Kathryn L Lunetta

List of Publications by Year
in descending order

264	36,294	5268	4117
papers	citations	83 h-index	175 g-index

292	292	292	40813
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Midlife lipid and glucose levels are associated with Alzheimer's disease. Alzheimer's and Dementia, 2023, 19, 181-193.	0.8	23
2	Genomeâ€wide association and multiâ€omics studies identify MGMT as a novel risk gene for Alzheimer's disease among women. Alzheimer's and Dementia, 2023, 19, 896-908.	0.8	19
3	Genome-wide analysis of mitochondrial DNA copy number reveals loci implicated in nucleotide metabolism, platelet activation, and megakaryocyte proliferation. Human Genetics, 2022, 141, 127-146.	3.8	30
4	Protein phosphatase 2A and complement component 4 are linked to the protective effect of APOE É2 for Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 2042-2054.	0.8	18
5	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	21.4	68
6	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
7	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
8	Cross-Sectional Association Between Blood Cell Phenotypes, Cognitive Function, and Brain Imaging Measures in the Community-Based Framingham Heart Study. Journal of Alzheimer's Disease, 2022, 87, 1291-1305.	2.6	1
9	Manifestations of Alzheimerâ€™s disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90. Scientific Reports, 2022, 12, 6117.	3.3	12
10	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. Human Molecular Genetics, 2022, 31, 3133-3143.	2.9	11
11	Alzheimerâ€™s disease associated AKAP9 I2558M mutation alters posttranslational modification and interactome of tau and cellular functions in CRISPRâ€edited human neuronal cells. Aging Cell, 2022, 21, e13617.	6.7	7
12	Resting heart rate and incident atrial fibrillation: A stratified Mendelian randomization in the AFGen consortium. PLoS ONE, 2022, 17, e0268768.	2.5	8
13	LMNA Variants and Risk of Adult-Onset Cardiac Disease. Journal of the American College of Cardiology, 2022, 80, 50-59.	2.8	14
14	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
15	Genetic variants in anti-MÃ¼llerian hormone-related genes and breast cancer risk: results from the AMBER consortium. Breast Cancer Research and Treatment, 2021, 185, 469-478.	2.5	1
16	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. Nature Communications, 2021, 12, 654.	12.8	75
17	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
18	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. Journal of the National Cancer Institute, 2021, 113, 1168-1176.	6.3	41

#	Article	IF	Citations
19	Set-Based Rare Variant Expression Quantitative Trait Loci in Blood and Brain from Alzheimer Disease Study Participants. Genes, 2021, 12, 419.	2.4	6
20	Cell-type-specific expression quantitative trait loci associated with Alzheimer disease in blood and brain tissue. Translational Psychiatry, 2021, 11, 250.	4.8	29
21	Large trans-ethnic meta-analysis identifies AKR1C4 as a novel gene associated with age at menarche. Human Reproduction, 2021, 36, 1999-2010.	0.9	10
22	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
23	Association of mitochondrial variants and haplogroups identified by whole exome sequencing with Alzheimer's disease. Alzheimer's and Dementia, 2021, , .	0.8	9
24	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	12.8	24
25	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	3.6	7
26	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	2.5	4
27	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
28	Predictive Accuracy of a Clinical and Genetic Risk Model for Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, e003355.	3.6	13
29	Integrative brain transcriptome analysis links complement component 4 and HSPA2 to the APOE Îµ2 protective effect in Alzheimer disease. Molecular Psychiatry, 2021, 26, 6054-6064.	7.9	27
30	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021, 144, 1899-1911.	1.6	35
31	Alzheimerâ€™s disease associated AKAP 9 I2558M mutation alters posttranslational modification and interactome of tau and cellular functions in CRISPRâ€edited human neuronal cells. Alzheimer's and Dementia, 2021, 17, e058592.	0.8	0
32	Genome-wide association and multi-omics studies identify MGMT as a novel risk gene for Alzheimer disease among women.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e054483.	0.8	0
33	Extended Rank Tests for Analyzing Recurrent Event Data. Statistics in Biopharmaceutical Research, 2020, 12, 90-98.	0.8	0
34	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191
35	Monogenic and Polygenic Contributions to Atrial Fibrillation Risk. Circulation Research, 2020, 126, 200-209.	4.5	79
36	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. Circulation Research, 2020, 126, 350-360.	4.5	41

