Roger L. Milne

List of Publications by Year
in descending order

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314 papers	29,299 citations	9254 74 h-index	6831 155 g-index
341 all docs	341 docs citations	341 times ranked	34721 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
2	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	3.8	1,898
3	Risk of COVID-19 among front-line health-care workers and the general community: a prospective cohort study. Lancet Public Health, The, 2020, 5, e475-e483.	4.7	1,595
4	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
5	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
6	Socioeconomic status and the 25â€ˆÃ—â€ˆ25 risk factors as determinants of premature mortality: a multicohort study and meta-analysis of 1Â·7 million men and women. Lancet, The, 2017, 389, 1229-1237.	6.3	825
7	Beyond GWASs: Illuminating the Dark Road from Association to Function. American Journal of Human Genetics, 2013, 93, 779-797.	2.6	688
8	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
9	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
10	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
11	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
12	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
13	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	9.4	472
14	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
15	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
16	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
17	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
18	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377

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19	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
20	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
21	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
22	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
23	Rapid implementation of mobile technology for real-time epidemiology of COVID-19. Science, 2020, 368, 1362-1367.	6.0	313
24	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
25	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
26	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	3.4	285
27	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
28	Common Breast Cancer-Predisposition Alleles Are Associated with Breast Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. American Journal of Human Genetics, 2008, 82, 937-948.	2.6	257
29	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
30	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
31	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
32	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	5.8	193
33	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
34	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
35	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. Scientific Reports, 2017, 7, 16266.	1.6	181
36	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178

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37	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
38	DNA methylationâ€based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. International Journal of Cancer, 2018, 142, 1611-1619.	2.3	153
39	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
40	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. Nature Genetics, 2018, 50, 1067-1071.	9.4	152
41	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	1.4	137
42	An international initiative to identify genetic modifiers of cancer risk in BRCA1 and BRCA2 mutation carriers: the Consortium of Investigators of Modifiers of BRCA1 and BRCA2 (CIMBA). Breast Cancer Research, 2007, 9, 104.	2.2	136
43	Oral Contraceptive Use and Risk of Early-Onset Breast Cancer in Carriers and Noncarriers of BRCA1 and BRCA2 Mutations. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 350-356.	1.1	133
44	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129
45	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
46	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	2.6	124
47	The Breast Cancer Susceptibility Mutation PALB2 1592delT Is Associated with an Aggressive Tumor Phenotype. Clinical Cancer Research, 2009, 15, 3214-3222.	3.2	122
48	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
49	10-year performance of four models of breast cancer risk: a validation study. Lancet Oncology, The, 2019, 20, 504-517.	5.1	116
50	Amount and Intensity of Leisure-Time Physical Activity and Lower Cancer Risk. Journal of Clinical Oncology, 2020, 38, 686-697.	0.8	114
51	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
52	ABCA Transporter Gene Expression and Poor Outcome in Epithelial Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	3.0	107
53	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	1.4	106
54	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. American Journal of Epidemiology, 2018, 187, 529-538.	1.6	106

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55	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
56	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
57	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.4	100
58	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	1.4	99
59	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
60	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
61	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	2.2	97
62	Breast Cancer Risk Prediction Using Clinical Models and 77 Independent Risk-Associated SNPs for Women Aged Under 50 Years: Australian Breast Cancer Family Registry. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 359-365.	1.1	96
63	Tumor PIK3CA Genotype and Prognosis in Early-Stage Breast Cancer: A Pooled Analysis of Individual Patient Data. Journal of Clinical Oncology, 2018, 36, 981-990.	0.8	95
64	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
65	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
66	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
67	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
68	Circulating Levels of Insulin-like Growth Factor 1 and Insulin-like Growth Factor Binding Protein 3 Associate With Risk of Colorectal Cancer Based on Serologic and Mendelian Randomization Analyses. Gastroenterology, 2020, 158, 1300-1312.e20.	0.6	90
69	Metaâ€analysis of 16 studies of the association of alcohol with colorectal cancer. International Journal of Cancer, 2020, 146, 861-873.	2.3	89
70	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
71	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
72	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87

