potential.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 11091-11094.	3.3	394
28	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	9.4	390
29	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	9.4	384
30	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	1.4	380
31	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	6.3	373
32	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	9.4	363
33	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
34	Evidence of genetic enrichment for exceptional survival using a family approach: the Leiden Longevity Study. European Journal of Human Genetics, 2006, 14, 79-84.	1.4	339
35	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
36	A genomic scanning method for higher organisms using restriction sites as landmarks.. Proceedings of the National Academy of Sciences of the United States of America, 1991, 88, 9523-9527.	3.3	326

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37	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. PLoS Genetics, 2013, 9, e1003225.	1.5	323
38	The continuing value of twin studies in the omics era. Nature Reviews Genetics, 2012, 13, 640-653.	7.7	314
39	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
40	Genetic and environmental influences interact with age and sex in shaping the human methylome. Nature Communications, 2016, 7, 11115.	5.8	299
41	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	5.8	295
42	Reduced insulin/IGF-1 signalling and human longevity. Aging Cell, 2005, 4, 79-85.	3.0	288
43	Variation, patterns, and temporal stability of DNA methylation: considerations for epigenetic epidemiology. FASEB Journal, 2010, 24, 3135-3144.	0.2	287
44	A genome-wide association study of anorexia nervosa. Molecular Psychiatry, 2014, 19, 1085-1094.	4.1	282
45	Telomere length predicts survival independent of genetic influences. Aging Cell, 2007, 6, 769-774.	3.0	271
46	Poly(ADP-ribose) polymerase activity in mononuclear leukocytes of 13 mammalian species correlates with species-specific life span.. Proceedings of the National Academy of Sciences of the United States of America, 1992, 89, 11759-11763.	3.3	262
47	Nonagenarian Siblings and Their Offspring Display Lower Risk of Mortality and Morbidity than Sporadic Nonagenarians: The Leiden Longevity Study. Journal of the American Geriatrics Society, 2009, 57, 1634-1637.	1.3	258
48	Epigenetic variation during the adult lifespan: crossâ€sectional and longitudinal data on monozygotic twin pairs. Aging Cell, 2012, 11, 694-703.	3.0	257
49	Rapid detection of human chromosome 21 aberrations by in situ hybridization.. Proceedings of the National Academy of Sciences of the United States of America, 1988, 85, 9664-9668.	3.3	254
50	Genome-wide association scan for five major dimensions of personality. Molecular Psychiatry, 2010, 15, 647-656.	4.1	250
51	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	1.7	250
52	A survey of the genomic distribution of alpha satellite DNA on all the human chromosomes, and derivation of a new consensus sequence. Nucleic Acids Research, 1991, 19, 1179-1182.	6.5	249
53	Genomeâ€wide association study identifies a single major locus contributing to survival into old age; the APOE locus revisited. Aging Cell, 2011, 10, 686-698.	3.0	249
54	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	1.4	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.. Molecular and Cellular Biology, 1987, 7, 349-356.	1.1	227
56	Variation in plasminogen-activator-inhibitor-1 gene and risk of meningococcal septic shock. Lancet, The, 1999, 354, 561-563.	6.3	227
57	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
58	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	2.6	222
59	DNA methylation as a mediator of the association between prenatal adversity and risk factors for metabolic disease in adulthood. Science Advances, 2018, 4, eaao4364.	4.7	219
60	Heritable rather than age-related environmental and stochastic factors dominate variation in DNA methylation of the human IGF2/H19 locus. Human Molecular Genetics, 2007, 16, 547-554.	1.4	218
61	The epigenome: Archive of the prenatal environment. Epigenetics, 2009, 4, 526-531.	1.3	218
62	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218
63	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	5.8	216
64	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	5.8	214
65	The number of p16INK4a positive cells in human skin reflects biological age. Aging Cell, 2012, 11, 722-725.	3.0	200
66	Nucleotide sequence heterogeneity of alpha satellite repetitive DNA: a survey of alphoid sequences from different human chromosomes. Nucleic Acids Research, 1987, 15, 7549-7569.	6.5	197
67	Variation in the human TP53 gene affects old age survival and cancer mortality. Experimental Gerontology, 2005, 40, 11-15.	1.2	196
68	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	1.5	194