#	Article	IF	Citations
37	A comparison of genetic imputation methods using Long Life Family Study genotypes and sequence data with the 1000 Genome reference panel. International Journal of Bioinformatics Research and Applications, 2020, 16, 59.	0.2	0
38	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
39	Mechanism for the protective effect of APOE Îµ2 against Alzheimer disease is linked to tau and the classical complement pathway. Alzheimer's and Dementia, 2020, 16, e044881.	0.8	0
40	Earlyâ€mid adulthood measures of HDL, triglycerides and fasting glucose are associated with lateâ€onset Alzheimer disease. Alzheimer's and Dementia, 2020, 16, e046125.	0.8	2
41	Genomeâ€wide interaction study of smoking in Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e046149.	0.8	0
42	Genome wide association study of chronic traumatic encephalopathy. Alzheimer's and Dementia, 2020, 16, e046505.	0.8	0
43	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
44	Gene discovery for high-density lipoprotein cholesterol level change over time in prospective family studies. Atherosclerosis, 2020, 297, 102-110.	0.8	9
45	Genome-Wide Association Study of Opioid Cessation. Journal of Clinical Medicine, 2020, 9, 180.	2.4	17
46	Exceptionally low likelihood of Alzheimerâ€™s dementia in APOE2 homozygotes from a 5,000-person neuropathological study. Nature Communications, 2020, 11, 667.	12.8	246
47	Abstract 2320: Evaluating a polygenic risk score for breast cancer in women of African ancestry. , 2020, , .		1
48	Abstract 4613: Cross-ancestry genome-wide association study identifies six new loci for breast cancer in women of African and european ancestry. , 2020, , .		1
49	Identifying factors associated with opioid cessation in a biracial sample using machine learning. , 2020, 1, 27-41.		1
50	Cross-Sectional Association of Frailty and Arterial Stiffness in Community-Dwelling Older Adults: The Framingham Heart Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 373-379.	3.6	51
51	Whole Blood Gene Expression Associated With Clinical Biological Age. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2019, 74, 81-88.	3.6	19
52	Correction for multiple testing in candidate-gene methylation studies. Epigenomics, 2019, 11, 1089-1105.	2.1	6
53	Refining the Association Between Body Mass Index and Atrial Fibrillation: Gâ€Formula and Restricted Mean Survival Times. Journal of the American Heart Association, 2019, 8, e013011.	3.7	12
54	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214

#	Article	IF	Citations
55	APOE Promoter Polymorphism-219T/G is an Effect Modifier of the Influence of APOE Îµ4 on Alzheimerâ€™s Disease Risk in a Multiracial Sample. Journal of Clinical Medicine, 2019, 8, 1236.	2.4	40
56	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. JAMA Neurology, 2019, 76, 1099.	9.0	32
57	CpGâ€related SNPs in the MS4A region have a doseâ€dependent effect on risk of lateâ€“onset Alzheimer disease. Aging Cell, 2019, 18, e12964.	6.7	8
58	Healthy diet is associated with gene expression in blood: the Framingham Heart Study. American Journal of Clinical Nutrition, 2019, 110, 742-749.	4.7	11
59	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
60	Association of Rare Coding Mutations With Alzheimer Disease and Other Dementias Among Adults of European Ancestry. JAMA Network Open, 2019, 2, e191350.	5.9	58
61	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
62	O3â€13â€01: HIGHLY PENETRANT LATEâ€ONSET ALZHEIMER DISEASE VARIANTS IN NOTCH3 IN ASHKENAZI JEWS. Alzheimer's and Dementia, 2019, 15, P918.	0.8	0
63	Genetic associations with age of menopause in familial longevity. Menopause, 2019, 26, 1204-1212.	2.0	17
64	A rare missense variant of CASP7 is associated with familial lateâ€onset Alzheimer's disease. Alzheimer's and Dementia, 2019, 15, 441-452.	0.8	39
65	Comparison of On-Site Versus Remote Mobile Device Support in the Framingham Heart Study Using the Health eHeart Study for Digital Follow-up: Randomized Pilot Study Set Within an Observational Study Design. JMIR MHealth and UHealth, 2019, 7, e13238.	3.7	16
66	Genetic Variation in Genes Underlying Diverse Dementias May Explain a Small Proportion of Cases in the Alzheimerâ€™s Disease Sequencing Project. Dementia and Geriatric Cognitive Disorders, 2018, 45, 1-17.	1.5	22
67	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
68	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	12.8	151
69	Genetic Variants in Immune-Related Pathways and Breast Cancer Risk in African American Women in the AMBER Consortium. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 321-330.	2.5	16
70	Genomeâ€wide association study of Alzheimer's disease endophenotypes at prediagnosis stages. Alzheimer's and Dementia, 2018, 14, 623-633.	0.8	64
71	Lifetime risk of atrial fibrillation according to optimal, borderline, or elevated levels of risk factors: cohort study based on longitudinal data from the Framingham Heart Study. BMJ: British Medical Journal, 2018, 361, k1453.	2.3	232
72	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 991-1004.	3.6	60

