Peter Kraft

List of Publications by Year in descending order

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310 papers	26,003 citations	9234 74 h-index	10708 138 g-index
319 all docs	319 docs citations	319 times ranked	35896 citing authors

#	Article	IF	Citations
1	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
2	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
3	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
4	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
5	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
6	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
7	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
8	Elevation of circulating branched-chain amino acids is an early event in human pancreatic adenocarcinoma development. Nature Medicine, 2014, 20, 1193-1198.	15.2	510
9	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
10	Cursesâ€”Winner's and Otherwiseâ€”in Genetic Epidemiology. Epidemiology, 2008, 19, 649-651.	1.2	431
11	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.	9.4	426
12	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	13.9	414
13	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
14	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	9.4	402
15	Genetic Risk Prediction â€” Are We There Yet?. New England Journal of Medicine, 2009, 360, 1701-1703.	13.9	388
16	Exploiting Gene-Environment Interaction to Detect Genetic Associations. Human Heredity, 2007, 63, 111-119.	0.4	387
17	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
18	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365

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19	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
20	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
21	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
22	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
23	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
24	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
25	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
26	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
27	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
28	Replication in Genome-Wide Association Studies. Statistical Science, 2009, 24, 561-573.	1.6	237
29	Meta-analysis of Genome-wide Association Studies Identifies 1q22 as a Susceptibility Locus for Intracerebral Hemorrhage. American Journal of Human Genetics, 2014, 94, 511-521.	2.6	235
30	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
31	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. American Journal of Human Genetics, 2015, 96, 329-339.	2.6	230
32	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	9.4	211
33	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
34	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
35	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
36	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

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37	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
38	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
39	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
40	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
41	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
42	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
43	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	2.6	149
44	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
45	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
46	Accounting for haplotype uncertainty in matched association studies: A comparison of simple and flexible techniques. Genetic Epidemiology, 2005, 28, 261-272.	0.6	131
47	Beyond odds ratios â€" communicating disease risk based on genetic profiles. Nature Reviews Genetics, 2009, 10, 264-269.	7.7	131
48	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	1.4	128
49	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.4	126
50	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	5.8	123
51	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. Trials, 2014, 15, 85.	0.7	122
52	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
53	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
54	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2016, 7, 12048.	5.8	117

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55	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
56	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
57	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
58	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
59	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
60	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. Depression and Anxiety, 2016, 33, 265-280.	2.0	99
61	Association of Prostate Cancer Risk Variants with Gene Expression in Normal and Tumor Tissue. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 255-260.	1.1	97
62	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
63	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
64	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. Nature Communications, 2016, 7, 12510.	5.8	94
65	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
66	Association of CAV1/CAV2 Genomic Variants with Primary Open-Angle Glaucoma Overall and by Gender and Pattern of Visual Field Loss. Ophthalmology, 2014, 121, 508-516.	2.5	91
67	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested caseâ€“control study. PLoS Medicine, 2018, 15, e1002644.	3.9	91
68	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
69	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90
70	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
71	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
72	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88

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73	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
74	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
75	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
76	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
77	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
78	Survival Among Patients With Pancreatic Cancer and Long-Standing or Recent-Onset Diabetes Mellitus. Journal of Clinical Oncology, 2015, 33, 29-35.	0.8	83
79	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
80	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	1.1	79
81	Cigarette Smoking and Pancreatic Cancer Survival. Journal of Clinical Oncology, 2017, 35, 1822-1828.	0.8	78
82	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075.	0.9	75
83	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
84	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
85	Evaluation of polygenic risk scores for predicting breast and prostate cancer risk. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	74
86	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	0.6	74
87	Development of a clinical polygenic risk score assay and reporting workflow. Nature Medicine, 2022, 28, 1006-1013.	15.2	74
88	Diabetes, Weight Change, and Pancreatic Cancer Risk. JAMA Oncology, 2020, 6, e202948.	3.4	72
89	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. Human Molecular Genetics, 2014, 23, 5294-5302.	1.4	71
90	Consumers report lower confidence in their genetics knowledge following direct-to-consumer personal genomic testing. Genetics in Medicine, 2016, 18, 65-72.	1.1	71