69	Identification and systematic annotation of tissue-specific differentially methylated regions using the Illumina 450k array. Epigenetics and Chromatin, 2013, 6, 26.	1.8	192
70	Identification of DIO2 as a new susceptibility locus for symptomatic osteoarthritis. Human Molecular Genetics, 2008, 17, 1867-1875.	1.4	190
71	Small nucleoli are a cellular hallmark of longevity. Nature Communications, 2017, 8, 16083.	5.8	190
72	N-glycomic biomarkers of biological aging and longevity: A link with inflammaging. Ageing Research Reviews, 2013, 12, 685-698.	5.0	189

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73	MARK-AGE biomarkers of ageing. Mechanisms of Ageing and Development, 2015, 151, 2-12.	2.2	189
74	Efficacy and toxicity of methotrexate in early rheumatoid arthritis are associated with single-nucleotide polymorphisms in genes coding for folate pathway enzymes. Arthritis and Rheumatism, 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. Nature Communications, 2019, 10, 3346.	5.8	188
76	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
77	A genome-wide association study on common SNPs and rare CNVs in anorexia nervosa. Molecular Psychiatry, 2011, 16, 949-959.	4.1	186
78	The Adult Netherlands Twin Register: Twenty-Five Years of Survey and Biological Data Collection. Twin Research and Human Genetics, 2013, 16, 271-281.	0.3	186
79	Largeâ€scale analysis of association between GDF5 and FRZB variants and osteoarthritis of the hip, knee, and hand. Arthritis and Rheumatism, 2009, 60, 1710-1721.	6.7	181
80	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	5.8	181
81	A genomeâ€wide association study identifies an osteoarthritis susceptibility locus on chromosome 7q22. Arthritis and Rheumatism, 2010, 62, 499-510.	6.7	178
82	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	5.8	178
83	Genomeâ€wide linkage analysis for human longevity: Genetics of Healthy Aging Study. Aging Cell, 2013, 12, 184-193.	3.0	170
84	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
85	Infection with cytomegalovirus but not herpes simplex virus induces the accumulation of late-differentiated CD4+ and CD8+ T-cells in humans. Journal of General Virology, 2011, 92, 2746-2756.	1.3	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 TERT and TERC influencing telomere length are associated with high-grade glioma risk. Nature Genetics, 2014, 46, 731-735.	9.4	161
88	Lipidomics of familial longevity. Aging Cell, 2013, 12, 426-434.	3.0	157
89	A meta-analysis of European and Asian cohorts reveals a global role of a functional SNP in the 5' UTR of GDF5 with osteoarthritis susceptibility. Human Molecular Genetics, 2008, 17, 1497-1504.	1.4	156
90	MethylAid: visual and interactive quality control of large Illumina 450k datasets. Bioinformatics, 2014, 30, 3435-3437.	1.8	154

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91	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	3.8	154
92	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
93	Relative validity of the food frequency questionnaire used to assess dietary intake in the Leiden Longevity Study. Nutrition Journal, 2013, 12, 75.	1.5	153
94	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
95	Dynamic changes in the higher-level chromatin organization of specific sequences revealed by in situ hybridization to nuclear halos.. Journal of Cell Biology, 1994, 126, 289-304.	2.3	150
96	Hallmark Features of Immunosenescence Are Absent in Familial Longevity. Journal of Immunology, 2010, 185, 4618-4624.	0.4	147
97	A whole genome association study of neuroticism using DNA pooling. Molecular Psychiatry, 2008, 13, 302-312.	4.1	145
98	Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243.	1.6	145
99	Human beta satellite DNA: genomic organization and sequence definition of a class of highly repetitive tandem DNA.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 6250-6254.	3.3	143
100	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.4	143
101	Genes Involved in the Osteoarthritis Process Identified through Genome Wide Expression Analysis in Articular Cartilage; the RAAK Study. PLoS ONE, 2014, 9, e103056.	1.1	142
102	The Netherlands Twin Register Biobank: A Resource for Genetic Epidemiological Studies. Twin Research and Human Genetics, 2010, 13, 231-245.	0.3	141
103	Early gestation as the critical time-window for changes in the prenatal environment to affect the adult human blood methylome. International Journal of Epidemiology, 2015, 44, 1211-1223.	0.9	139
104	Genome-wide association study (GWAS)-identified disease risk alleles do not compromise human longevity. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 18046-18049.	3.3	138
105	Gut Microbial Associations to Plasma Metabolites Linked to Cardiovascular Phenotypes and Risk. Circulation Research, 2019, 124, 1808-1820.	2.0	137
106	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. Nature Genetics, 2014, 46, 498-502.	9.4	136