#	Article	IF	Citations
73	Tau Phosphorylation is Impacted by Rare AKAP9 Mutations Associated with Alzheimer Disease in African Americans. Journal of NeuroImmune Pharmacology, 2018, 13, 254-264.	4.1	19
74	Genetic variants associated with earlier age at menopause increase the risk of cardiovascular events in women. Menopause, 2018, 25, 451-457.	2.0	22
75	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. Circulation, 2018, 137, 1027-1038.	1.6	196
76	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	7.4	144
77	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2018, 10, 22.	6.2	27
78	Targeted Sequencing of Alzheimer Disease Genes in African Americans Implicates Novel Risk Variants. Frontiers in Neuroscience, 2018, 12, 592.	2.8	24
79	A survey of microRNA single nucleotide polymorphisms identifies novel breast cancer susceptibility loci in a case-control, population-based study of African-American women. Breast Cancer Research, 2018, 20, 45.	5.0	15
80	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
81	Genetic ancestry and population differences in levels of inflammatory cytokines in women: Role for evolutionary selection and environmental factors. PLoS Genetics, 2018, 14, e1007368.	3.5	47
82	Measures of Biologic Age in a Community Sample Predict Mortality and Age-Related Disease: The Framingham Offspring Study. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2018, 73, 757-762.	3.6	59
83	Genome-wide Association Study of Parental Life Span. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2017, 72, glw206.	3.6	6
84	Methylome-wide Association Study of Atrial Fibrillation in Framingham Heart Study. Scientific Reports, 2017, 7, 40377.	3.3	48
85	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.8	166
86	Demographic, lifestyle, and genetic determinants of circulating concentrations of 25-hydroxyvitamin D and vitamin Dâ€“binding protein in African American and European American women,. American Journal of Clinical Nutrition, 2017, 105, 1362-1371.	4.7	36
87	Alcohol Intake and Breast Cancer Risk in African American Women from the AMBER Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 787-794.	2.5	19
88	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
89	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
90	Crossâ€sectional relations of wholeâ€blood mi<scp>RNA</scp> expression levels and hand grip strength in a community sample. Aging Cell, 2017, 16, 888-894.	6.7	13

#	Article	IF	Citations
91	Characterizing Genetic Susceptibility to Breast Cancer in Women of African Ancestry. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1016-1026.	2.5	24
92	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
93	Genetic Obesity and the Risk of Atrial Fibrillation. Circulation, 2017, 135, 741-754.	1.6	96
94	Diminished PRRX1 Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	33
95	Genetic Interactions with Age, Sex, Body Mass Index, and Hypertension in Relation to Atrial Fibrillation: The AFGen Consortium. Scientific Reports, 2017, 7, 11303.	3.3	15
96	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
97	[O2â€“08â€“04]: NOVEL GENETIC VARIANTS ASSOCIATED WITH FAMILIAL LATEâ€ONSET ALZHEIMER DISEASE IN THE ALZHEIMER's DISEASE SEQUENCING PROJECT. Alzheimer's and Dementia, 2017, 13, P572.	0.8	0
98	Association Between Leukocyte Telomere Length and the Risk of Incident Atrial Fibrillation: The Framingham Heart Study. Journal of the American Heart Association, 2017, 6, .	3.7	14
99	A functionally significant SNP in TP53 and breast cancer risk in African-American women. Npj Breast Cancer, 2017, 3, 5.	5.2	44
100	Evaluation of logistic regression models and effect of covariates for caseâ€“control study in RNA-Seq analysis. BMC Bioinformatics, 2017, 18, 91.	2.6	21
101	Cardiovascular risk factors among women with self-reported infertility. Fertility Research and Practice, 2017, 3, 7.	4.2	49
102	Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2017, 13, 119-129.	0.8	87
103	Genetic Risk Prediction of Atrial Fibrillation. Circulation, 2017, 135, 1311-1320.	1.6	87
104	Heritability of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	72
105	A novel TCF7L2 type 2 diabetes SNP identified from fine mapping in African American women. PLoS ONE, 2017, 12, e0172577.	2.5	9
106	The complex genetics of gait speed: genome-wide meta-analysis approach. Aging, 2017, 9, 209-246.	3.1	21
107	Transcriptome-wide association study of inflammatory biologic age. Aging, 2017, 9, 2288-2301.	3.1	12
108	Admixture Mapping of Africanâ€“American Women in the AMBER Consortium Identifies New Loci for Breast Cancer and Estrogen-Receptor Subtypes. Frontiers in Genetics, 2016, 7, 170.	2.3	19