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73	Anti-MÃ¼llerian hormone serum concentrations of women with germlineBRCA1orBRCA2mutations. Human Reproduction, 2016, 31, 1126-1132.	0.4	84
74	Associations of alcohol intake, smoking, physical activity and obesity with survival following colorectal cancer diagnosis by stage, anatomic site and tumor molecular subtype. International Journal of Cancer, 2018, 142, 238-250.	2.3	83
75	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
76	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	2.2	78
77	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
78	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77
79	Heritable DNA methylation marks associated with susceptibility to breast cancer. Nature Communications, 2018, 9, 867.	5.8	76
80	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396.	2.3	76
81	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
82	Low Free Testosterone and Prostate Cancer Risk: A Collaborative Analysis of 20 Prospective Studies. European Urology, 2018, 74, 585-594.	0.9	75
83	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
84	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
85	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	1.4	68
86	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
87	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. Cancer Research, 2018, 78, 6011-6021.	0.4	67
88	Association Between Single-Nucleotide Polymorphisms in Hormone Metabolism and DNA Repair Genes and Epithelial Ovarian Cancer: Results from Two Australian Studies and an Additional Validation Set. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2557-2565.	1.1	65
89	Modifiers of breast and ovarian cancer risks for BRCA1 and BRCA2 mutation carriers. Endocrine-Related Cancer, 2016, 23, T69-T84.	1.6	63
90	Genetics of epilepsy. Neurology, 2014, 83, 1042-1048.	1.5	61

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91	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
92	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
93	Reliability of DNA methylation measures from dried blood spots and mononuclear cells using the HumanMethylation450k BeadArray. Scientific Reports, 2016, 6, 30317.	1.6	58
94	Sustained Weight Loss and Risk of Breast Cancer in Women 50 Years and Older: A Pooled Analysis of Prospective Data. Journal of the National Cancer Institute, 2020, 112, 929-937.	3.0	58
95	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
96	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
97	Pooled analysis of active cigarette smoking and invasive breast cancer risk in 14 cohort studies. International Journal of Epidemiology, 2017, 46, dyw288.	0.9	56
98	Smoking and blood DNA methylation: an epigenome-wide association study and assessment of reversibility. Epigenetics, 2020, 15, 358-368.	1.3	56
99	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
100	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
101	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
102	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
103	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	1.6	51
104	Age-specific breast cancer risk by body mass index and familial risk: prospective family study cohort (ProF-SC). Breast Cancer Research, 2018, 20, 132.	2.2	51
105	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
106	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
107	Past recreational physical activity, body size, and all-cause mortality following breast cancer diagnosis: results from the breast cancer family registry. Breast Cancer Research and Treatment, 2010, 123, 531-542.	1.1	50
108	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49

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109	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of crossâ€sectional and longitudinal data. Addiction Biology, 2021, 26, e12855.	1.4	49
110	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	1.1	48
111	Inference about causation between body mass index and DNA methylation in blood from a twin family study. International Journal of Obesity, 2019, 43, 243-252.	1.6	48
112	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
113	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
114	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
115	Regular use of aspirin and other non-steroidal anti-inflammatory drugs and breast cancer risk for women at familial or genetic risk: a cohort study. Breast Cancer Research, 2019, 21, 52.	2.2	44
116	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	1.8	44
117	Special Report: The Biology of Inequalities in Health: The Lifepath Consortium. Frontiers in Public Health, 2020, 8, 118.	1.3	44
118	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44
119	No Increased Risk of Breast Cancer Associated with Alcohol Consumption among Carriers of BRCA1 and BRCA2 Mutations Ages <50 Years. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 1565-1567.	1.1	42
120	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2020, 22, 8.	2.2	41
121	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
122	Biological Aging Measures Based on Blood DNA Methylation and Risk of Cancer: A Prospective Study. JNCI Cancer Spectrum, 2021, 5, pkaa109.	1.4	40
123	Preventing breast and ovarian cancers in highâ€risk BRCA1 and BRCA2 mutation carriers. Medical Journal of Australia, 2013, 199, 680-683.	0.8	39
124	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
125	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
126	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38

