

Qihua Tan

List of Publications by Year in descending order

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Version: 2024-02-01

239
papers

7,058
citations

61945

43
h-index

91828

69
g-index

245
all docs

245
docs citations

245
times ranked

11303
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of genetic and environmental correlation between leisure activities and cognitive function in aging Chinese twins. <i>Aging and Mental Health</i> , 2022, 26, 493-498.	1.5	1
2	Early life affects late-life health through determining DNA methylation across the lifespan: A twin study. <i>EBioMedicine</i> , 2022, 77, 103927.	2.7	15
3	Epigenetic age acceleration as an effective predictor of diseases and mortality in the elderly. <i>EBioMedicine</i> , 2021, 63, 103174.	2.7	4
4	Genome-wide DNA methylation analysis of cognitive function in middle and old-aged Chinese monozygotic twins. <i>Journal of Psychiatric Research</i> , 2021, 136, 571-580.	1.5	13
5	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	5.8	75
6	Novel DNA methylation marker discovery by assumption-free genome-wide association analysis of cognitive function in twins. <i>Aging Cell</i> , 2021, 20, e13293.	3.0	7
7	Skewness of X-chromosome inactivation increases with age and varies across birth cohorts in elderly Danish women. <i>Scientific Reports</i> , 2021, 11, 4326.	1.6	16
8	Genetic and environmental determinants of O6-methylguanine DNA-methyltransferase (MGMT) gene methylation: a 10-year longitudinal study of Danish twins. <i>Clinical Epigenetics</i> , 2021, 13, 35.	1.8	6
9	Genome-wide association analysis of cognitive function in Danish long-lived individuals. <i>Mechanisms of Ageing and Development</i> , 2021, 195, 111463.	2.2	1
10	Epigenome-wide association study shows that smoking alters DNA methylation in blood cells triggering aggressive bone resorption of osteoclasts in vivo and in vitro. <i>Bone Reports</i> , 2021, 14, 100796.	0.2	0
11	Gene expression profiling of morphologic subtypes of pancreatic ductal adenocarcinoma using surgical and EUS-FNB specimens. <i>Pancreatology</i> , 2021, 21, 530-543.	0.5	6
12	Global Gene Expression Profiling and Transcription Factor Network Analysis of Cognitive Aging in Monozygotic Twins. <i>Frontiers in Genetics</i> , 2021, 12, 675587.	1.1	6
13	Age patterns of intra-pair DNA methylation discordance in twins: Sex difference in epigenomic instability and implication on survival. <i>Aging Cell</i> , 2021, 20, e13460.	3.0	2
14	Differential lncRNA expression profiling of cognitive function in middle and old aged monozygotic twins using generalized association analysis. <i>Journal of Psychiatric Research</i> , 2021, 140, 197-204.	1.5	3
15	Genome-wide DNA methylation and gene expression analyses in monozygotic twins identify potential biomarkers of depression. <i>Translational Psychiatry</i> , 2021, 11, 416.	2.4	31
16	EWAS of Monozygotic Twins Implicate a Role of mTOR Pathway in Pathogenesis of Tic Spectrum Disorder. <i>Genes</i> , 2021, 12, 1510.	1.0	5
17	Comparison of the Metastasis Predictive Potential of mRNA and Long Non-Coding RNA Profiling in Systemically Untreated Breast Cancer. <i>Cancers</i> , 2021, 13, 4907.	1.7	0
18	Educational attainment of same-sex and opposite-sex dizygotic twins: An individual-level pooled study of 19 twin cohorts. <i>Hormones and Behavior</i> , 2021, 136, 105054.	1.0	1

