Jack A Taylor

List of Publications by Year
in descending order

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220	17,572	17429	17580
papers	citations	63 h-index	121 g-index

233	233	233	21909
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
3	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
4	SNPinfo: integrating GWAS and candidate gene information into functional SNP selection for genetic association studies. Nucleic Acids Research, 2009, 37, W600-W605.	6.5	655
5	Genetic Risk and Carcinogen Exposure: a Common Inherited Defect of the Carcinogen-Metabolism Gene Glutathione S-Transferase M1 (GSTM1) That Increases Susceptibility to Bladder Cancer. Journal of the National Cancer Institute, 1993, 85, 1159-1164.	3.0	630
6	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	9.4	493
7	Non-hierarchical logistic models and case-only designs for assessing susceptibility in population-based case-control studies. Statistics in Medicine, 1994, 13, 153-162.	0.8	441
8	Cadmium is a mutagen that acts by inhibiting mismatch repair. Nature Genetics, 2003, 34, 326-329.	9.4	440
9	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	13.9	414
10	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
11	Folic acid supplements and risk of facial clefts: national population based case-control study. BMJ: British Medical Journal, 2007, 334, 464.	2.4	341
12	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
13	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
14	SHORT COMMUNICATION: Genotype/phenotype discordance for human arylamine N-acetyltransferase (NAT2) reveals a new slow-acetylator allele common in African-Americans. Carcinogenesis, 1993, 14, 1689-1692.	1.3	281
15	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
16	Increased risk for myelodysplastic syndromes in individuals with glutathione transferase theta 1 (GSTT1) gene defect. Lancet, The, 1996, 347, 295-297.	6.3	272
17	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. Nucleic Acids Research, 2016, 44, e20-e20.	6.5	267
18	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265

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19	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
20	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	1.4	211
21	Pooled Analysis and Meta-analysis of Glutathione S-Transferase M1 and Bladder Cancer: A HuGE Review. American Journal of Epidemiology, 2002, 156, 95-109.	1.6	209
22	XRCC1 and DNA polymerase Î² in cellular protection against cytotoxic DNA single-strand breaks. Cell Research, 2008, 18, 48-63.	5.7	190
23	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
24	Long-Term Use of Procaine Amide following Acute Myocardial Infarction. Circulation, 1973, 47, 1204-1210.	1.6	183
25	Prostate cancer risk and polymorphism in 17 hydroxylase (CYP17) and steroid reductase (SRD5A2). Carcinogenesis, 1999, 20, 1727-1731.	1.3	175
26	Identification of DNA Methylation Changes in Newborns Related to Maternal Smoking during Pregnancy. Environmental Health Perspectives, 2014, 122, 1147-1153.	2.8	171
27	Obesity and Weight Gain in Adulthood and Telomere Length. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 816-820.	1.1	163
28	The Sister Study Cohort: Baseline Methods and Participant Characteristics. Environmental Health Perspectives, 2017, 125, 127003.	2.8	160
29	Expression of CYP1A1 and CYP1A2 genes in human liver. Pharmacogenetics and Genomics, 1993, 3, 239-249.	5.7	159
30	Ethnic variation in the CYP2E1 gene: polymorphism analysis of 695 African-Americans, European-Americans and Taiwanese. Pharmacogenetics and Genomics, 1994, 4, 185-192.	5.7	158
31	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	5.8	140
32	Zebrafish behavioral profiling identifies multitarget antipsychotic-like compounds. Nature Chemical Biology, 2016, 12, 559-566.	3.9	124
33	Methylation-Based Biological Age and Breast Cancer Risk. Journal of the National Cancer Institute, 2019, 111, 1051-1058.	3.0	124
34	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
35	Epigenome-wide Association Study of Breast Cancer Using Prospectively Collected Sister Study Samples. Journal of the National Cancer Institute, 2013, 105, 694-700.	3.0	119
36	p53 mutation hotspot in radon-associated lung cancer. Lancet, The, 1994, 343, 86-87.	6.3	113