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91	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	1.1	69
92	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. PLoS Medicine, 2016, 13, e1002118.	3.9	69
93	Integrating epidemiology and genetic association: the challenge of geneâ€“environment interaction. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1609-1616.	1.8	67
94	Genome-wide association study of selenium concentrations. Human Molecular Genetics, 2015, 24, 1469-1477.	1.4	67
95	Genetic Variation in the HSD17B1 Gene and Risk of Prostate Cancer. PLoS Genetics, 2005, 1, e68.	1.5	66
96	A Cross-Cancer Genetic Association Analysis of the DNA Repair and DNA Damage Signaling Pathways for Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 193-200.	1.1	66
97	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. American Journal of Human Genetics, 2020, 107, 352-363.	2.6	64
98	Precision Prevention and Early Detection of Cancer: Fundamental Principles. Cancer Discovery, 2018, 8, 803-811.	7.7	62
99	Transcriptomeâ€wide association studies accounting for colocalization using Egger regression. Genetic Epidemiology, 2018, 42, 418-433.	0.6	59
100	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
101	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	5.8	58
102	Inclusion of Endogenous Hormone Levels in Risk Prediction Models of Postmenopausal Breast Cancer. Journal of Clinical Oncology, 2014, 32, 3111-3117.	0.8	57
103	<scp>TERT</scp> gene harbors multiple variants associated with pancreatic cancer susceptibility. International Journal of Cancer, 2015, 137, 2175-2183.	2.3	57
104	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
105	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.4	55
106	Aggregate penetrance of genomic variants for actionable disorders in European and African Americans. Science Translational Medicine, 2016, 8, 364ra151.	5.8	55
107	Using genetics to test the causal relationship of total adiposity and periodontitis: Mendelian randomization analyses in the Gene-Lifestyle Interactions and Dental Endpoints (GLIDE) Consortium. International Journal of Epidemiology, 2015, 44, 638-650.	0.9	54
108	Associations of dairy intake with risk of mortality in women and men: three prospective cohort studies. BMJ: British Medical Journal, 2019, 367, l6204.	2.4	54

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109	A Prospective Analysis of Circulating Plasma Metabolites Associated with Ovarian Cancer Risk. Cancer Research, 2020, 80, 1357-1367.	0.4	54
110	Gainâ€ofâ€function mutations in SMAD4 cause a distinctive repertoire of cardiovascular phenotypes in patients with Myhre syndrome. American Journal of Medical Genetics, Part A, 2016, 170, 2617-2631.	0.7	53
111	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. Genetics in Medicine, 2017, 19, 30-35.	1.1	53
112	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676.	1.4	52
113	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
114	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. PLoS ONE, 2017, 12, e0173997.	1.1	52
115	Circulating vitamin D concentrations and risk of breast and prostate cancer: a Mendelian randomization study. International Journal of Epidemiology, 2019, 48, 1416-1424.	0.9	51
116	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
117	Circulating vitamin D, vitamin Dâ€“related genetic variation, and risk of fatal prostate cancer in the <scp>N</scp>ational <scp>C</scp>ancer <scp>I</scp>nstitute <scp>B</scp>reast and <scp>P</scp>rostate <scp>C</scp>ancer <scp>C</scp>ohort <scp>C</scp>onsortium. Cancer, 2015, 121, 1949-1956.	2.0	50
118	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50
119	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
120	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. Nature Communications, 2019, 10, 569.	5.8	50
121	Prediagnostic Plasma 25-Hydroxyvitamin D and Pancreatic Cancer Survival. Journal of Clinical Oncology, 2016, 34, 2899-2905.	0.8	49
122	Impact of Pre-analytic Blood Sample Collection Factors on Metabolomics. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 823-829.	1.1	48
123	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
124	Genetic Predictors of Cardiovascular Mortality During Intensive Glycemic Control in Type 2 Diabetes: Findings From the ACCORD Clinical Trial. Diabetes Care, 2016, 39, 1915-1924.	4.3	47
125	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. Metabolites, 2019, 9, 117.	1.3	47
126	The genetics of vitamin D. Bone, 2019, 126, 59-77.	1.4	47