#	Article	IF	Citations
109	Evaluation of a Twoâ€Stage Approach in Transâ€Ethnic Metaâ€Analysis in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2016, 40, 284-292.	1.3	8
110	Somatic, positive and negative domains of the Center for Epidemiological Studies Depression (CES-D) scale: a meta-analysis of genome-wide association studies. Psychological Medicine, 2016, 46, 1613-1623.	4.5	17
111	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	3.1	174
112	Gene-based analysis of the fibroblast growth factor receptor signaling pathway in relation to breast cancer in African American women: the AMBER consortium. Breast Cancer Research and Treatment, 2016, 155, 355-363.	2.5	12
113	Genome-wide association studies in women of African ancestry identified 3q26.21 as a novel susceptibility locus for oestrogen receptor negative breast cancer. Human Molecular Genetics, 2016, 25, ddw305.	2.9	50
114	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
115	Genetic variations in the Hippo signaling pathway and breast cancer risk in African American women in the AMBER Consortium. Carcinogenesis, 2016, 37, 951-956.	2.8	20
116	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
117	Gene-gene Interaction Analyses for Atrial Fibrillation. Scientific Reports, 2016, 6, 35371.	3.3	15
118	Genetic variation in the insulin, insulin-like growth factor, growth hormone, and leptin pathways in relation to breast cancer in African-American women: the AMBER consortium. Npj Breast Cancer, 2016, 2, .	5.2	10
119	Phenotypically Enriched Genotypic Imputation in Genetic Association Tests. Human Heredity, 2016, 81, 35-45.	0.8	0
120	Imputing rare variants in families using a two-stage approach. BMC Proceedings, 2016, 10, 209-214.	1.6	5
121	Genetic variations in vitamin D-related pathways and breast cancer risk in African American women in the AMBER consortium. International Journal of Cancer, 2016, 138, 2118-2126.	5.1	21
122	An exome-wide analysis of low frequency and rare variants in relation to risk of breast cancer in African American Women: the AMBER Consortium. Carcinogenesis, 2016, 37, 870-877.	2.8	22
123	Association of an Index of Healthy Aging With Incident Cardiovascular Disease and Mortality in a Community-Based Sample of Older Adults. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 1695-1701.	3.6	21
124	Genetic variants in the mTOR pathway and breast cancer risk in African American women. Carcinogenesis, 2016, 37, 49-55.	2.8	10
125	Family History of Cancer in Relation to Breast Cancer Subtypes in African American Women. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 366-373.	2.5	18
126	Global and local ancestry in Africanâ€Americans: Implications for Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 233-243.	0.8	42

#	Article	IF	Citations
127	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
128	Whole Exome Sequencing in Atrial Fibrillation. PLoS Genetics, 2016, 12, e1006284.	3.5	35
129	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
130	Trans-ethnic follow-up of breast cancer GWAS hits using the preferential linkage disequilibrium approach. Oncotarget, 2016, 7, 83160-83176.	1.8	9
131	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
132	Rarity of the Alzheimer Diseaseâ€“ProtectiveAPPA673T Variant in the United States. JAMA Neurology, 2015, 72, 209.	9.0	41
133	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
134	Protective variant for hippocampal atrophy identified by whole exome sequencing. Annals of Neurology, 2015, 77, 547-552.	5.3	48
135	Gene expression markers of age-related inflammation in two human cohorts. Experimental Gerontology, 2015, 70, 37-45.	2.8	23
136	A caseâ€“control analysis of oral contraceptive use and breast cancer subtypes in the African American Breast Cancer Epidemiology and Risk Consortium. Breast Cancer Research, 2015, 17, 22.	5.0	47
137	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
138	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.	3.6	250
139	Genome-Wide Association Study and Linkage Analysis of the Healthy Aging Index. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 1003-1008.	3.6	14
140	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
141	Hormone-related pathways and risk of breast cancer subtypes in African American women. Breast Cancer Research and Treatment, 2015, 154, 145-154.	2.5	30
142	Association of Long Runs of Homozygosity With Alzheimer Disease Among African American Individuals. JAMA Neurology, 2015, 72, 1313.	9.0	39
143	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
144	Correction for multiple testing in a gene region. European Journal of Human Genetics, 2014, 22, 414-418.	2.8	39