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127	Genome-wide measures of DNA methylation in peripheral blood and the risk of urothelial cell carcinoma: a prospective nested caseâ€“control study. British Journal of Cancer, 2016, 115, 664-673.	2.9	38
128	Genome-wide average DNA methylation is determined in utero. International Journal of Epidemiology, 2018, 47, 908-916.	0.9	38
129	Factors Explaining Socio-Economic Inequalities in Cancer Survival: A Systematic Review. Cancer Control, 2021, 28, 107327482110119.	0.7	38
130	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. Journal of Clinical Investigation, 2021, 131, .	3.9	38
131	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	0.5	37
132	Recreational Physical Activity Is Associated with Reduced Breast Cancer Risk in Adult Women at High Risk for Breast Cancer: A Cohort Study of Women Selected for Familial and Genetic Risk. Cancer Research, 2020, 80, 116-125.	0.4	37
133	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	0.6	36
134	A Common Cancer Risk-Associated Allele in the hTERT Locus Encodes a Dominant Negative Inhibitor of Telomerase. PLoS Genetics, 2015, 11, e1005286.	1.5	35
135	Global measures of peripheral blood-derived DNA methylation as a risk factor in the development of mature B-cell neoplasms. Epigenomics, 2016, 8, 55-66.	1.0	35
136	Dietary intake of one-carbon metabolism nutrients and DNA methylation in peripheral blood. American Journal of Clinical Nutrition, 2018, 108, 611-621.	2.2	35
137	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780.	0.9	35
138	The Risk of Ovarian Cancer Increases with an Increase in the Lifetime Number of Ovulatory Cycles: An Analysis from the Ovarian Cancer Cohort Consortium (OC3). Cancer Research, 2020, 80, 1210-1218.	0.4	35
139	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
140	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	1.8	34
141	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. Breast Cancer Research, 2019, 21, 62.	2.2	34
142	The COronavirus Pandemic Epidemiology (COPE) Consortium: A Call to Action. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1283-1289.	1.1	34
143	Association Between Molecular Subtypes of Colorectal Tumors and Patient Survival, Based on Pooled Analysis of 7 International Studies. Gastroenterology, 2020, 158, 2158-2168.e4.	0.6	34
144	Oral contraceptive use and ovarian cancer risk for BRCA1/2 mutation carriers: an international cohort study. American Journal of Obstetrics and Gynecology, 2021, 225, 51.e1-51.e17.	0.7	34

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145	Differences in cancer survival by area-level socio-economic disadvantage: A population-based study using cancer registry data. PLoS ONE, 2020, 15, e0228551.	1.1	34
146	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. Clinical Cancer Research, 2015, 21, 5264-5276.	3.2	33
147	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
148	Body Size Indicators and Risk of Gallbladder Cancer: Pooled Analysis of Individual-Level Data from 19 Prospective Cohort Studies. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 597-606.	1.1	33
149	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. JNCI Cancer Spectrum, 2018, 2, pky023.	1.4	33
150	Genetic and environmental causes of variation in epigenetic aging across the lifespan. Clinical Epigenetics, 2020, 12, 158.	1.8	33
151	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
152	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
153	Genomeâ€Wide Measures of Peripheral Blood Dna Methylation and Prostate Cancer Risk in a Prospective Nested Caseâ€Control Study. Prostate, 2017, 77, 471-478.	1.2	31
154	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	2.1	31
155	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
156	Anthropometric Risk Factors for Cancers of the Biliary Tract in the Biliary Tract Cancers Pooling Project. Cancer Research, 2019, 79, 3973-3982.	0.4	31
157	Trajectories of body mass index in adulthood and all-cause and cause-specific mortality in the Melbourne Collaborative Cohort Study. BMJ Open, 2019, 9, e030078.	0.8	31
158	Risk-Reducing Oophorectomy and Breast Cancer Risk Across the Spectrum of Familial Risk. Journal of the National Cancer Institute, 2019, 111, 331-334.	3.0	31
159	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
160	Body size and weight change over adulthood and risk of breast cancer by menopausal and hormone receptor status: a pooled analysis of 20 prospective cohort studies. European Journal of Epidemiology, 2021, 36, 37-55.	2.5	30
161	eQTL Colocalization Analyses Identify NTN4 as a Candidate Breast Cancer Risk Gene. American Journal of Human Genetics, 2020, 107, 778-787.	2.6	29
162	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	0.8	29

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163	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
164	Ovarian cancer risk factors by tumor aggressiveness: An analysis from the Ovarian Cancer Cohort Consortium. International Journal of Cancer, 2019, 145, 58-69.	2.3	28
165	Association of Markers of Inflammation, the Kynurenine Pathway and B Vitamins with Age and Mortality, and a Signature of Inflammaging. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 826-836.	1.7	28
166	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
167	Alcohol consumption, cigarette smoking, and familial breast cancer risk: findings from the Prospective Family Study Cohort (ProF-SC). Breast Cancer Research, 2019, 21, 128.	2.2	27
168	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
169	Genetically predicted circulating concentrations of micronutrients and risk of colorectal cancer among individuals of European descent: a Mendelian randomization study. American Journal of Clinical Nutrition, 2021, 113, 1490-1502.	2.2	27
170	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
171	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
172	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
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