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127	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
128	Study Designs for Genomeâ€Wide Association Studies. Advances in Genetics, 2008, 60, 465-504.	0.8	46
129	Pancreatic Cancer Risk Associated with Prediagnostic Plasma Levels of Leptin and Leptin Receptor Genetic Polymorphisms. Cancer Research, 2016, 76, 7160-7167.	0.4	46
130	Investigating the genetic relationship between Alzheimerâ€™s disease and cancer using GWAS summary statistics. Human Genetics, 2017, 136, 1341-1351.	1.8	46
131	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
132	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
133	Assessing the Association of Mitochondrial Genetic Variation With Primary Open-Angle Glaucoma Using Gene-Set Analyses. , 2016, 57, 5046.		44
134	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
135	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
136	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	0.9	43
137	Yield of whole exome sequencing in undiagnosed patients facing insurance coverage barriers to genetic testing. Journal of Genetic Counseling, 2019, 28, 1107-1118.	0.9	42
138	Identification of a melanoma susceptibility locus and somatic mutation inTET2. Carcinogenesis, 2014, 35, 2097-2101.	1.3	41
139	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	0.9	41
140	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
141	Leucocyte telomere length, genetic variants at theTERTgene region and risk of pancreatic cancer. Gut, 2017, 66, 1116-1122.	6.1	39
142	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	0.9	39
143	Prescription medication changes following direct-to-consumer personal genomic testing: findings from the Impact of Personal Genomics (PGen) Study. Genetics in Medicine, 2017, 19, 537-545.	1.1	39
144	Red Meat Intake, NAT2, and Risk of Colorectal Cancer: A Pooled Analysis of 11 Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 198-205.	1.1	38

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145	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
146	Post-GWAS geneâ€“environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79 000 women. Human Molecular Genetics, 2014, 23, 5260-5270.	1.4	37
147	A genomeâ€wide investigation of food addiction. Obesity, 2016, 24, 1336-1341.	1.5	37
148	Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. Carcinogenesis, 2016, 37, 96-105.	1.3	36
149	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36
150	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	4.7	36
151	Breast Cancer Screening Strategies for Women With ATM, CHEK2, and PALB2 Pathogenic Variants. JAMA Oncology, 2022, 8, 587.	3.4	36
152	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. PLoS Genetics, 2019, 15, e1007530.	1.5	35
153	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
154	Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies. PLoS Genetics, 2021, 17, e1008973.	1.5	35
155	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	1.5	34
156	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. Genetics in Medicine, 2015, 17, 536-544.	1.1	34
157	A Genome-Wide Association Study of Cutaneous Squamous Cell Carcinoma among European Descendants. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 714-720.	1.1	34
158	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096.	0.4	34
159	Circulating Lysophosphatidylcholines, Phosphatidylcholines, Ceramides, and Sphingomyelins and Ovarian Cancer Risk: A 23-Year Prospective Study. Journal of the National Cancer Institute, 2020, 112, 628-636.	3.0	34
160	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. Journal of the National Cancer Institute, 2021, 113, 434-442.	3.0	34
161	Returning actionable genomic results in a research biobank: Analytic validity, clinical implementation, and resource utilization. American Journal of Human Genetics, 2021, 108, 2224-2237.	2.6	34
162	Finding the missing geneâ€“environment interactions. European Journal of Epidemiology, 2015, 30, 353-355.	2.5	33

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163	Association of breast cancer risk loci with breast cancer survival. International Journal of Cancer, 2015, 137, 2837-2845.	2.3	33
164	Statin use and pancreatic cancer risk in two prospective cohort studies. Journal of Gastroenterology, 2018, 53, 959-966.	2.3	33
165	Genetic Tools for Coronary Risk Assessment in Type 2 Diabetes: A Cohort Study From the ACCORD Clinical Trial. Diabetes Care, 2018, 41, 2404-2413.	4.3	32
166	Association of a Primary Open-Angle Glaucoma Genetic Risk Score With Earlier Age at Diagnosis. JAMA Ophthalmology, 2019, 137, 1190.	1.4	32
167	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
168	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	2.2	31
169	Explicit Modeling of Ancestry Improves Polygenic Risk Scores and BLUP Prediction. Genetic Epidemiology, 2015, 39, 427-438.	0.6	30
170	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
171	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2020, 11, 820.	5.8	30
172	De Novo Pathogenic Variants in N-cadherin Cause a Syndromic Neurodevelopmental Disorder with Corpus Callosum, Axon, Cardiac, Ocular, and Genital Defects. American Journal of Human Genetics, 2019, 105, 854-868.	2.6	29
173	De novo mutations in TOMM70, a receptor of the mitochondrial import translocase, cause neurological impairment. Human Molecular Genetics, 2020, 29, 1568-1579.	1.4	29
174	Androgen Receptor CAG Repeat Polymorphism and Risk of TMPRSS2:ERGâ€“Positive Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2027-2031.	1.1	28
175	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. Carcinogenesis, 2015, 36, 999-1007.	1.3	28
176	Inherited variation in circadian rhythm genes and risks of prostate cancer and three other cancer sites in combined cancer consortia. International Journal of Cancer, 2017, 141, 1794-1802.	2.3	28
177	Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863.	0.6	28
178	PPARA Polymorphism Influences the Cardiovascular Benefit of Fenofibrate in Type 2 Diabetes: Findings From ACCORD-Lipid. Diabetes, 2020, 69, 771-783.	0.3	28
179	Complex Diseases, Complex Genes. Epidemiology, 2009, 20, 508-511.	1.2	27
180	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27