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19	Differential regulation of the DNA methylome in adults born during the Great Chinese Famine in 1959–1961. <i>Genomics</i> , 2021, 113, 3907-3918.	1.3	10
20	Age-dependent DNA methylation patterns on the Y chromosome in elderly males. <i>Aging Cell</i> , 2020, 19, e12907.	3.0	27
21	Network based analysis of microarray gene expression profiles in response to electroacupuncture. <i>Journal of Traditional and Complementary Medicine</i> , 2020, 10, 471-477.	1.5	1
22	Harnessing the power of twins in epigenetic association studies: causal inference and more. <i>Epigenomics</i> , 2020, 12, 1-3.	1.0	2
23	EWASex: an efficient R-package to predict sex in epigenome-wide association studies. <i>Bioinformatics</i> , 2020, , .	1.8	1
24	Genetic and environmental variation in educational attainment: an individual-based analysis of 28 twin cohorts. <i>Scientific Reports</i> , 2020, 10, 12681.	1.6	59
25	A decade of epigenetic change in aging twins: Genetic and environmental contributions to longitudinal DNA methylation. <i>Aging Cell</i> , 2020, 19, e13197.	3.0	29
26	Differential long noncoding RNA profiling of BMI in twins. <i>Epigenomics</i> , 2020, 12, 1531-1541.	1.0	4
27	Genetic and environmental causes of variation in epigenetic aging across the lifespan. <i>Clinical Epigenetics</i> , 2020, 12, 158.	1.8	33
28	Exploratory analysis of age and sex dependent DNA methylation patterns on the X-chromosome in whole blood samples. <i>Genome Medicine</i> , 2020, 12, 39.	3.6	26
29	Weighted Gene Coregulation Network Analysis of Promoter DNA Methylation on All-Cause Mortality in Old-Aged Birth Cohorts Finds Modules of High-Risk Associated Biomarkers. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2020, 75, 2249-2257.	1.7	3
30	Cohort Differences in the Associations of Selected Candidate Genes With Risk of All-Cause Mortality at Advanced Ages. <i>American Journal of Epidemiology</i> , 2020, 189, 708-716.	1.6	1
31	Deciphering the DNA Methylome of Polycystic Ovary Syndrome. <i>Molecular Diagnosis and Therapy</i> , 2020, 24, 245-250.	1.6	5
32	A Genome-Wide Integrative Association Study of DNA Methylation and Gene Expression Data and Later Life Cognitive Functioning in Monozygotic Twins. <i>Frontiers in Neuroscience</i> , 2020, 14, 233.	1.4	5
33	The sex chromosomes of the aging epigenome. <i>Aging</i> , 2020, 12, 16667-16668.	1.4	1
34	Generalized correlation coefficient for genome-wide association analysis of cognitive ability in twins. <i>Aging</i> , 2020, 12, 22457-22494.	1.4	3
35	Gene Co-expression Network Analysis Associated with Acupuncture Treatment of Rheumatoid Arthritis: An Animal Model. <i>Journal of Acupuncture Research</i> , 2020, 37, 128-135.	0.1	0
36	Heritability of Age-Related Hearing Loss in Middle-Aged and Elderly Chinese: A Population-Based Twin Study. <i>Ear and Hearing</i> , 2019, 40, 253-259.	1.0	20