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37	Avoided and avoidable risks of cancer. Carcinogenesis, 1997, 18, 97-105.	1.3	111
38	Polymorphisms in DNA Repair Genes, Smoking, and Bladder Cancer Risk: Findings from the International Consortium of Bladder Cancer. Cancer Research, 2009, 69, 6857-6864.	0.4	107
39	RCP: a novel probe design bias correction method for Illumina Methylation BeadChip. Bioinformatics, 2016, 32, 2659-2663.	1.8	107
40	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
41	Genome-wide age-related DNA methylation changes in blood and other tissues relate to histone modification, expression and cancer. Carcinogenesis, 2014, 35, 356-364.	1.3	104
42	Microsomal epoxide hydrolase polymorphism as a risk factor for ovarian cancer. , 1996, 17, 160-162.		99
43	Lead Exposure as a Risk Factor for Amyotrophic Lateral Sclerosis. Neurodegenerative Diseases, 2005, 2, 195-201.	0.8	99
44	Serum microRNA expression as an early marker for breast cancer risk in prospectively collected samples from the Sister Study cohort. Breast Cancer Research, 2013, 15, R42.	2.2	96
45	RELIC: a novel dye-bias correction method for Illumina Methylation BeadChip. BMC Genomics, 2017, 18, 4.	1.2	96
46	CTNNB1 mutations and ?-catenin protein accumulation in human hepatocellular carcinomas associated with high exposure to aflatoxin B1. Molecular Carcinogenesis, 2001, 31, 68-73.	1.3	91
47	CpG Sites Associated with Cigarette Smoking: Analysis of Epigenome-Wide Data from the Sister Study. Environmental Health Perspectives, 2014, 122, 673-678.	2.8	91
48	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
49	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
50	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
51	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	5.8	86
52	Application of the GA/KNN method to SELDI proteomics data. Bioinformatics, 2004, 20, 1638-1640.	1.8	85
53	Maternal Smoking and Oral Clefts. Epidemiology, 2008, 19, 606-615.	1.2	83
54	Amyotrophic Lateral Sclerosis. Archives of Neurology, 1990, 47, 38.	4.9	82

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55	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. PLoS Genetics, 2016, 12, e1006385.	1.5	82
56	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
57	Variants of developmental genes (TGFA, TGFB3, andMSX1) and their associations with orofacial clefts: A case-parent triad analysis. Genetic Epidemiology, 2003, 24, 230-239.	0.6	80
58	Exploring the Effects of Methylenetetrahydrofolate Reductase Gene Variants C677T and A1298C on the Risk of Orofacial Clefts in 261 Norwegian Case-Parent Triads. American Journal of Epidemiology, 2003, 157, 1083-1091.	1.6	79
59	Genetic monitoring of human polymorphic cancer susceptibility genes by polymerase chain reaction: application to glutathione transferase mu.. Environmental Health Perspectives, 1992, 98, 113-117.	2.8	76
60	Blood DNA Methylation and Breast Cancer: A Prospective Case-Cohort Analysis in the Sister Study. Journal of the National Cancer Institute, 2020, 112, 87-94.	3.0	76
61	Glutathione S-transferase Î¼ in human lymphocyte and liver: role in modulating formation of carcinogen-derived DNA adducts. Carcinogenesis, 1991, 12, 2269-2275.	1.3	75
62	ras Oncogene Activation and Occupational Exposures in Acute Myeloid Leukemia. Journal of the National Cancer Institute, 1992, 84, 1626-1632.	3.0	73
63	Genetic polymorphism and prostate cancer aggressiveness: A caseâ€only study of 1,536 GWAS and candidate SNPs in Africanâ€Americans and Europeanâ€Americans. Prostate, 2013, 73, 11-22.	1.2	72
64	Recreational and household physical activity at different time points and DNA global methylation. European Journal of Cancer, 2013, 49, 2199-2206.	1.3	71
65	Antimutagenicity of cinnamaldehyde and vanillin in human cells: Global gene expression and possible role of DNA damage and repair. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2007, 616, 60-69.	0.4	70
66	Amyotrophic lateral sclerosis, lead, and genetic susceptibility: polymorphisms in the delta-aminolevulinic acid dehydratase and vitamin D receptor genes.. Environmental Health Perspectives, 2003, 111, 1335-1339.	2.8	67
67	Approximate Bayesian inference for quantiles. Journal of Nonparametric Statistics, 2005, 17, 385-400.	0.4	67
68	Roadmap for investigating epigenome deregulation and environmental origins of cancer. International Journal of Cancer, 2018, 142, 874-882.	2.3	64
69	Air pollution, particulate matter composition and methylation-based biologic age. Environment International, 2019, 132, 105071.	4.8	64
70	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	1.0	64
71	Vitamin D receptor polymorphisms and prostate cancer. Molecular Carcinogenesis, 2000, 27, 18-23.	1.3	63
72	Insulin-Like Growth Factor-I: a Key Regulator of Human Cancer Risk?. Journal of the National Cancer Institute, 1999, 91, 579-581.	3.0	62