107	Senescent human melanocytes drive skin ageing via paracrine telomere dysfunction. EMBO Journal, 2019, 38, e101982.	3.5	136
108	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	4.1	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. PLoS ONE, 2012, 7, e37933.	1.1	132
110	High-yield noninvasive human genomic DNA isolation method for genetic studies in geographically dispersed families and populations. American Journal of Human Genetics, 1995, 57, 1252-4.	2.6	131
111	Age-related DNA methylation changes are tissue-specific with ELOVL2 promoter methylation as exception. Epigenetics and Chromatin, 2018, 11, 25.	1.8	130
112	RNA sequencing data integration reveals an miRNA interactome of osteoarthritis cartilage. Annals of the Rheumatic Diseases, 2019, 78, 270-277.	0.5	130
113	Effects of a Web-Based Intervention on Physical Activity and Metabolism in Older Adults: Randomized Controlled Trial. Journal of Medical Internet Research, 2013, 15, e233.	2.1	130
114	Evidence for familial aggregation of hand, hip, and spine but not knee osteoarthritis in siblings with multiple joint involvement: the GARP study. Annals of the Rheumatic Diseases, 2004, 64, 438-443.	0.5	129
115	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. Biological Psychiatry, 2020, 87, 409-418.	0.7	129
116	Heritabilities of radiologic osteoarthritis in peripheral joints and of disc degeneration of the spine. Arthritis and Rheumatism, 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. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.5	126
118	DNA methylation ofIGF2,GNASAS,INSIGFandLEPand being born small for gestational age. Epigenetics, 2011, 6, 171-176.	1.3	126
119	Genome-wide Association Study of Smoking Initiation and Current Smoking. American Journal of Human Genetics, 2009, 84, 367-379.	2.6	125
120	Gene Variants in the Novel Type 2 Diabetes Loci CDC123/CAMK1D, THADA, ADAMTS9, BCL11A, and MTNR1B Affect Different Aspects of Pancreatic Î²-Cell Function. Diabetes, 2010, 59, 293-301.	0.3	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.. Proceedings of the National Academy of Sciences of the United States of America, 1986, 83, 5611-5615.	3.3	123
122	Subclass-specific IgG glycosylation is associated with markers of inflammation and metabolic health. Scientific Reports, 2017, 7, 12325.	1.6	123
123	Association between leptin, adiponectin and resistin and long-term progression of hand osteoarthritis. Annals of the Rheumatic Diseases, 2011, 70, 1282-1284.	0.5	120
124	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	3.8	120
125	Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. Annals of the Rheumatic Diseases, 2011, 70, 864-867.	0.5	119
126	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. Diabetologia, 2013, 56, 298-310.	2.9	119

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127	Association of the frizzled-related protein gene with symptomatic osteoarthritis at multiple sites. Arthritis and Rheumatism, 2005, 52, 1077-1080.	6.7	118
128	VDR gene variants associate with cognitive function and depressive symptoms in old age. Neurobiology of Aging, 2009, 30, 466-473.	1.5	118
129	Novel genetic variants associated with lumbar disc degeneration in northern Europeans: a meta-analysis of 4600 subjects. Annals of the Rheumatic Diseases, 2013, 72, 1141-1148.	0.5	118
130	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	5.8	118
131	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	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. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2010, 65A, 478-487.	1.7	117
133	A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots. Journal of Investigative Dermatology, 2015, 135, 1735-1742.	0.3	117
134	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
135	Quantitative comparison of mRNA levels in mammalian tissues: 28S ribosomal RNA level as an accurate internal control. Nucleic Acids Research, 1989, 17, 10137-10138.	6.5	115
136	Mental Performance in Old Age Dependent on Cortisol and Genetic Variance in the Mineralocorticoid and Glucocorticoid Receptors. Neuropsychopharmacology, 2007, 32, 1295-1301.	2.8	115
137	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	2.4	115
138	Familial Longevity Is Associated with Decreased Thyroid Function. Journal of Clinical Endocrinology and Metabolism, 2010, 95, 4979-4984.	1.8	112
139	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. Annals of the Rheumatic Diseases, 2013, 72, 427-436.	0.5	112
140	Metabolic biomarker profiling for identification of susceptibility to severe pneumonia and COVID-19 in the general population. ELife, 2021, 10, .	2.8	112
141	Heritabilities of Apolipoprotein and Lipid Levels in Three Countries. Twin Research and Human Genetics, 2002, 5, 87-97.	1.3	111
142	A Genomewide Scan for Intelligence Identifies Quantitative Trait Loci on 2q and 6p. American Journal of Human Genetics, 2005, 77, 318-326.	2.6	110