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37	Epigenome-wide exploratory study of monozygotic twins suggests differentially methylated regions to associate with hand grip strength. <i>Biogerontology</i> , 2019, 20, 627-647.	2.0	9
38	Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. <i>European Journal of Human Genetics</i> , 2019, 27, 631-636.	1.4	4
39	Sex and age specific reduction in stress resistance and mitochondrial DNA copy number in <i>Drosophila melanogaster</i> . <i>Scientific Reports</i> , 2019, 9, 12305.	1.6	25
40	Epigenome-wide association study of depression symptomatology in elderly monozygotic twins. <i>Translational Psychiatry</i> , 2019, 9, 214.	2.4	48
41	Global expression profiling of cognitive level and decline in middle-aged monozygotic twins. <i>Neurobiology of Aging</i> , 2019, 84, 141-147.	1.5	10
42	The epigenome of twins as a perfect laboratory for studying behavioural traits. <i>Neuroscience and Biobehavioral Reviews</i> , 2019, 107, 192-195.	2.9	10
43	DNA methylome profiling in identical twin pairs discordant for body mass index. <i>International Journal of Obesity</i> , 2019, 43, 2491-2499.	1.6	16
44	Impact of obesity and physical inactivity on the long-term change in grip strength among middle-aged and older European adults. <i>Journal of Epidemiology and Community Health</i> , 2019, 73, 619-624.	2.0	8
45	Epigenetic Consequences of Low Birth-Weight and Preterm Birth in Adult Twins. , 2019, , 1263-1275.		0
46	Longitudinal changes in the genetic and environmental influences on the epigenetic clocks across old age: Evidence from two twin cohorts. <i>EBioMedicine</i> , 2019, 40, 710-716.	2.7	27
47	DNA methylome profiling of all-cause mortality in comparison with age-associated methylation patterns. <i>Clinical Epigenetics</i> , 2019, 11, 23.	1.8	13
48	Longitudinal analysis of sibling correlation on blood pressure using mixed modeling. <i>Annals of Epidemiology</i> , 2019, 33, 49-53.	0.9	1
49	Epigenetic association analysis of clinical sub-phenotypes in patients with polycystic ovary syndrome (PCOS). <i>Gynecological Endocrinology</i> , 2019, 35, 691-694.	0.7	8
50	Global microRNA profiling of metastatic conjunctival melanoma. <i>Melanoma Research</i> , 2019, 29, 465-473.	0.6	20
51	Weak Grip Strength and Cognition Predict Functional Limitation in Older Europeans. <i>Journal of the American Geriatrics Society</i> , 2019, 67, 93-99.	1.3	27
52	White blood cell mitochondrial DNA copy number is decreased in rheumatoid arthritis and linked with risk factors. A twin study. <i>Journal of Autoimmunity</i> , 2019, 96, 142-146.	3.0	16
53	Adenoid cystic carcinomas of the salivary gland, lacrimal gland, and breast are morphologically and genetically similar but have distinct microRNA expression profiles. <i>Modern Pathology</i> , 2018, 31, 1211-1225.	2.9	33
54	Circulating, Cell-Free Micro-RNA Profiles Reflect Discordant Development of Dementia in Monozygotic Twins. <i>Journal of Alzheimer's Disease</i> , 2018, 63, 591-601.	1.2	9

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55	Circulating microRNAs disclose biology of normal cognitive function in healthy elderly people – a discovery twin study. <i>European Journal of Human Genetics</i> , 2018, 26, 1378-1387.	1.4	9
56	DNA methylation age and perceived age in elderly Danish twins. <i>Mechanisms of Ageing and Development</i> , 2018, 169, 40-44.	2.2	13
57	Genetic and environmental influences on cardiovascular risk factors and cognitive function: A Chinese twin aging study. <i>Geriatrics and Gerontology International</i> , 2018, 18, 352-359.	0.7	32
58	Weighted gene co-expression network analysis of microarray mRNA expression profiling in response to electroacupuncture. , 2018, , .		1
59	Differential effect of surgical manipulation on gene expression in normal breast tissue and breast tumor tissue. <i>Molecular Medicine</i> , 2018, 24, 57.	1.9	7
60	DNA Methylation and All-Cause Mortality in Middle-Aged and Elderly Danish Twins. <i>Genes</i> , 2018, 9, 78.	1.0	27
61	Association of miR-548c-5p, miR-7-5p, miR-210-3p, miR-128-3p with recurrence in systemically untreated breast cancer. <i>Oncotarget</i> , 2018, 9, 9030-9042.	0.8	22
62	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018, 1, e181670.	2.8	60
63	MicroRNA dysregulation in adenoid cystic carcinoma of the salivary gland in relation to prognosis and gene fusion status: a cohort study. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2018, 473, 329-340.	1.4	26
64	Heritability and Genome-Wide Association Analyses of Serum Uric Acid in Middle and Old-Aged Chinese Twins. <i>Frontiers in Endocrinology</i> , 2018, 9, 75.	1.5	45
65	Genetics of Obesity Traits: A Bivariate Genome-Wide Association Analysis. <i>Frontiers in Genetics</i> , 2018, 9, 179.	1.1	29
66	Association of current and former smoking with body mass index: A study of smoking discordant twin pairs from 21 twin cohorts. <i>PLoS ONE</i> , 2018, 13, e0200140.	1.1	57
67	Epigenetic signature of preterm birth in adult twins. <i>Clinical Epigenetics</i> , 2018, 10, 87.	1.8	16
68	Surfactant protein-D, a potential mediator of inflammation in axial spondyloarthritis. <i>Rheumatology</i> , 2018, 57, 1861-1865.	0.9	6
69	On the power of epigenome-wide association studies using a disease-discordant twin design. <i>Bioinformatics</i> , 2018, 34, 4073-4078.	1.8	31
70	A case-only genome-wide association study on gene-sex interaction in allergic rhinitis. <i>Annals of Allergy, Asthma and Immunology</i> , 2018, 121, 366-367.e2.	0.5	3
71	Online Interactive Microbial Classification and Geospatial Distributional Analysis Using BioAtlas. <i>Methods in Molecular Biology</i> , 2018, 1807, 21-35.	0.4	2
72	Genetic rearrangements, hotspot mutations, and microRNA expression in the progression of metastatic adenoid cystic carcinoma of the salivary gland. <i>Oncotarget</i> , 2018, 9, 19675-19687.	0.8	15

