

Jonine D Figueroa

List of Publications by Year in Descending Order

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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.

250
papers

14,886
citations

63
h-index

115
g-index

302
ext. papers

18,442
ext. citations

8.7
avg, IF

4.95
L-index

#	Paper	IF	Citations
250	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , 2022 , 5, 65	6.7	0
249	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , 2022 , 24, 2	8.3	3
248	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. <i>JAMA Oncology</i> , 2022 ,	13.4	4
247	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study.. <i>Breast Cancer Research</i> , 2022 , 24, 9	8.3	1
246	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
245	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. <i>Scientific Reports</i> , 2022 , 12, 6199	4.9	
244	Disinfection By-Products in Drinking Water and Bladder Cancer: Evaluation of Risk Modification by Common Genetic Polymorphisms in Two Case-Control Studies.. <i>Environmental Health Perspectives</i> , 2022 , 130, 57006	8.4	1
243	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. <i>Genome Medicine</i> , 2022 , 14, 51	14.4	0
242	The impact of measures to curb COVID-19 on patient attendance at 10 hospitals in Machakos County, Kenya. <i>Journal of Global Health</i> , 2021 , 11, 05016	4.3	2
241	Might changes in diagnostic practice explain increasing incidence of brain and central nervous system tumors? A population-based study in Wales (United Kingdom) and the United States. <i>Neuro-Oncology</i> , 2021 , 23, 979-989	1	3
240	Risk factors for breast cancer development by tumor characteristics among women with benign breast disease. <i>Breast Cancer Research</i> , 2021 , 23, 34	8.3	5
239	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 1168-1176	9.7	9
238	Tumor-Associated Stromal Cellular Density as a Predictor of Recurrence and Mortality in Breast Cancer: Results from Ethnically Diverse Study Populations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 1397-1407	4	2
237	Breast cancer risk factors in relation to molecular subtypes in breast cancer patients from Kenya. <i>Breast Cancer Research</i> , 2021 , 23, 68	8.3	3
236	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021 , 12, 4198	17.4	1
235	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021 , 108, 1190-1203	11	1
234	Risk of missing colorectal cancer with a COVID-adapted diagnostic pathway using quantitative faecal immunochemical testing. <i>BJS Open</i> , 2021 , 5,	3.9	1

233	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 329-337	9.7	14
232	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021 , 124, 842-854	8.7	2
231	Relation of Quantitative Histologic and Radiologic Breast Tissue Composition Metrics With Invasive Breast Cancer Risk. <i>JNCI Cancer Spectrum</i> , 2021 , 5, pkab015	4.6	1
230	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
229	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. <i>International Journal of Cancer</i> , 2021 , 148, 2712-2723	7.5	3
228	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data from > 2000 women of African-ancestry. <i>Human Genetics</i> , 2021 , 140, 1449-1457	6.3	1
227	Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. <i>Npj Precision Oncology</i> , 2021 , 5, 83	9.8	0
226	Raised cardiovascular disease mortality after central nervous system tumor diagnosis: analysis of 171,926 patients from UK and USA. <i>Neuro-Oncology Advances</i> , 2021 , 3, vdab136	0.9	0
225	The impact of the Covid-19 pandemic on breast cancer early detection and screening. <i>Preventive Medicine</i> , 2021 , 151, 106585	4.3	10
224	Variation in chemotherapy prescribing rates and mortality in early breast cancer over two decades: a national data linkage study. <i>ESMO Open</i> , 2021 , 6, 100331	6	
223	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
222	Distinguishing between direct and indirect consequences of covid-19. <i>BMJ, The</i> , 2020 , 369, m2377	5.9	7
221	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020 , 10, 9688	4.9	2
220	Distinct temporal trends in breast cancer incidence from 1997 to 2016 by molecular subtypes: a population-based study of Scottish cancer registry data. <i>British Journal of Cancer</i> , 2020 , 123, 852-859	8.7	11
219	Reproductive factors and risk of breast cancer by tumor subtypes among Ghanaian women: A population-based case-control study. <i>International Journal of Cancer</i> , 2020 , 147, 1535-1547	7.5	9
218	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
217	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. <i>Breast Cancer Research and Treatment</i> , 2020 , 181, 423-434	4.4	7
216	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. <i>BMC Bioinformatics</i> , 2020 , 21, 30	3.6	18