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73	Folate and oneâ€carbon metabolism gene polymorphisms and their associations with oral facial clefts. American Journal of Medical Genetics, Part A, 2008, 146A, 440-449.	0.7	62
74	Maternal Age at Delivery Is Associated with an Epigenetic Signature in Both Newborns and Adults. PLoS ONE, 2016, 11, e0156361.	1.1	62
75	Maternal Alcohol Consumption, Alcohol Metabolism Genes, and the Risk of Oral Clefts: A Population-based Case-Control Study in Norway, 1996-2001. American Journal of Epidemiology, 2010, 172, 924-931.	1.6	60
76	Serum Vitamin D and Risk of Breast Cancer within Five Years. Environmental Health Perspectives, 2017, 125, 077004.	2.8	60
77	Potential for Selection Bias with Tumor Tissue Retrieval in Molecular Epidemiology Studies. Annals of Epidemiology, 2002, 12, 1-6.	0.9	58
78	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
79	Genetic Analysis of Complex Diseases. Science, 1997, 275, 1327-1330.	6.0	55
80	Associations of Body Composition and Physical Activity Level With Multiple Measures of Epigenetic Age Acceleration. American Journal of Epidemiology, 2021, 190, 984-993.	1.6	53
81	Progesterone receptor gene polymorphism and risk for breast and ovarian cancer. British Journal of Cancer, 1998, 78, 277-277.	2.9	51
82	Oral facial clefts and gene polymorphisms in metabolism of folate/oneâ€carbon and vitamin A: a pathwayâ€wide association study. Genetic Epidemiology, 2009, 33, 247-255.	0.6	51
83	An epigenome-wide study of body mass index and DNA methylation in blood using participants from the Sister Study cohort. International Journal of Obesity, 2017, 41, 194-199.	1.6	50
84	Association of Neighborhood Deprivation With Epigenetic Aging Using 4 Clock Metrics. JAMA Network Open, 2020, 3, e2024329.	2.8	50
85	Vitamin D, DNA methylation, and breast cancer. Breast Cancer Research, 2018, 20, 70.	2.2	49
86	Global DNA methylation and one-carbon metabolism gene polymorphisms and the risk of breast cancer in the Sister Study. Carcinogenesis, 2014, 35, 333-338.	1.3	48
87	Mini-and microsatellite mutations in children from Chernobyl accident cleanup workers. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2004, 559, 143-151.	0.9	47
88	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. Journal of Clinical Oncology, 2021, 39, 2564-2573.	0.8	47
89	Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. Human Genetics, 2015, 134, 439-450.	1.8	45
90	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45