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73	Efficient detection of differentially methylated regions using DiMmeR. <i>Bioinformatics</i> , 2017, 33, 549-551.	1.8	9
74	Blood DNA methylation age is not associated with cognitive functioning in middle-aged monozygotic twins. <i>Neurobiology of Aging</i> , 2017, 50, 60-63.	1.5	28
75	Genetic and Environmental Influences on Pulmonary Function and Muscle Strength: The Chinese Twin Study of Aging. <i>Twin Research and Human Genetics</i> , 2017, 20, 53-59.	0.3	6
76	Genetic and Environmental Basis in Phenotype Correlation Between Physical Function and Cognition in Aging Chinese Twins. <i>Twin Research and Human Genetics</i> , 2017, 20, 60-65.	0.3	49
77	Familial Risk and Heritability of Colorectal Cancer in the Nordic Twin Study of Cancer. <i>Clinical Gastroenterology and Hepatology</i> , 2017, 15, 1256-1264.	2.4	77
78	Genetic interplay between human longevity and metabolic pathways â€” a large-scale eQTL study. <i>Aging Cell</i> , 2017, 16, 716-725.	3.0	14
79	The gene expression and immunohistochemical time-course of diphenylcyclopropenone-induced contact allergy in healthy humans following repeated epicutaneous challenges. <i>Experimental Dermatology</i> , 2017, 26, 926-933.	1.4	7
80	Disease-Concordant Twins Empower Genetic Association Studies. <i>Annals of Human Genetics</i> , 2017, 81, 20-26.	0.3	46
81	Education in Twins and Their Parents Across Birth Cohorts Over 100 years: An Individual-Level Pooled Analysis of 42-Twin Cohorts. <i>Twin Research and Human Genetics</i> , 2017, 20, 395-405.	0.3	8
82	Identification, replication and characterization of epigenetic remodelling in the aging genome: a cross population analysis. <i>Scientific Reports</i> , 2017, 7, 8183.	1.6	27
83	Genetic and Environmental Influences on Correlations Between Hearing and Cognitive Functions in Middle and Older Chinese Twins. <i>Twin Research and Human Genetics</i> , 2017, 20, 374-379.	0.3	38
84	Generalized Correlation Coefficient for Non-Parametric Analysis of Microarray Time-Course Data. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	4
85	Handling blood cell composition in epigenetic studies on ageing. <i>International Journal of Epidemiology</i> , 2017, 46, 1717-1718.	0.9	6
86	A genome-wide association study of cognitive function in Chinese adult twins. <i>Biogerontology</i> , 2017, 18, 811-819.	2.0	18
87	Differences in genetic and environmental variation in adult BMI by sex, age, time period, and region: an individual-based pooled analysis of 40 twin cohorts. <i>American Journal of Clinical Nutrition</i> , 2017, 106, 457-466.	2.2	107
88	Does the sex of one's co-twin affect height and BMI in adulthood? A study of dizygotic adult twins from 31 cohorts. <i>Biology of Sex Differences</i> , 2017, 8, 14.	1.8	8
89	Efficient Management of High-Throughput Screening Libraries with SAVANAH. <i>SLAS Discovery</i> , 2017, 22, 196-202.	1.4	5
90	Differential DNA methylation patterns of polycystic ovarian syndrome in whole blood of Chinese women. <i>Oncotarget</i> , 2017, 8, 20656-20666.	0.8	32