#	Article	IF	Citations
181	The causal relevance of body mass index in different histological types of lung cancer: A Mendelian randomization study. Scientific Reports, 2016, 6, 31121.	1.6	27
182	Covariate selection for association screening in multiphenotype genetic studies. Nature Genetics, 2017, 49, 1789-1795.	9.4	27
183	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
184	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27
185	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
186	Testing calibration of risk models at extremes of disease risk. Biostatistics, 2015, 16, 143-154.	0.9	26
187	Reclassification of genetic-based risk predictions as GWAS data accumulate. Genome Medicine, 2016, 8, 20.	3.6	26
188	Metabolome-Wide Association Study of the Relationship Between Habitual Physical Activity and Plasma Metabolite Levels. American Journal of Epidemiology, 2019, 188, 1932-1943.	1.6	26
189	Genetic risk variants associated with in situ breast cancer. Breast Cancer Research, 2015, 17, 82.	2.2	25
190	Quantifying the Polygenic Contribution to Cutaneous Squamous Cell Carcinoma Risk. Journal of Investigative Dermatology, 2018, 138, 1507-1510.	0.3	25
191	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
192	Particulate Matter and Traffic-Related Exposures in Relation to Breast Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 751-759.	1.1	24
193	Association of Prostate Cancer Risk Variants with TMPRSS2:ERG Status: Evidence for Distinct Molecular Subtypes. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 745-749.	1.1	23
194	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
195	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
196	Genomic correlation, shared loci, and causal relationship between obesity and polycystic ovary syndrome: a large-scale genome-wide cross-trait analysis. BMC Medicine, 2022, 20, 66.	2.3	22
197	RHD maternalâ€“fetal genotype incompatibility and schizophrenia: extending the MFG test to include multiple siblings and birth order. European Journal of Human Genetics, 2004, 12, 192-198.	1.4	21
198	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657.	0.9	21

#	Article	IF	Citations
199	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	0.8	21
200	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. Journal of the National Cancer Institute, 2019, 111, 557-567.	3.0	21
201	The Use of Genetic Correlation and Mendelian Randomization Studies to Increase Our Understanding of Relationships between Complex Traits. Current Epidemiology Reports, 2020, 7, 104-112.	1.1	21
202	Multivariate variance-components analysis of longitudinal blood pressure measurements from the Framingham Heart Study. BMC Genetics, 2003, 4, S55.	2.7	20
203	Vitamin Dâ€“Associated Genetic Variation and Risk of Breast Cancer in the Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 627-630.	1.1	20
204	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. Human Molecular Genetics, 2018, 27, 853-859.	1.4	20
205	Case-sibling gene-association studies for diseases with variable age at onset. Statistics in Medicine, 2004, 23, 3697-3712.	0.8	19
206	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
207	Residential particulate matter and distance to roadways in relation to mammographic density: results from the Nursesâ€™ Health Studies. Breast Cancer Research, 2017, 19, 124.	2.2	19
208	Genetic and Circulating Biomarker Data Improve Risk Prediction for Pancreatic Cancer in the General Population. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 999-1008.	1.1	19
209	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	1.1	19
210	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. Breast Cancer Research and Treatment, 2013, 138, 529-542.	1.1	18
211	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. Carcinogenesis, 2014, 35, 2068-2073.	1.3	18
212	Lack of geneâ€“diuretic interactions on the risk of incident gout: the Nursesâ€™ Health Study and Health Professionals Follow-up Study. Annals of the Rheumatic Diseases, 2015, 74, 1394-1398.	0.5	18
213	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. BMC Bioinformatics, 2017, 18, 304.	1.2	18
214	Genetic correlations between intraocular pressure, blood pressure and primary open-angle glaucoma: a multi-cohort analysis. European Journal of Human Genetics, 2017, 25, 1261-1267.	1.4	18
215	The impact of direct-to-consumer personal genomic testing on perceived risk of breast, prostate, colorectal, and lung cancer: findings from the PGen study. BMC Medical Genomics, 2015, 8, 63.	0.7	17
216	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