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91	Inhibition of Fried Meat-Induced Colorectal DNA Damage and Altered Systemic Genotoxicity in Humans by Crucifera, Chlorophyllin, and Yogurt. PLoS ONE, 2011, 6, e18707.	1.1	44
92	Association between Urinary Prostaglandin E2 Metabolite and Breast Cancer Risk: A Prospective, Caseâ€“Cohort Study of Postmenopausal Women. Cancer Prevention Research, 2013, 6, 511-518.	0.7	43
93	Alcohol and DNA Methylation: An Epigenome-Wide Association Study in Blood and Normal Breast Tissue. American Journal of Epidemiology, 2019, 188, 1055-1065.	1.6	43
94	Lifetime use of nonsteroidal anti-inflammatory drugs and breast cancer risk: results from a prospective study of women with a sister with breast cancer. BMC Cancer, 2015, 15, 960.	1.1	42
95	Molecular Mechanisms of Lung Cancer. Chest, 1996, 109, 14S-19S.	0.4	41
96	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. Journal of the National Cancer Institute, 2021, 113, 1168-1176.	3.0	41
97	Lycopene Intake and Prostate Cancer Risk: Effect Modification by Plasma Antioxidants and the XRCC1 Genotype. Nutrition and Cancer, 2006, 55, 13-20.	0.9	39
98	Cleft palate, transforming growth factor alpha gene variants, and maternal exposures: Assessing gene-environment interactions in case-parent triads. Genetic Epidemiology, 2003, 25, 367-374.	0.6	38
99	Telomere length in peripheral blood and breast cancer risk in a prospective case-cohort analysis: results from the Sister Study. Cancer Causes and Control, 2011, 22, 1061-1066.	0.8	38
100	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
101	Shift work, DNA methylation and epigenetic age. International Journal of Epidemiology, 2019, 48, 1536-1544.	0.9	38
102	Tag SNP selection for candidate gene association studies using HapMap and gene resequencing data. European Journal of Human Genetics, 2007, 15, 1063-1070.	1.4	37
103	A Novel Host Cell Reactivation Assay to Assess Homologous Recombination Capacity in Human Cancer Cell Lines. Biochemical and Biophysical Research Communications, 2001, 281, 212-219.	1.0	36
104	VEGF PROMOTER HAPLOTYPE AND AMYOTROPHIC LATERAL SCLEROSIS (ALS). Journal of Neurogenetics, 2004, 18, 429-434.	0.6	36
105	TAGster: efficient selection of LD tag SNPs in single or multiple populations. Bioinformatics, 2007, 23, 3254-3255.	1.8	36
106	Soy Formula and Epigenetic Modifications: Analysis of Vaginal Epithelial Cells from Infant Girls in the IFED Study. Environmental Health Perspectives, 2017, 125, 447-452.	2.8	36
107	Breast Cancer Screening Strategies for Women With ATM, CHEK2, and PALB2 Pathogenic Variants. JAMA Oncology, 2022, 8, 587.	3.4	36
108	The ENmix DNA methylation analysis pipeline for Illumina BeadChip and comparisons with seven other preprocessing pipelines. Clinical Epigenetics, 2021, 13, 216.	1.8	35

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109	Homozygous deletions but no sequence mutations in coding regions ofp15 orp16 in human primary bladder tumors. Molecular Carcinogenesis, 1995, 14, 147-151.	1.3	33
110	Genome-Wide Association Study of Serum 25-Hydroxyvitamin D in US Women. Frontiers in Genetics, 2018, 9, 67.	1.1	32
111	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. European Urology, 2020, 78, 316-320.	0.9	32
112	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
113	XPD codon 751 polymorphism, metabolism genes, smoking, and bladder cancer risk. Cancer Epidemiology Biomarkers and Prevention, 2002, 11, 1004-11.	1.1	32
114	ipDMR: identification of differentially methylated regions with interval P-values. Bioinformatics, 2021, 37, 711-713.	1.8	31
115	p53 mutations in bladder cancer: evidence for exogenous versus endogenous risk factors. Cancer Research, 2003, 63, 7530-8.	0.4	31
116	L-myc Proto-oncogene alleles and susceptibility to hepatocellular carcinoma. International Journal of Cancer, 1993, 54, 927-930.	2.3	30
117	GWAS SNP Replication among African American and European American men in the North Carolinaâ€“Louisiana prostate cancer project (PCaP). Prostate, 2011, 71, 881-891.	1.2	30
118	Genetic Ancestry, Self-Reported Race and Ethnicity in African Americans and European Americans in the PCaP Cohort. PLoS ONE, 2012, 7, e30950.	1.1	30
119	Polymorphisms in CYP17 and CYP3A4 and prostate cancer in men of African descent. Prostate, 2013, 73, 668-676.	1.2	30
120	Epigenetic mortality predictors and incidence of breast cancer. Aging, 2019, 11, 11975-11987.	1.4	30
121	APE1 genotype and risk of bladder cancer: Evidence for effect modification by smoking. International Journal of Cancer, 2006, 118, 3170-3173.	2.3	28
122	Long-term use of calcium channel blocking drugs and breast cancer risk in a prospective cohort of US and Puerto Rican women. Breast Cancer Research, 2016, 18, 61.	2.2	28
123	oxBS-MLE: an efficient method to estimate 5-methylcytosine and 5-hydroxymethylcytosine in paired bisulfite and oxidative bisulfite treated DNA. Bioinformatics, 2016, 32, 3667-3669.	1.8	27
124	Reproduction, DNA methylation and biological age. Human Reproduction, 2019, 34, 1965-1973.	0.4	27
125	Zebrafish behavioural profiling identifies GABA and serotonin receptor ligands related to sedation and paradoxical excitation. Nature Communications, 2019, 10, 4078.	5.8	27
126	Alcohol Consumption and Methylation-Based Measures of Biological Age. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 2107-2111.	1.7	27