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91	Epigenome-Wide Association Study of Cognitive Functioning in Middle-Aged Monozygotic Twins. <i>Frontiers in Aging Neuroscience</i> , 2017, 9, 413.	1.7	52
92	Weighted gene co-expression network analysis of expression data of monozygotic twins identifies specific modules and hub genes related to BMI. <i>BMC Genomics</i> , 2017, 18, 872.	1.2	53
93	Lung function discordance in monozygotic twins and associated differences in blood DNA methylation. <i>Clinical Epigenetics</i> , 2017, 9, 132.	1.8	18
94	Epigenetic Consequences of Low Birth-Weight and Preterm Birth in Adult Twins. , 2017, , 1-13.		1
95	Lung function discordance in monozygotic twins and associated differences in blood DNA methylation. , 2017, , .		0
96	Genetic and environmental influences on adult human height across birth cohorts from 1886 to 1994. <i>ELife</i> , 2016, 5, .	2.8	42
97	Differentially Methylated DNA Regions in Monozygotic Twin Pairs Discordant for Rheumatoid Arthritis: An Epigenome-Wide Study. <i>Frontiers in Immunology</i> , 2016, 7, 510.	2.2	29
98	Genetic and Environmental Regulation on Longitudinal Change of Metabolic Phenotypes in Danish and Chinese Adult Twins. <i>PLoS ONE</i> , 2016, 11, e0148396.	1.1	2
99	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016, 6, 21243.	1.6	145
100	Change in Depression Symptomatology and Cognitive Function in Twins: A 10-Year Follow-Up Study. <i>Twin Research and Human Genetics</i> , 2016, 19, 104-111.	0.3	11
101	Copy number variation associates with mortality in long-lived individuals: a genome-wide assessment. <i>Aging Cell</i> , 2016, 15, 49-55.	3.0	21
102	<scp>DNA</scp> methylation age is associated with mortality in a longitudinal Danish twin study. <i>Aging Cell</i> , 2016, 15, 149-154.	3.0	260
103	Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs. <i>Annals of Human Genetics</i> , 2016, 80, 81-87.	0.3	19
104	Epigenetic drift in the aging genome: a ten-year follow-up in an elderly twin cohort. <i>International Journal of Epidemiology</i> , 2016, 45, dyw132.	0.9	82
105	The epigenomics of polycystic ovarian syndrome: from pathogenesis to clinical manifestations. <i>Gynecological Endocrinology</i> , 2016, 32, 942-946.	0.7	25
106	Illumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and Infinium MethylationEPIC BeadChip data processing. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 24-32.	1.0	2
107	Comprehensive analysis of high-throughput screens with HiTSeekR. <i>Nucleic Acids Research</i> , 2016, 44, 6639-6648.	6.5	17
108	Association between the surfactant protein D (SFTPD) gene and subclinical carotid artery atherosclerosis. <i>Atherosclerosis</i> , 2016, 246, 7-12.	0.4	20

