

Roger L. Milne

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

304
papers

19,320
citations

62
h-index

134
g-index

341
ext. papers

25,026
ext. citations

9.5
avg, IF

5.45
L-index

#	Paper	IF	Citations
304	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007 , 447, 1087-93	50.4	1957
303	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 317, 2402-2416	27.4	1140
302	Risk of COVID-19 among front-line health-care workers and the general community: a prospective cohort study. <i>Lancet Public Health, The</i> , 2020 , 5, e475-e483	22.4	899
301	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
300	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
299	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007 , 39, 352-836.3	36.3	557
298	Beyond GWASs: illuminating the dark road from association to function. <i>American Journal of Human Genetics</i> , 2013 , 93, 779-97	11	515
297	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 250-63	9.7	513
296	Socioeconomic status and the 25 D25 risk factors as determinants of premature mortality: a multicohort study and meta-analysis of 17 million men and women. <i>Lancet, The</i> , 2017 , 389, 1229-1237	40	511
295	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013 , 45, 371-84, 384e1-2	36.3	422
294	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
293	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009 , 41, 585-906.3	36.3	393
292	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
291	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
290	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. <i>PLoS Genetics</i> , 2008 , 4, e1000054	6	280
289	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017 , 49, 834-841	36.3	257
288	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256

287	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017 , 49, 1126-1132	36.3	246
286	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237
285	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
284	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014 , 46, 994-1000	36.3	226
283	Common breast cancer-predisposition alleles are associated with breast cancer risk in BRCA1 and BRCA2 mutation carriers. <i>American Journal of Human Genetics</i> , 2008 , 82, 937-48	11	218
282	Rapid implementation of mobile technology for real-time epidemiology of COVID-19. <i>Science</i> , 2020 , 368, 1362-1367	33.3	208
281	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190
280	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016 , 2, 1295-1302	13.4	189
279	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
278	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
277	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019 , 51, 76-83	36.3	177
276	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. <i>American Journal of Human Genetics</i> , 2016 , 98, 830-842	11	153
275	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021 , 384, 428-439	59.2	143
274	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). <i>Breast Cancer Research</i> , 2007 , 9, 104	8.3	121
273	Social adversity and epigenetic aging: a multi-cohort study on socioeconomic differences in peripheral blood DNA methylation. <i>Scientific Reports</i> , 2017 , 7, 16266	4.9	118
272	Oral contraceptive use and risk of early-onset breast cancer in carriers and noncarriers of BRCA1 and BRCA2 mutations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005 , 14, 350-6	4	113
271	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 2750-60	2.2	107
270	The breast cancer susceptibility mutation PALB2 1592delT is associated with an aggressive tumor phenotype. <i>Clinical Cancer Research</i> , 2009 , 15, 3214-22	12.9	106

269	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016 , 6, 1052-67	24.4	104
268	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018 , 9, 556	17.4	103
267	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018 , 50, 968-978	36.3	101
266	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
265	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. <i>Cancer Research</i> , 2012 , 72, 1795-803	33.1	93
264	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2009 , 18, 4442-56	5.6	91
263	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. <i>PLoS Genetics</i> , 2013 , 9, e1003173	6	90
262	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
261	Genome-wide association study of intraocular pressure uncovers new pathways to glaucoma. <i>Nature Genetics</i> , 2018 , 50, 1067-1071	36.3	86
260	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
259	DNA methylation-based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. <i>International Journal of Cancer</i> , 2018 , 142, 1611-1619	7.5	83
258	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014 , 16, 3419	8.3	82
257	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013 , 93, 1046-60	11	80
256	ABCA transporter gene expression and poor outcome in epithelial ovarian cancer. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	79
255	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020 , 52, 572-581	36.3	76
254	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
253	10-year performance of four models of breast cancer risk: a validation study. <i>Lancet Oncology</i> , 2019 , 20, 504-517	21.7	73
252	Anti-Müllerian hormone serum concentrations of women with germline BRCA1 or BRCA2 mutations. <i>Human Reproduction</i> , 2016 , 31, 1126-32	5.7	72