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127	Evidence for clustering of amyotrophic lateral sclerosis in wisconsin. Journal of Clinical Epidemiology, 1989, 42, 569-575.	2.4	26
128	p53 polymorphism in ovarian and bladder cancer. Lancet, The, 1995, 346, 182.	6.3	26
129	Bayesian Latent Variable Models for Median Regression on Multiple Outcomes. Biometrics, 2003, 59, 296-304.	0.8	26
130	Smoking is associated with increased telomerase activity in short-term cultures of human bronchial epithelial cells. Cancer Letters, 2007, 246, 24-33.	3.2	26
131	DNA repair gene XRCC3 codon 241 polymorphism, its interaction with smoking and XRCC1 polymorphisms, and bladder cancer risk. Cancer Epidemiology Biomarkers and Prevention, 2002, 11, 939-43.	1.1	26
132	Mutations in tetranucleotide repeats following DNA damage depend on repeat sequence and carcinogenic agent. Cancer Research, 2002, 62, 6052-60.	0.4	26
133	ONCOGENES AND THEIR APPLICATIONS IN EPIDEMIOLOGIC STUDIES. American Journal of Epidemiology, 1989, 130, 6-13.	1.6	25
134	Body mass index associated with genome-wide methylation in breast tissue. Breast Cancer Research and Treatment, 2015, 151, 453-463.	1.1	25
135	Prediagnostic Immune Cell Profiles and Breast Cancer. JAMA Network Open, 2020, 3, e1919536.	2.8	25
136	Admixture mapping of prostate cancer in African Americans participating in the North Carolinaâ€Łouisiana Prostate Cancer Project (PCaP). Prostate, 2014, 74, 1-9.	1.2	24
137	Africanâ€specific improvement of a polygenic hazard score for age at diagnosis of prostate cancer. International Journal of Cancer, 2021, 148, 99-105.	2.3	24
138	Healthy eating patterns and epigenetic measures of biological age. American Journal of Clinical Nutrition, 2022, 115, 171-179.	2.2	24
139	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	5.8	24
140	Association between Genetic Variants in DNA and Histone Methylation and Telomere Length. PLoS ONE, 2012, 7, e40504.	1.1	24
141	International pooled study on diet and bladder cancer: the bladder cancer, epidemiology and nutritional determinants (BLEND) study: design and baseline characteristics. Archives of Public Health, 2016, 74, 30.	1.0	23
142	Risk of Miscarriage and a Common Variant of the Estrogen Receptor Gene. American Journal of Epidemiology, 1993, 137, 1361-1364.	1.6	22
143	Genome-wide association study of anti-MÃ¼llerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. Human Molecular Genetics, 2019, 28, 1392-1401.	1.4	22
144	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. Journal of Clinical Oncology, 2021, 39, 3918-3926.	0.8	22