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109	Propranolol Targets Hemangioma Stem Cells via cAMP and Mitogen-Activated Protein Kinase Regulation. <i>Stem Cells Translational Medicine</i> , 2016, 5, 45-55.	1.6	49
110	Interaction Between the <i>FOXO1A-209</i> Genotype and Tea Drinking Is Significantly Associated with Reduced Mortality at Advanced Ages. <i>Rejuvenation Research</i> , 2016, 19, 195-203.	0.9	14
111	Robust de novo pathway enrichment with KeyPathwayMiner 5. <i>F1000Research</i> , 2016, 5, 1531.	0.8	30
112	Longitudinal Investigation into Genetics in the Conservation of Metabolic Phenotypes in Danish and Chinese Twins. <i>PLoS ONE</i> , 2016, 11, e0162805.	1.1	4
113	Generalized Measure of Dependency for Analysis of Omics Data. <i>Journal of Data Mining in Genomics & Proteomics</i> , 2016, 07, .	0.5	0
114	Illumina - A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and MethylationEPIC data processing. <i>Journal of Integrative Bioinformatics</i> , 2016, 13, 294.	1.0	4
115	Zygoty Differences in Height and Body Mass Index of Twins From Infancy to Old Age: A Study of the CODATwins Project. <i>Twin Research and Human Genetics</i> , 2015, 18, 557-570.	0.3	24
116	The CODATwins Project: The Cohort Description of Collaborative Project of Development of Anthropometrical Measures in Twins to Study Macro-Environmental Variation in Genetic and Environmental Effects on Anthropometric Traits. <i>Twin Research and Human Genetics</i> , 2015, 18, 348-360.	0.3	55
117	DNA Methylation Changes in the <i>IGF1R</i> Gene in Birth Weight Discordant Adult Monozygotic Twins. <i>Twin Research and Human Genetics</i> , 2015, 18, 635-646.	0.3	23
118	The 82-plex plasma protein signature that predicts increasing inflammation. <i>Scientific Reports</i> , 2015, 5, 14882.	1.6	8
119	Efficient Sample Tracking With OpenLabFramework. <i>Scientific Reports</i> , 2015, 4, 4278.	1.6	14
120	Long non-coding RNA expression profiles predict metastasis in lymph node-negative breast cancer independently of traditional prognostic markers. <i>Breast Cancer Research</i> , 2015, 17, 55.	2.2	49
121	Therapeutic effects and associated adverse events of multikinase inhibitors in metastatic renal cell carcinoma: A meta-analysis. <i>Experimental and Therapeutic Medicine</i> , 2015, 9, 2275-2280.	0.8	8
122	The Genetic Basis for Cognitive Ability, Memory, and Depression Symptomatology in Middle-Aged and Elderly Chinese Twins. <i>Twin Research and Human Genetics</i> , 2015, 18, 79-85.	0.3	12
123	Twin methodology in epigenetic studies. <i>Journal of Experimental Biology</i> , 2015, 218, 134-139.	0.8	92
124	Global gene expression profiling of telangiectasial tissue from patients with hereditary hemorrhagic telangiectasia. <i>Microvascular Research</i> , 2015, 99, 118-126.	1.1	13
125	Multivariate Modeling of Body Mass Index, Pulse Pressure, Systolic and Diastolic Blood Pressure in Chinese Twins. <i>Twin Research and Human Genetics</i> , 2015, 18, 73-78.	0.3	12
126	Gene, environment and cognitive function: a Chinese twin ageing study. <i>Age and Ageing</i> , 2015, 44, 452-457.	0.7	12