251	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016 , 7, 10933	17.4	70
250	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
249	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2012 , 14, R33	8.3	70
248	Breast Cancer Risk Prediction Using Clinical Models and 77 Independent Risk-Associated SNPs for Women Aged Under 50 Years: Australian Breast Cancer Family Registry. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 359-65	4	68
247	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
246	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , 2019 , 11, 2045-2070	5.6	67
245	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016 , 7, 66328-66343	3.3	66
244	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
243	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
242	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2011 , 20, 3304-21	5.6	62
241	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. <i>American Journal of Epidemiology</i> , 2018 , 187, 529-538	3.8	61
240	Tumor PIK3CA Genotype and Prognosis in Early-Stage Breast Cancer: A Pooled Analysis of Individual Patient Data. <i>Journal of Clinical Oncology</i> , 2018 , 36, 981-990	2.2	61
239	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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007 , 16, 2557-65	4	58
238	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56
237	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. <i>Human Molecular Genetics</i> , 2016 , 25, 2256-2268	5.6	55
236	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017 , 8, 14175	17.4	54
235	Associations of alcohol intake, smoking, physical activity and obesity with survival following colorectal cancer diagnosis by stage, anatomic site and tumor molecular subtype. <i>International Journal of Cancer</i> , 2018 , 142, 238-250	7.5	53
234	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53

233	Heritable DNA methylation marks associated with susceptibility to breast cancer. <i>Nature Communications</i> , 2018 , 9, 867	17.4	52
232	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019 , 48, 795-806	7.8	52
231	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599-603	6.3	51
230	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012 , 7, e42380	3.7	49
229	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
228	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
227	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. <i>Gastroenterology</i> , 2020 , 158, 1274-1286.e12	13.3	47
226	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. <i>Nature Communications</i> , 2018 , 9, 4774	17.4	47
225	Modifiers of breast and ovarian cancer risks for BRCA1 and BRCA2 mutation carriers. <i>Endocrine-Related Cancer</i> , 2016 , 23, T69-84	5.7	46
224	Genetics of epilepsy: The testimony of twins in the molecular era. <i>Neurology</i> , 2014 , 83, 1042-8	6.5	46
223	Amount and Intensity of Leisure-Time Physical Activity and Lower Cancer Risk. <i>Journal of Clinical Oncology</i> , 2020 , 38, 686-697	2.2	46
222	Pooled analysis of active cigarette smoking and invasive breast cancer risk in 14 cohort studies. <i>International Journal of Epidemiology</i> , 2017 , 46, 881-893	7.8	46
221	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
220	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. <i>Gastroenterology</i> , 2020 , 158, 1300-1312.e20	13.3	45
219	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 884-95	7.8	45
218	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015 , 2, 681-9	8.8	44
217	Past recreational physical activity, body size, and all-cause mortality following breast cancer diagnosis: results from the Breast Cancer Family Registry. <i>Breast Cancer Research and Treatment</i> , 2010 , 123, 531-42	4.4	43
216	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016 , 99, 903-911	11	43

215	Functional polymorphisms in the TERT promoter are associated with risk of serous epithelial ovarian and breast cancers. <i>PLoS ONE</i> , 2011 , 6, e24987	3.7	41
214	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. <i>Cancer Research</i> , 2018 , 78, 6011-6021	10.1	40
213	Meta-analysis of 16 studies of the association of alcohol with colorectal cancer. <i>International Journal of Cancer</i> , 2020 , 146, 861-873	7.5	39
212	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
211	Reliability of DNA methylation measures from dried blood spots and mononuclear cells using the HumanMethylation450k BeadArray. <i>Scientific Reports</i> , 2016 , 6, 30317	4.9	38
210	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
209	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
208	Low Free Testosterone and Prostate Cancer Risk: A Collaborative Analysis of 20 Prospective Studies. <i>European Urology</i> , 2018 , 74, 585-594	10.2	36
207	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
206	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. <i>Nature Communications</i> , 2020 , 11, 597	17.4	36
205	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 285-98	5.6	35
204	Preventing breast and ovarian cancers in high-risk BRCA1 and BRCA2 mutation carriers. <i>Medical Journal of Australia</i> , 2013 , 199, 680-3	4	35
203	No increased risk of breast cancer associated with alcohol consumption among carriers of BRCA1 and BRCA2 mutations ages . <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 1565-7	4	34
202	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
201	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. <i>Genetics in Medicine</i> , 2017 , 19, 30-35	8.1	31
200	A Common Cancer Risk-Associated Allele in the hTERT Locus Encodes a Dominant Negative Inhibitor of Telomerase. <i>PLoS Genetics</i> , 2015 , 11, e1005286	6	31
199	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. <i>American Journal of Human Genetics</i> , 2020 , 107, 432-444	11	31
198	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. <i>Human Genetics</i> , 2015 , 134, 231-45	6.3	30