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145	A Rare Germline HOXB13 Variant Contributes to Risk of Prostate Cancer in Men of African Ancestry. European Urology, 2022, 81, 458-462.	0.9	22
146	Analytical and statistical methods to evaluate microsatellite allelic imbalance in small amounts of DNA. Laboratory Investigation, 2004, 84, 649-657.	1.7	21
147	Long-term ambient fine particulate matter and DNA methylation in inflammation pathways: results from the Sister Study. Epigenetics, 2020, 15, 524-535.	1.3	21
148	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. Journal of Clinical Oncology, 2021, 39, 3430-3440.	0.8	21
149	B region variant of the estrogen receptor gene. Nucleic Acids Research, 1992, 20, 2895-2895.	6.5	20
150	Xenobiotic Metabolism Genes and the Risk of Recurrent Spontaneous Abortion. Epidemiology, 1996, 7, 206-208.	1.2	20
151	No Association Between SOD2 or NQO1 Genotypes and Risk of Bladder Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 753-754.	1.1	20
152	DNA repair gene polymorphisms and probability of p53 mutation in bladder cancer. Molecular Carcinogenesis, 2006, 45, 715-719.	1.3	20
153	Symposium overview: the role of genetic polymorphism and repair deficiencies in environmental disease [published erratum appears in Toxicol Sci 1999 Oct;51(2):317]. Toxicological Sciences, 1999, 47, 135-143.	1.4	19
154	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
155	Blood DNA methylation profiles improve breast cancer prediction. Molecular Oncology, 2022, 16, 42-53.	2.1	19
156	Vitamin D receptor polymorphisms and prostate cancer. Molecular Carcinogenesis, 2000, 27, 18.	1.3	19
157	Genetic determinism and the overprotection of human subjects. Nature Genetics, 1999, 21, 362-362.	9.4	18
158	Val153Met Polymorphism of Catechol-O-Methyltransferase and Prevalence of Uterine Leiomyomata. Reproductive Sciences, 2007, 14, 117-120.	1.1	18
159	Reliability of DNA methylation measures using Illumina methylation BeadChip. Epigenetics, 2021, 16, 495-502.	1.3	18
160	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	1.4	17
161	A comparison of DNA methylation in newborn blood samples from infants with and without orofacial clefts. Clinical Epigenetics, 2019, 11, 40.	1.8	17
162	Epigenomeâ€wide analysis uncovers a bloodâ€based DNA methylation biomarker of lifetime cannabis use. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 173-182.	1.1	17

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163	In Utero Exposure to Diethylstilbestrol and Blood DNA Methylation in Women Ages 40â€“59 Years from the Sister Study. PLoS ONE, 2015, 10, e0118757.	1.1	16
164	How Well Do HapMap Haplotypes Identify Common Haplotypes of Genes? A Comparison with Haplotypes of 334 Genes Resequenced in the Environmental Genome Project. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 133-137.	1.1	15
165	Reliability and Short-Term Intra-Individual Variability of Telomere Length Measurement Using Monochrome Multiplexing Quantitative PCR. PLoS ONE, 2011, 6, e25774.	1.1	15
166	Single-Nucleotide Polymorphisms in Vitamin Dâ€“Related Genes May Modify Vitamin Dâ€“Breast Cancer Associations. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1761-1771.	1.1	15
167	Systemic Levels of Estrogens and PGE2 Synthesis in Relation to Postmenopausal Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 383-388.	1.1	15
168	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
169	Reproductive history and blood cell telomere length. Aging, 2018, 10, 2383-2393.	1.4	13
170	Bayesian hierarchically weighted finite mixture models for samples of distributions. Biostatistics, 2008, 10, 155-171.	0.9	11
171	A family-based, genome-wide association study of young-onset breast cancer: inherited variants and maternally mediated effects. European Journal of Human Genetics, 2016, 24, 1316-1323.	1.4	11
172	Previous GWAS hits in relation to young-onset breast cancer. Breast Cancer Research and Treatment, 2017, 161, 333-344.	1.1	11
173	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.	1.4	11
174	The association between coffee consumption and bladder cancer in the bladder cancer epidemiology and nutritional determinants (BLEND) international pooled study. Cancer Causes and Control, 2019, 30, 859-870.	0.8	10
175	Persistent epigenetic changes in adult daughters of older mothers. Epigenetics, 2019, 14, 467-476.	1.3	10
176	Geneâ€“methylation interactions: discovering region-wise DNA methylation levels that modify SNP-associated disease risk. Clinical Epigenetics, 2020, 12, 109.	1.8	9
177	A data mining approach to investigate food groups related to incidence of bladder cancer in the BLadder cancer Epidemiology and Nutritional Determinants International Study. British Journal of Nutrition, 2020, 124, 611-619.	1.2	9
178	Performance of African-ancestry-specific polygenic hazard score varies according to local ancestry in 8q24. Prostate Cancer and Prostatic Diseases, 2022, 25, 229-237.	2.0	9
179	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
180	HRAS1 variable number of tandem repeats polymorphism and risk of bladder cancer. International Journal of Cancer, 2002, 100, 414-418.	2.3	8

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