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127	GxE Interactions between FOXO Genotypes and Tea Drinking Are Significantly Associated with Cognitive Disability at Advanced Ages in China. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 426-433.	1.7	34
128	OpenLabNotes--An Electronic Laboratory Notebook Extension for OpenLabFramework. <i>Journal of Integrative Bioinformatics</i> , 2015, 12, 274.	1.0	3
129	Long Non-Coding RNA Expression Profiles in Hereditary Haemorrhagic Telangiectasia. <i>PLoS ONE</i> , 2014, 9, e90272.	1.1	21
130	Epigenetic signature of birth weight discordance in adult twins. <i>BMC Genomics</i> , 2014, 15, 1062.	1.2	48
131	Probing genetic overlap in the regulation of systolic and diastolic blood pressure in Danish and Chinese twins. <i>Hypertension Research</i> , 2014, 37, 954-959.	1.5	4
132	Surfactant protein D is a candidate biomarker for subclinical tobacco smoke-induced lung damage. <i>American Journal of Physiology - Lung Cellular and Molecular Physiology</i> , 2014, 306, L887-L895.	1.3	31
133	Prevalence and Clinical Outcomes for Patients With ALK-Positive Resected Stage I to III Adenocarcinoma: Results From the European Thoracic Oncology Platform Lungscape Project. <i>Journal of Clinical Oncology</i> , 2014, 32, 2780-2787.	0.8	163
134	Power Estimation for Gene-Longevity Association Analysis Using Concordant Twins. <i>Genetics Research International</i> , 2014, 2014, 1-8.	2.0	1
135	Microarray R-based analysis of complex lysate experiments with MIRACLE. <i>Bioinformatics</i> , 2014, 30, i631-i638.	1.8	8
136	Microarray-Based RNA Profiling of Breast Cancer: Batch Effect Removal Improves Cross-Platform Consistency. <i>BioMed Research International</i> , 2014, 2014, 1-11.	0.9	21
137	Contribution of genetic polymorphisms on functional status at very old age: A gene-based analysis of 38 genes (311 SNPs) in the oxidative stress pathway. <i>Experimental Gerontology</i> , 2014, 52, 23-29.	1.2	25
138	RNA profiling reveals familial aggregation of molecular subtypes in non-BRCA1/2 breast cancer families. <i>BMC Medical Genomics</i> , 2014, 7, 9.	0.7	18
139	Birth cohort differences in the prevalence of longevity-associated variants in APOE and FOXO3A in Danish long-lived individuals. <i>Experimental Gerontology</i> , 2014, 57, 41-46.	1.2	28
140	Surfactant Protein-D-encoding Gene Variant Polymorphisms Are Linked to Respiratory Outcome in Premature Infants. <i>Journal of Pediatrics</i> , 2014, 165, 683-689.	0.9	27
141	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.	1.4	227
142	Hierarchical linear modeling of longitudinal pedigree data for genetic association analysis. <i>BMC Proceedings</i> , 2014, 8, S82.	1.8	8
143	Testosterone treatment increases androgen receptor and aromatase gene expression in myotubes from patients with PCOS and controls, but does not induce insulin resistance. <i>Biochemical and Biophysical Research Communications</i> , 2014, 451, 622-626.	1.0	17
144	Human longevity and variation in DNA damage response and repair: study of the contribution of sub-processes using competitive gene-set analysis. <i>European Journal of Human Genetics</i> , 2014, 22, 1131-1136.	1.4	31

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145	Classification of breast cancer subtypes by combining gene expression and DNA methylation data. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 236.	1.0	23
146	Interactions between Social/ behavioral factors and ADRB2 genotypes may be associated with health at advanced ages in China. <i>BMC Geriatrics</i> , 2013, 13, 91.	1.1	17
147	Long non-coding RNA HOTAIR is an independent prognostic marker of metastasis in estrogen receptor-positive primary breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 142, 529-536.	1.1	242
148	Genetic investigation into ethnic disparity in polycystic ovarian syndrome. <i>Gynecological Endocrinology</i> , 2013, 29, 878-882.	0.7	5
149	Genome-wide linkage analysis for human longevity: Genetics of Healthy Aging Study. <i>Aging Cell</i> , 2013, 12, 184-193.	3.0	170
150	Evidence from case-control and longitudinal studies supports associations of genetic variation in APOE, CETP, and IL6 with human longevity. <i>Age</i> , 2013, 35, 487-500.	3.0	82
151	Twins for epigenetic studies of human aging and development. <i>Ageing Research Reviews</i> , 2013, 12, 182-187.	5.0	51
152	Circulating surfactant protein D is associated to mortality in elderly women: A twin study. <i>Immunobiology</i> , 2013, 218, 712-717.	0.8	12
153	The Danish Twin Registry: Linking Surveys, National Registers, and Biological Information. <i>Twin Research and Human Genetics</i> , 2013, 16, 104-111.	0.3	74
154	A novel permutation test for case-only analysis identifies epistatic effects on human longevity in the FOXO gene family. <i>Aging Cell</i> , 2013, 12, 690-694.	3.0	17
155	Effects of the APOE ϵ 2 Allele on Mortality and Cognitive Function in the Oldest Old. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2013, 68, 389-394.	1.7	25
156	AKT1 fails to replicate as a longevity-associated gene in Danish and German nonagenarians and centenarians. <i>European Journal of Human Genetics</i> , 2013, 21, 574-577.	1.4	4
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