#	Article	IF	Citations
217	Prediagnostic Leukocyte Telomere Length and Pancreatic Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1868-1875.	1.1	17
218	Inherited variants at 3q13.33 and 3p24.1 are associated with risk of diffuse large B-cell lymphoma and implicate immune pathways. Human Molecular Genetics, 2020, 29, 70-79.	1.4	17
219	Polygenic scores, diet quality, and type 2 diabetes risk: An observational study among 35,759 adults from 3 US cohorts. PLoS Medicine, 2022, 19, e1003972.	3.9	17
220	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
221	Interaction of a genetic risk score with physical activity, physical inactivity, and body mass index in relation to venous thromboembolism risk. Genetic Epidemiology, 2018, 42, 354-365.	0.6	16
222	Modulation of GLP-1 Levels by a Genetic Variant That Regulates the Cardiovascular Effects of Intensive Glycemic Control in ACCORD. Diabetes Care, 2018, 41, 348-355.	4.3	16
223	Multitrait GWAS to connect disease variants and biological mechanisms. PLoS Genetics, 2021, 17, e1009713.	1.5	16
224	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. Lupus Science and Medicine, 2017, 4, e000187.	1.1	15
225	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for WaldenstrÃ¶m macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
226	Homozygous TRPV4 mutation causes congenital distal spinal muscular atrophy and arthrogryposis. Neurology: Genetics, 2019, 5, e312.	0.9	15
227	Associations between smoking behavior-related alleles and the risk of melanoma. Oncotarget, 2016, 7, 47366-47375.	0.8	15
228	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
229	A genome-wide association study of energy intake and expenditure. PLoS ONE, 2018, 13, e0201555.	1.1	14
230	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets. , 2018, 59, 629.		14
231	Allergy, asthma, and the risk of breast and prostate cancer: a Mendelian randomization study. Cancer Causes and Control, 2020, 31, 273-282.	0.8	14
232	Simplified Breast Risk Tool Integrating Questionnaire Risk Factors, Mammographic Density, and Polygenic Risk Score: Development and Validation. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 600-607.	1.1	14
233	Somatic mutational profiles and germline polygenic risk scores in human cancer. Genome Medicine, 2022, 14, 14.	3.6	14
234	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	3.0	14

#	Article	IF	Citations
235	Noncirrhotic hyperammonemia after deceased donor kidney transplantation: A case report. American Journal of Transplantation, 2019, 19, 3197-3201.	2.6	13
236	Colorectal cancer susceptibility variants and risk of conventional adenomas and serrated polyps: results from three cohort studies. International Journal of Epidemiology, 2020, 49, 259-269.	0.9	13
237	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	2.3	13
238	Circulating carotenoids and breast cancer among high-risk individuals. American Journal of Clinical Nutrition, 2021, 113, 525-533.	2.2	13
239	Heterozygous loss-of-function variants significantly expand the phenotypes associated with loss of GDF11. Genetics in Medicine, 2021, 23, 1889-1900.	1.1	13
240	Genome-wide association study meta-analysis identifies three novel loci for circulating anti-MÃ¼llerian hormone levels in women. Human Reproduction, 2022, 37, 1069-1082.	0.4	13
241	Joint Effects of Colorectal Cancer Susceptibility Loci, Circulating 25-Hydroxyvitamin D and Risk of Colorectal Cancer. PLoS ONE, 2014, 9, e92212.	1.1	12
242	Exome-Wide Association Study of Endometrial Cancer in a Multiethnic Population. PLoS ONE, 2014, 9, e97045.	1.1	12
243	Joint Effects of PON1 Polymorphisms and Vegetable Intake on Ischemic Stroke: A Family-Based Case Control Study. International Journal of Molecular Sciences, 2017, 18, 2652.	1.8	12
244	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. American Journal of Ophthalmology, 2019, 206, 245-255.	1.7	12
245	Joint Analysis of Multiple Interaction Parameters in Genetic Association Studies. Genetics, 2019, 211, 483-494.	1.2	12
246	Sex-Stratified Polygenic Risk Score Identifies Individuals at Increased Risk of Basal Cell Carcinoma. Journal of Investigative Dermatology, 2020, 140, 971-975.	0.3	12
247	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
248	Estimating the effective sample size in association studies of quantitative traits. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	12
249	Sniffing out significant â€œPee valuesâ€• genome wide association study of asparagus anosmia. BMJ, The, 2016, 355, i6071.	3.0	11
250	Family history of cancer, Ashkenazi Jewish ancestry, and pancreatic cancer risk. British Journal of Cancer, 2019, 120, 848-854.	2.9	11
251	Instrumental variable estimation for a time-varying treatment and a time-to-event outcome via structural nested cumulative failure time models. BMC Medical Research Methodology, 2021, 21, 258.	1.4	11
252	Genome-Wide Association Studies of Multiple Keratinocyte Cancers. PLoS ONE, 2017, 12, e0169873.	1.1	10