143	What evidence is there for the existence of individual genes with antagonistic pleiotropic effects?. Mechanisms of Ageing and Development, 2005, 126, 421-429.	2.2	109
144	Assessment of Osteoarthritis Candidate Genes in a Metaâ€Analysis of Nine Genomeâ€Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949.	2.9	108

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145	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.5	108
146	Reduced Response to Activated Protein C Is Associated with Increased Risk for Cerebrovascular Disease. Annals of Internal Medicine, 1996, 125, 265.	2.0	107
147	Genes encoding longevity: from model organisms to humans. Aging Cell, 2008, 7, 270-280.	3.0	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. Diabetologia, 2012, 55, 1971-1977.	2.9	107
149	ApoE Plasma Levels and Risk of Cardiovascular Mortality in Old Age. PLoS Medicine, 2006, 3, e176.	3.9	107
150	Familial longevity is marked by enhanced insulin sensitivity. Aging Cell, 2011, 10, 114-121.	3.0	106
151	Associations between age and gray matter volume in anatomical brain networks in middleâ€aged to older adults. Aging Cell, 2014, 13, 1068-1074.	3.0	106
152	A common variant of the methylenetetrahydrofolate reductase gene (1p36) is associated with an increased risk of cancer. Cancer Research, 2003, 63, 1249-53.	0.4	106
153	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. Age, 2013, 35, 235-249.	3.0	105
154	Decreased Levels of Bisecting GlcNAc Glycoforms of IgG Are Associated with Human Longevity. PLoS ONE, 2010, 5, e12566.	1.1	104
155	Gene expression analysis of <scp>mTOR</scp> pathway: association with human longevity. Aging Cell, 2013, 12, 24-31.	3.0	104
156	Homologous subfamilies of human alphoid repetitive DNA on different nucleolus organizing chromosomes.. Proceedings of the National Academy of Sciences of the United States of America, 1987, 84, 1075-1079.	3.3	103
157	Netherlands twin family study of anxious depression (NETSAD). Twin Research and Human Genetics, 2000, 3, 323-334.	1.3	103
158	Haplotypes in the human Foxo1a and Foxo3a genes; impact on disease and mortality at old age. European Journal of Human Genetics, 2007, 15, 294-301.	1.4	103
159	Latent Infection with Cytomegalovirus Is Associated with Poor Memory CD4 Responses to Influenza A Core Proteins in the Elderly. Journal of Immunology, 2014, 193, 3624-3631.	0.4	103
160	Negative selection in humans and fruit flies involves synergistic epistasis. Science, 2017, 356, 539-542.	6.0	103
161	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	5.8	99
162	Association of the interleukin-1 gene cluster with radiographic signs of osteoarthritis of the hip. Arthritis and Rheumatism, 2004, 50, 1179-1186.	6.7	98

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163	Homologous alpha satellite sequences on human acrocentric chromosomes with selectivity for chromosomes 13, 14 and 21: implications for recombination between nonhomologues and Robertsonian translocations. Nucleic Acids Research, 1988, 16, 1273-1284.	6.5	96
164	Duration of breastfeeding and gender are associated with methylation of the LEPTIN gene in very young children. Pediatric Research, 2013, 74, 344-349.	1.1	96
165	The CTRB1/2 Locus Affects Diabetes Susceptibility and Treatment via the Incretin Pathway. Diabetes, 2013, 62, 3275-3281.	0.3	96
166	Knee and hip articular cartilage have distinct epigenomic landscapes: implications for future cartilage regeneration approaches. Annals of the Rheumatic Diseases, 2014, 73, 2208-2212.	0.5	96
167	Leukocyte telomere length associates with prospective mortality independent of immune-related parameters and known genetic markers. International Journal of Epidemiology, 2014, 43, 878-886.	0.9	95
168	Urinary CTX-II levels are associated with radiographic subtypes of osteoarthritis in hip, knee, hand, and facet joints in subject with familial osteoarthritis at multiple sites: the GARP study. Annals of the Rheumatic Diseases, 2006, 65, 360-365.	0.5	94
169	Zygosity diagnosis in young twins by parental report. Twin Research and Human Genetics, 2000, 3, 134-141.	1.3	94
170	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	15.2	93
171	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	1.4	92
172	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
173	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
174	Plasma protein N-glycan profiles are associated with calendar age, familial longevity and health. Journal of Proteome Research, 2011, 10, 1667-1674.	1.8	87
175	A nonsynonymous mutation in PLCG2 reduces the risk of Alzheimerâ€™s disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. Acta Neuropathologica, 2019, 138, 237-250.	3.9	87
176	Longer genotypically-estimated leukocyte telomere length is associated with increased adult glioma risk. Oncotarget, 2015, 6, 42468-42477.	0.8	87
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