#	Article	IF	Citations
145	Whole blood gene expression and interleukin-6 levels. Genomics, 2014, 104, 490-495.	2.9	24
146	Genetic diversity is a predictor of mortality in humans. BMC Genetics, 2014, 15, 159.	2.7	12
147	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	9.0	166
148	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	2.8	127
149	Targeted sequencing in candidate genes for atrial fibrillation: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. Heart Rhythm, 2014, 11, 452-457.	0.7	24
150	Genome-Wide Association Study of <scp>l</scp> -Arginine and Dimethylarginines Reveals Novel Metabolic Pathway for Symmetric Dimethylarginine. Circulation: Cardiovascular Genetics, 2014, 7, 864-872.	5.1	53
151	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
152	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. Circulation, 2014, 130, 1225-1235.	1.6	183
153	<scp>PLXNA</scp>4 is associated with <scp>A</scp>lzheimer disease and modulates tau phosphorylation. Annals of Neurology, 2014, 76, 379-392.	5.3	60
154	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
155	Sex- and age-interacting eQTLs in human complex diseases. Human Molecular Genetics, 2014, 23, 1947-1956.	2.9	66
156	Two rare AKAP9 variants are associated with Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2014, 10, 609.	0.8	94
157	A search for age-related macular degeneration risk variants in Alzheimer disease genes and pathways. Neurobiology of Aging, 2014, 35, 1510.e7-1510.e18.	3.1	53
158	Gene expression and genetic variation in human atria. Heart Rhythm, 2014, 11, 266-271.	0.7	48
159	A novel trafficking-defective HCN4 mutation is associated with early-onset atrial fibrillation. Heart Rhythm, 2014, 11, 1055-1062.	0.7	64
160	The heritability of circulating testosterone, oestradiol, oestrone and sex hormone binding globulin concentrations in men: the Framingham Heart Study. Clinical Endocrinology, 2014, 80, 277-282.	2.4	36
161	Whole Blood Gene Expression and Atrial Fibrillation: The Framingham Heart Study. PLoS ONE, 2014, 9, e96794.	2.5	23
162	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155

#	Article	IF	Citations
163	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
164	APOE genotype and MRI markers of cerebrovascular disease. Neurology, 2013, 81, 292-300.	1.1	149
165	Association of heat shock proteins with all-cause mortality. Age, 2013, 35, 1367-1376.	3.0	5
166	A Genome-Wide Association Study of Depressive Symptoms. Biological Psychiatry, 2013, 73, 667-678.	1.3	149
167	Methods for Metaâ€Analysis of Genetic Data. Current Protocols in Human Genetics, 2013, 77, Unit1.24.	3.5	3
168	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
169	Variants in the ATP-Binding Cassette Transporter (ABCA7), Apolipoprotein E Ïµ4, and the Risk of Late-Onset Alzheimer Disease in African Americans. JAMA - Journal of the American Medical Association, 2013, 309, 1483.	7.4	360
170	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	2.9	104
171	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. American Journal of Epidemiology, 2013, 178, 451-460.	3.4	51
172	Incremental value of rare genetic variants for the prediction of multifactorial diseases. Genome Medicine, 2013, 5, 76.	8.2	10
173	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
174	A Comparison of Gene Region Simulation Methods. PLoS ONE, 2012, 7, e40925.	2.5	5
175	Assessment of cortical and striatal involvement in 523 Huntington disease brains. Neurology, 2012, 79, 1708-1715.	1.1	52
176	Reproductive aging-associated common genetic variants and the risk of breast cancer. Breast Cancer Research, 2012, 14, R54.	5.0	17
177	Serum paraoxonase activity is associated with variants in the PON gene cluster and risk of Alzheimer disease. Neurobiology of Aging, 2012, 33, 1015.e7-1015.e23.	3.1	32
178	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.1	144
179	Transferability and fine-mapping of glucose and insulin quantitative trait loci across populations: CARe, the Candidate Gene Association Resource. Diabetologia, 2012, 55, 2970-2984.	6.3	23
180	Comprehensive Search for Alzheimer Disease Susceptibility Loci in the APOE Region. Archives of Neurology, 2012, 69, 1270.	4.5	97