#	Article	IF	Citations
253	Metaâ€Analysis of Rare Variant Association Tests in Multiethnic Populations. Genetic Epidemiology, 2016, 40, 57-65.	0.6	9
254	Analysis of a Genetic Polymorphism in the CostimulatoryÂMolecule TNFSF4 with Hematopoietic StemÂCellÂTransplant Outcomes. Biology of Blood and Marrow Transplantation, 2016, 22, 27-36.	2.0	9
255	Polygenic risk score of shorter telomere length and risk of depression and anxiety in women. Journal of Psychiatric Research, 2018, 103, 182-188.	1.5	9
256	Prediagnostic Inflammation and Pancreatic Cancer Survival. Journal of the National Cancer Institute, 2021, 113, 1186-1193.	3.0	9
257	Multitrait transcriptomeâ€wide association study (TWAS) tests. Genetic Epidemiology, 2021, 45, 563-576.	0.6	9
258	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. American Journal of Clinical Nutrition, 2021, 114, 1408-1417.	2.2	9
259	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
260	Mendelian Randomization With Repeated Measures of a Time-varying Exposure. Epidemiology, 2022, 33, 84-94.	1.2	9
261	Reassessing the causal role of obesity in breast cancer susceptibility: a comprehensive multivariable Mendelian randomization investigating the distribution and timing of exposure. International Journal of Epidemiology, 2023, 52, 58-70.	0.9	9
262	EFFICIENT TWO-STAGE GENOME-WIDE ASSOCIATION DESIGNS BASED ON FALSE POSITIVE REPORT PROBABILITIES. , 2005, , .		8
263	A Genome-Wide â€œPleiotropy Scanâ€•Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. PLoS ONE, 2014, 9, e85955.	1.1	8
264	A Genomeâ€Wide Association Study of Childhood Body Fatness. Obesity, 2021, 29, 446-453.	1.5	8
265	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143.	0.4	8
266	Genome-Wide Association Study for Urinary and Fecal Incontinence in Women. Journal of Urology, 2020, 203, 978-983.	0.2	8
267	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	2.9	7
268	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. European Journal of Human Genetics, 2020, 28, 656-668.	1.4	7
269	The Association of Modifiable Breast Cancer Risk Factors and Somatic Genomic Alterations in Breast Tumors: The Cancer Genome Atlas Network. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 599-605.	1.1	7
270	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7