197	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. <i>Breast Cancer Research</i> , 2019 , 21, 52	8.3	29
196	Inference about causation between body mass index and DNA methylation in blood from a twin family study. <i>International Journal of Obesity</i> , 2019 , 43, 243-252	5.5	29
195	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019 , 120, 647-657	8.7	28
194	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
193	Genome-wide measures of DNA methylation in peripheral blood and the risk of urothelial cell carcinoma: a prospective nested case-control study. <i>British Journal of Cancer</i> , 2016 , 115, 664-73	8.7	27
192	Global measures of peripheral blood-derived DNA methylation as a risk factor in the development of mature B-cell neoplasms. <i>Epigenomics</i> , 2016 , 8, 55-66	4.4	26
191	Evidence of a genetic link between endometriosis and ovarian cancer. <i>Fertility and Sterility</i> , 2016 , 105, 35-43.e1-10	4.8	26
190	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
189	Genome-wide average DNA methylation is determined in utero. <i>International Journal of Epidemiology</i> , 2018 , 47, 908-916	7.8	26
188	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 1003-1012	9.7	25
187	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016 , 18, 64	8.3	25
186	Genome-Wide Measures of Peripheral Blood Dna Methylation and Prostate Cancer Risk in a Prospective Nested Case-Control Study. <i>Prostate</i> , 2017 , 77, 471-478	4.2	24
185	Body Size Indicators and Risk of Gallbladder Cancer: Pooled Analysis of Individual-Level Data from 19 Prospective Cohort Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 597-606	4	24
184	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015 , 21, 5264-76	12.9	24
183	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016 , 25, 3863-3876	5.6	24
182	Dietary intake of one-carbon metabolism nutrients and DNA methylation in peripheral blood. <i>American Journal of Clinical Nutrition</i> , 2018 , 108, 611-621	7	24
181	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24
180	Age-specific breast cancer risk by body mass index and familial risk: prospective family study cohort (ProF-SC). <i>Breast Cancer Research</i> , 2018 , 20, 132	8.3	24

179	The COronavirus Pandemic Epidemiology (COPE) Consortium: A Call to Action. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1283-1289	4	22
178	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2020 , 22, 8	8.3	22
177	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015 , 2,		22
176	Risk-Reducing Oophorectomy and Breast Cancer Risk Across the Spectrum of Familial Risk. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 331-334	9.7	22
175	Smoking and blood DNA methylation: an epigenome-wide association study and assessment of reversibility. <i>Epigenetics</i> , 2020 , 15, 358-368	5.7	22
174	Special Report: The Biology of Inequalities in Health: The Lifepath Consortium. <i>Frontiers in Public Health</i> , 2020 , 8, 118	6	21
173	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. <i>Breast Cancer Research</i> , 2019 , 21, 62	8.3	20
172	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
171	Paclitaxel sensitivity in relation to ABCB1 expression, efflux and single nucleotide polymorphisms in ovarian cancer. <i>Scientific Reports</i> , 2014 , 4, 4669	4.9	20
170	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018 , 8, 6574	4.9	19
169	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 6353-68	3.3	19
168	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. <i>Breast Cancer Research</i> , 2019 , 21, 68	8.3	18
167	Mixed ductal-lobular carcinomas: evidence for progression from ductal to lobular morphology. <i>Journal of Pathology</i> , 2018 , 244, 460-468	9.4	18
166	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
165	Sustained Weight Loss and Risk of Breast Cancer in Women 50 Years and Older: A Pooled Analysis of Prospective Data. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 929-937	9.7	18
164	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. <i>International Journal of Epidemiology</i> , 2019 , 48, 767-780	7.8	18
163	Pancreatic cancer risk is modulated by inflammatory potential of diet and ABO genotype: a consortia-based evaluation and replication study. <i>Carcinogenesis</i> , 2018 , 39, 1056-1067	4.6	18
162	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1680-91	4	17