#	Article	IF	Citations
181	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
182	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	21.4	533
183	Multiple loci influencing hippocampal degeneration identified by genome scan. Annals of Neurology, 2012, 72, 65-75.	5.3	59
184	The Search for Longevity and Healthy Aging Genes: Insights From Epidemiological Studies and Samples of Long-Lived Individuals. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2012, 67A, 470-479.	3.6	155
185	Genetics of Human Longevity and Healthy Aging. , 2012, , 215-235.		1
186	Lack of replication in polymorphisms reported to be associated with atrial fibrillation. Heart Rhythm, 2011, 8, 403-409.	0.7	22
187	A genome-wide association study of aging. Neurobiology of Aging, 2011, 32, 2109.e15-2109.e28.	3.1	127
188	A Comprehensive Genetic Association Study of Alzheimer Disease in African Americans. Archives of Neurology, 2011, 68, 1569.	4.5	221
189	Association of TTR polymorphisms with hippocampal atrophy in Alzheimer disease families. Neurobiology of Aging, 2011, 32, 249-256.	3.1	17
190	Magnetic resonance imagingâ€measured atrophy and its relationship to cognitive functioning in vascular dementia and Alzheimer's disease patients. Alzheimer's and Dementia, 2011, 7, 493-500.	0.8	13
191	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	21.4	1,676
192	Choice of population structure informative principal components for adjustment in a case-control study. BMC Genetics, 2011, 12, 64.	2.7	15
193	Frailty models: Applications to biomedical and genetic studies. Statistics in Medicine, 2011, 30, 2754-2764.	1.6	38
194	Evaluation of methods accounting for population structure with pedigree data and continuous outcomes. Genetic Epidemiology, 2011, 35, n/a-n/a.	1.3	3
195	Circulating Testosterone and SHBG Concentrations Are Heritable in Women: The Framingham Heart Study. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E1491-E1495.	3.6	23
196	CYP2D6 Inhibition and Breast Cancer Recurrence in a Population-Based Study in Denmark. Journal of the National Cancer Institute, 2011, 103, 489-500.	6.3	84
197	Large-Scale Candidate Gene Analysis in Whites and African Americans Identifies IL6R Polymorphism in Relation to Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2011, 4, 557-564.	5.1	74
198	A Common Connexin-40 Gene Promoter Variant Affects Connexin-40 Expression in Human Atria and Is Associated With Atrial Fibrillation. Circulation: Arrhythmia and Electrophysiology, 2011, 4, 87-93.	4.8	76

#	Article	IF	Citations
199	Large common deletions associate with mortality at old age. Human Molecular Genetics, 2011, 20, 4290-4296.	2.9	35
200	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. PLoS Genetics, 2011, 7, e1002025.	3.5	87
201	Genetic Determinants of Serum Testosterone Concentrations in Men. PLoS Genetics, 2011, 7, e1002313.	3.5	178
202	Functional Polymorphisms in UDP-Glucuronosyl Transferases and Recurrence in Tamoxifen-Treated Breast Cancer Survivors. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1937-1943.	2.5	21
203	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
204	Common variants in KCNN3 are associated with lone atrial fibrillation. Nature Genetics, 2010, 42, 240-244.	21.4	438
205	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
206	Concordance of metabolic enzyme genotypes assayed from paraffin-embedded, formalin-fixed breast tumors and normal lymphatic tissue. Clinical Epidemiology, 2010, 2, 241.	3.0	17
207	Independent Susceptibility Markers for Atrial Fibrillation on Chromosome 4q25. Circulation, 2010, 122, 976-984.	1.6	137
208	Breast cancer recurrence risk related to concurrent use of SSRI antidepressants and tamoxifen. Acta OncolÃ³gica, 2010, 49, 305-312.	1.8	82
209	Meta-analysis Confirms CR1, CLU, and PICALM as Alzheimer Disease Risk Loci and Reveals Interactions With APOE Genotypes. Archives of Neurology, 2010, 67, 1473.	4.5	376
210	Head circumference, atrophy, and cognition. Neurology, 2010, 75, 137-142.	1.1	88
211	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.	3.6	117
212	Education Attenuates the Effect of Medial Temporal Lobe Atrophy on Cognitive Function in Alzheimer's Disease: The MIRAGE Study. Journal of Alzheimer's Disease, 2009, 17, 855-862.	2.6	42
213	The Relation of Genetic and Environmental Factors to Systemic Inflammatory Biomarker Concentrations. Circulation: Cardiovascular Genetics, 2009, 2, 229-237.	5.1	58
214	Principal-component-based population structure adjustment in the North American Rheumatoid Arthritis Consortium data: impact of single-nucleotide polymorphism set and analysis method. BMC Proceedings, 2009, 3, S108.	1.6	10
215	Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Circulation: Cardiovascular Genetics, 2009, 2, 73-80.	5.1	519
216	Intergenerational and striatal CAG repeat instability in Huntington's disease knock-in mice involve different DNA repair genes. Neurobiology of Disease, 2009, 33, 37-47.	4.4	189