#	Article	IF	Citations
271	A targeted genetic association study of epithelial ovarian cancer susceptibility. Oncotarget, 2016, 7, 7381-7389.	0.8	7
272	Genetic variation in the HSD17B1 gene and risk of prostate cancer. PLoS Genetics, 2005, preprint, e68.	1.5	6
273	Deep targeted sequencing of 12 breast cancer susceptibility regions in 4611 women across four different ethnicities. Breast Cancer Research, 2016, 18, 109.	2.2	6
274	Mendelian Randomization Analysis of n-6 Polyunsaturated Fatty Acid Levels and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2735-2739.	1.1	6
275	Validating Breast Cancer Risk Prediction Models in the Korean Cancer Prevention Study-II Biobank. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1271-1277.	1.1	6
276	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
277	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
278	A Metabolomics Analysis of Circulating Carotenoids and Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 85-96.	1.1	6
279	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
280	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	0.7	6
281	Hierarchical modeling of melanocortin 1 receptor variants with skin cancer risk. Genetic Epidemiology, 2018, 42, 571-586.	0.6	5
282	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
283	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5
284	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	2.9	5
285	Obesity, Adiposity, and Risk of Symptomatic Gallstone Disease According to Genetic Susceptibility. Clinical Gastroenterology and Hepatology, 2022, 20, e1083-e1120.	2.4	5
286	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci.. Journal of Clinical Oncology, 2017, 2017, 1-1.	0.8	5
287	Efficient two-stage genome-wide association designs based on false positive report probabilities. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 523-34.	0.7	5
288	A novel DPH5-related diphthamide-deficiency syndrome causing embryonic lethality or profound neurodevelopmental disorder. Genetics in Medicine, 2022, 24, 1567-1582.	1.1	5

#	Article	IF	Citations
289	Prediagnostic 25-Hydroxyvitamin D Concentrations in Relation to Tumor Molecular Alterations and Risk of Breast Cancer Recurrence. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1253-1263.	1.1	4
290	Multilocus Heterozygosity and Coronary Heart Disease: Nested Case-Control Studies in Men and Women. PLoS ONE, 2015, 10, e0124847.	1.1	3
291	Exhaustive screens for disease susceptibility loci incorporating statistical interaction of genotypes: a comparison of likelihood-ratio-based and Akaike and Bayesian information criteria-based methods. BMC Proceedings, 2007, 1, S25.	1.8	2
292	Interactions between breast cancer susceptibility loci and menopausal hormone therapy in relationship to breast cancer in the Breast and Prostate Cancer Cohort Consortium. Breast Cancer Research and Treatment, 2016, 155, 531-540.	1.1	2
293	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. Bioinformatics, 2017, 33, 1389-1391.	1.8	2
294	Identification of an Identical de Novo SCAMP5 Missense Variant in Four Unrelated Patients With Seizures and Severe Neurodevelopmental Delay. Frontiers in Pharmacology, 2020, 11, 599191.	1.6	2
295	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
296	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
297	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	1.6	2
298	Response to Day etÂal.. American Journal of Human Genetics, 2016, 98, 394-395.	2.6	1
299	Fine Tuning the Risk of Hereditary Cancer Using Genome-Wide Association Studies. Journal of Clinical Oncology, 2017, 35, 2224-2225.	0.8	1
300	Height, nevus count, and risk of cutaneous malignant melanoma: Results from 2 large cohorts of US women. Journal of the American Academy of Dermatology, 2020, 83, 1049-1056.	0.6	1
301	Rare Inherited Defects of the Complement System in Purpura Fulminans. Blood, 2020, 136, 35-36.	0.6	1
302	A comprehensive analysis of polymorphic variants in steroid hormone and insulinâ€like growth factorâ€1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. International Journal of Cancer, 2018, 142, 1182-1188.	2.3	0
303	A Pathway Analysis of Hereditary Hemochromatosis-related Genes and Pancreatic Ductal Adenocarcinoma Risk (FS11-05-19). Current Developments in Nutrition, 2019, 3, nzz037.FS11-05-19.	0.1	0
304	Involvement of fine particulate matter exposure with gene expression pathways in breast tumor and adjacent-normal breast tissue. Environmental Research, 2020, 186, 109535.	3.7	0
305	Germline pathogenic variants in cancer predisposition genes among women with invasive lobular cancer of breast.. Journal of Clinical Oncology, 2021, 39, 10581-10581.	0.8	0
306	Breast cancer screening for carriers of ATM, CHEK2, and PALB2 pathogenic variants: A comparative modeling analysis.. Journal of Clinical Oncology, 2021, 39, 10500-10500.	0.8	0

#	Article	IF	Citations
307	Circadian dysrhythm and advanced prostate cancer.. Journal of Clinical Oncology, 2014, 32, 199-199.	0.8	0
308	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci.. Journal of Clinical Oncology, 2017, 35, 1-1.	0.8	0
309	Genetic predisposition to breast cancer among African American women.. Journal of Clinical Oncology, 2019, 37, 104-104.	0.8	0
310	Abstract P3-13-02: A genome-wide association study of mammographic texture variation. Cancer Research, 2022, 82, P3-13-02-P3-13-02.	0.4	0