161	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). <i>Cancer Research</i> , 2020 , 80, 1210-1218	10.1	17
160	Association Between Molecular Subtypes of Colorectal Tumors and Patient Survival, Based on Pooled Analysis of 7 International Studies. <i>Gastroenterology</i> , 2020 , 158, 2158-2168.e4	13.3	17
159	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. <i>BMC Medicine</i> , 2020 , 18, 396	11.4	17
158	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. <i>Human Genetics</i> , 2019 , 138, 307-326	6.3	17
157	The Premenopausal Breast Cancer Collaboration: A Pooling Project of Studies Participating in the National Cancer Institute Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1360-1369	4	16
156	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. <i>Nature Communications</i> , 2020 , 11, 1217	17.4	16
155	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016 , 6, 32512	4.9	16
154	No evidence for an association between the earwax-associated polymorphism in ABCC11 and breast cancer risk in Caucasian women. <i>Breast Cancer Research and Treatment</i> , 2011 , 126, 235-9	4.4	16
153	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 557-567	9.7	16
152	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
151	Genetic and environmental causes of variation in epigenetic aging across the lifespan. <i>Clinical Epigenetics</i> , 2020 , 12, 158	7.7	15
150	Sex specific associations in genome wide association analysis of renal cell carcinoma. <i>European Journal of Human Genetics</i> , 2019 , 27, 1589-1598	5.3	15
149	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. <i>Cancer Research</i> , 2020 , 80, 116-125	10.1	15
148	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021 , 160, 1164-1178.e6	13.3	15
147	Tools for translational epigenetic studies involving formalin-fixed paraffin-embedded human tissue: applying the Infinium HumanMethylation450 Beadchip assay to large population-based studies. <i>BMC Research Notes</i> , 2015 , 8, 543	2.3	14
146	Deletion at 6q24.2-26 predicts longer survival of high-grade serous epithelial ovarian cancer patients. <i>Molecular Oncology</i> , 2015 , 9, 422-36	7.9	14
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57	Linking Physical Activity to Breast Cancer via Sex Steroid Hormones, Part 2: The Effect of Sex Steroid Hormones on Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 ,	4	2
56	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study		2
55	Fine-mapping of 150 breast cancer risk regions identifies 178 high confidence target genes		2
54	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2

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46	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , 2021 , 114, 1408-1417		2
45	Methylation marks of prenatal exposure to maternal smoking and risk of cancer in adulthood. <i>International Journal of Epidemiology</i> , 2021 , 50, 105-115	7.8	2
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35	Associations between reproductive factors and biliary tract cancers in women from the Biliary Tract Cancers Pooling Project. <i>Journal of Hepatology</i> , 2020 , 73, 863-872	13.4	1
34	Biological aging measures based on blood DNA methylation and risk of cancer: a prospective study		1
33	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1
32	Exploratory Genome-Wide Interaction Analysis of Nonsteroidal Anti-inflammatory Drugs and Predicted Gene Expression on Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1800-1808	4	1
31	Ovarian Cancer Risk Factor Associations by Primary Anatomic Site: The Ovarian Cancer Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 2010-2018	4	1
30	Response to Li and Hopper. <i>American Journal of Human Genetics</i> , 2021 , 108, 527-529	11	1
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20	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 2197-2206	4	1
19	Diet and risk of gastro-oesophageal reflux disease in the Melbourne Collaborative Cohort Study. <i>Public Health Nutrition</i> , 2021 , 24, 5034-5046	3.3	1
18	Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. <i>Npj Breast Cancer</i> , 2021 , 7, 153	7.8	1

17	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. <i>Breast Cancer Research</i> , 2022 , 24, 27	8.3	1
16	Epigenome erosion and SOX10 drive neural crest phenotypic mimicry in triple-negative breast cancer.. <i>Npj Breast Cancer</i> , 2022 , 8, 57	7.8	1
15	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , 2022 , 5, 65	6.7	0
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12	Evolving Practice Pattern of Palliative Radiation Therapy for Bone Metastases from Lung Cancer in Australia. <i>Clinical Oncology</i> , 2021 , 33, e530-e539	2.8	0
11	A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. <i>Cancer Research Communications</i> , 2022 , 2, 211-219		0
10	Recreational Physical Activity and Outcomes After Breast Cancer in Women at High Familial Risk.. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkab090	4.6	0
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1	Underutilisation of breast cancer prevention medication in Australia. <i>Breast</i> , 2021 , 60, 35-37	3.6	