#	Article	IF	Citations
217	Performance of random forest when SNPs are in linkage disequilibrium. BMC Bioinformatics, 2009, 10, 78.	2.6	76
218	Estimating the probability of de novo HD cases from transmissions of expanded penetrant CAG alleles in the Huntington disease gene from male carriers of high normal alleles (27â€“35 CAG). American Journal of Medical Genetics, Part A, 2009, 149A, 1375-1381.	1.2	48
219	Combined haplotype relative risk (CHRR): a general and simple genetic association test that combines trios and unrelated caseâ€controls. Genetic Epidemiology, 2009, 33, 54-62.	1.3	12
220	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	21.4	1,234
221	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. Nature Genetics, 2009, 41, 648-650.	21.4	266
222	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. Nature Genetics, 2009, 41, 879-881.	21.4	363
223	Clinical and genetic factors associated with lipoprotein-associated phospholipase A2 in the Framingham Heart Study. Atherosclerosis, 2009, 204, 601-607.	0.8	34
224	Clinical and genetic correlates of soluble Pâ€selectin in the community. Journal of Thrombosis and Haemostasis, 2008, 6, 20-31.	3.8	31
225	Tamoxifen's protection against breast cancer recurrence is not reduced by concurrent use of the SSRI citalopram. British Journal of Cancer, 2008, 99, 616-621.	6.4	56
226	Genetic Association Studies. Circulation, 2008, 118, 96-101.	1.6	71
227	Association of Distinct Variants in SORL1 With Cerebrovascular and Neurodegenerative Changes Related to Alzheimer Disease. Archives of Neurology, 2008, 65, 1640.	4.5	60
228	Large scale replication and meta-analysis of variants on chromosome 4q25 associated with atrial fibrillation. European Heart Journal, 2008, 30, 813-819.	2.2	193
229	Relations of Inflammatory Biomarkers and Common Genetic Variants With Arterial Stiffness and Wave Reflection. Hypertension, 2008, 51, 1651-1657.	2.7	141
230	Heritability of Magnetic Resonance Imaging (MRI) Traits in Alzheimer Disease Cases and Their Siblings in the MIRAGE Study. Alzheimer Disease and Associated Disorders, 2007, 21, 85-91.	1.3	28
231	Two-stage approach for identifying single-nucleotide polymorphisms associated with rheumatoid arthritis using random forests and Bayesian networks. BMC Proceedings, 2007, 1, S56.	1.6	27
232	Informative-Transmission Disequilibrium Test (i-TDT): combined linkage and association mapping that includes unaffected offspring as well as affected offspring. Genetic Epidemiology, 2007, 31, 115-133.	1.3	13
233	The Framingham Heart Study 100K SNP genome-wide association study resource: overview of 17 phenotype working group reports. BMC Medical Genetics, 2007, 8, S1.	2.1	169
234	Genome-wide association with select biomarker traits in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S11.	2.1	111

#	Article	IF	Citations
235	Genetic correlates of longevity and selected age-related phenotypes: a genome-wide association study in the Framingham Study. BMC Medical Genetics, 2007, 8, S13.	2.1	171
236	Genome-wide association with bone mass and geometry in the Framingham Heart Study. BMC Medical Genetics, 2007, 8, S14.	2.1	232
237	The neuronal sortilin-related receptor SORL1 is genetically associated with Alzheimer disease. Nature Genetics, 2007, 39, 168-177.	21.4	1,045
238	Polymorphisms in the PON gene cluster are associated with Alzheimer disease. Human Molecular Genetics, 2006, 15, 77-85.	2.9	87
239	Genetic association between endothelial nitric oxide synthase and Alzheimer disease. Clinical Genetics, 2006, 70, 49-56.	2.0	28
240	Estrogen Receptor Î± Gene Variation Is Associated With Risk of Myocardial Infarction in More Than Seven Thousand Men From Five Cohorts. Circulation Research, 2006, 98, 590-592.	4.5	86
241	Demonstrating stratification in a European American population. Nature Genetics, 2005, 37, 868-872.	21.4	424
242	Identifying SNPs predictive of phenotype using random forests. Genetic Epidemiology, 2005, 28, 171-182.	1.3	321
243	Expectation Maximization Algorithm Based Haplotype Relative Risk (EM-HRR): Test of Linkage Disequilibrium Using Incomplete Case-Parents Trios. Human Heredity, 2005, 59, 125-135.	0.8	15
244	Screening large-scale association study data: exploiting interactions using random forests. BMC Genetics, 2004, 5, 32.	2.7	369
245	Testing for Population Subdivision and Association in Four Case-Control Studies. American Journal of Human Genetics, 2002, 71, 304-311.	6.2	210
246	Abnormalities of bone marrow mesenchymal cells in multiple myeloma patients. Cancer, 2001, 91, 1219-1230.	4.1	106
247	On the validity of the TDT test in the presence of comorbidity and ascertainment bias. Genetic Epidemiology, 2001, 21, 326-336.	1.3	9
248	HIN-1, a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 9796-9801.	7.1	122
249	Implications of comorbidity and ascertainment bias for identifying disease genes. American Journal of Medical Genetics Part A, 2000, 96, 817-822.	2.4	34
250	Somatic mitochondrial DNA (mtDNA) mutations in papillary thyroid carcinomas and differential mtDNA sequence variants in cases with thyroid tumours. Oncogene, 2000, 19, 2060-2066.	5.9	160
251	Family-Based Tests of Association and Linkage That Use Unaffected Sibs, Covariates, and Interactions. American Journal of Human Genetics, 2000, 66, 605-614.	6.2	163
252	PTEN Mutation Spectrum and Genotype-Phenotype Correlations in Bannayan-Riley-Ruvalcaba Syndrome Suggest a Single Entity With Cowden Syndrome. Human Molecular Genetics, 1999, 8, 1461-1472.	2.9	562

#	Article	IF	Citations
253	Using recursive partitioning for exploration and followâ€up of linkage and association analyses. Genetic Epidemiology, 1999, 17, S391-6.	1.3	6
254	Strategy for mapping minor histocompatibility genes involved in graft-versus-host disease: A novel application of discordant sib pair methodology. , 1998, 15, 595-607.		12
255	Mutation spectrum and genotype-phenotype analyses in Cowden disease and Bannayan-Zonana syndrome, two hamartoma syndromes with germline PTEN mutation. Human Molecular Genetics, 1998, 7, 507-515.	2.9	578
256	An Allelic Variant at theATMLocus Is Implicated in Breast Cancer Susceptibility. Genetic Testing and Molecular Biomarkers, 1997, 1, 165-170.	1.7	38
257	Exclusion of PTEN and 10q22-24 as the susceptibility locus for juvenile polyposis syndrome. Cancer Research, 1997, 57, 5017-21.	0.9	58
258	Linkage Study of Best‘s Vitelliform Macular Dystrophy (VMD2) in a Large North American Family. Human Heredity, 1996, 46, 211-220.	0.8	10
259	Selected locus and multiple panel models for radiation hybrid mapping. American Journal of Human Genetics, 1996, 59, 717-25.	6.2	40
260	Refined Genetic Mapping of Juvenile X-Linked Retinoschisis. Human Heredity, 1995, 45, 206-210.	0.8	9
261	Statistical methods for polyploid radiation hybrid mapping.. Genome Research, 1995, 5, 136-150.	5.5	162
262	Experimental design and error detection for polyploid radiation hybrid mapping.. Genome Research, 1995, 5, 151-163.	5.5	44
263	Multipoint Radiation Hybrid Mapping: Comparison of Methods, Sample Size Requirements, and Optimal Study Characteristics. Genomics, 1994, 21, 92-103.	2.9	43
264	Inheritance of human plasma dopamine-Î²-hydroxylase thermal stability. Genetic Epidemiology, 1991, 8, 237-251.	1.3	3