215	Monitoring indirect impact of COVID-19 pandemic on services for cardiovascular diseases in the UK. <i>Heart</i> , 2020 , 106, 1890-1897	5.1	33
214	Longer-term (12 years) survival in patients with glioblastoma in population-based studies pre- and post-2005: a systematic review and meta-analysis. <i>Scientific Reports</i> , 2020 , 10, 11622	4.9	60
213	Breast cancer gene expression datasets do not reflect the disease at the population level. <i>Npj Breast Cancer</i> , 2020 , 6, 39	7.8	2
212	Polygenic risk score for the prediction of breast cancer is related to lesser terminal duct lobular unit involution of the breast. <i>Npj Breast Cancer</i> , 2020 , 6, 41	7.8	0
211	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019 , 9, 12524	4.9	2
210	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. <i>PLoS ONE</i> , 2019 , 14, e0215347	3.7	5
209	Combined quantitative measures of ER, PR, HER2, and Ki67 provide more prognostic information than categorical combinations in luminal breast cancer. <i>Modern Pathology</i> , 2019 , 32, 1244-1256	9.8	24
208	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
207	The p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019 , 5, 38	7.8	12
206	Involution of Breast Lobules, Mammographic Breast Density and Prognosis Among Tamoxifen-Treated Estrogen Receptor-Positive Breast Cancer Patients. <i>Journal of Clinical Medicine</i> , 2019 , 8,	5.1	3
205	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019 , 21, 144	8.3	11
204	The relationship between terminal duct lobular unit features and mammographic density among Chinese breast cancer patients. <i>International Journal of Cancer</i> , 2019 , 145, 70-77	7.5	4
203	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
202	Reply to Mosaic loss of chromosome Y in leukocytes matters? <i>Nature Genetics</i> , 2019 , 51, 7-9	36.3	6
201	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
200	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018 , 39, 729-741	4.7	16
199	Serum insulin-like growth factor (IGF)-I and IGF binding protein-3 in relation to terminal duct lobular unit involution of the normal breast in Caucasian and African American women: The Susan G. Komen Tissue Bank. <i>International Journal of Cancer</i> , 2018 , 143, 496-507	7.5	2
198	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018 , 143, 746-757	7.5	9

197	Skin lighteners and hair relaxers as risk factors for breast cancer: results from the Ghana breast health study. <i>Carcinogenesis</i> , 2018 , 39, 571-579	4.6	13
196	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 526-536	7.8	53
195	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
194	The Relation of Type 2 Diabetes and Breast Cancer Incidence in Asian, Hispanic and African American Populations-A Review. <i>Canadian Journal of Diabetes</i> , 2018 , 42, 100-105	2.1	5
193	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
192	Epidemiology of Bladder Cancer: A Systematic Review and Contemporary Update of Risk Factors in 2018. <i>European Urology</i> , 2018 , 74, 784-795	10.2	265
191	Relationship between crown-like structures and sex-steroid hormones in breast adipose tissue and serum among postmenopausal breast cancer patients. <i>Breast Cancer Research</i> , 2017 , 19, 8	8.3	41
190	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 2789-2799	10.1	49
189	Design considerations for identifying breast cancer risk factors in a population-based study in Africa. <i>International Journal of Cancer</i> , 2017 , 140, 2667-2677	7.5	17
188	Factors contributing to delays in diagnosis of breast cancers in Ghana, West Africa. <i>Breast Cancer Research and Treatment</i> , 2017 , 162, 105-114	4.4	30
187	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
186	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
185	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. <i>Carcinogenesis</i> , 2017 , 38, 1167-1179	4.6	9
184	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017 , 19, 119	8.3	26
183	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017 , 141, 1830-1840	7.5	13
182	Age-related terminal duct lobular unit involution in benign tissues from Chinese breast cancer patients with luminal and triple-negative tumors. <i>Breast Cancer Research</i> , 2017 , 19, 61	8.3	9
181	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. <i>International Journal of Cancer</i> , 2017 , 140, 825-832	7.5	9
180	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599-603		51

179	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
178	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2017 , 8, 18381-18398	3.3	7
177	- a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017 , 8, 102769-102782	3.3	3
176	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
175	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
174	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016 , 6, 36874	4.9	2
173	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. <i>Nature Genetics</i> , 2016 , 48, 1330-1338	36.3	104
172	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
171	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016 , 7, 11843	17.4	59
170	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
169	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
168	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
167	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016 , 18, 104	8.3	44
166	Smoking status, usual adult occupation, and risk of recurrent urothelial bladder carcinoma: data from The Cancer Genome Atlas (TCGA) Project. <i>Cancer Causes and Control</i> , 2016 , 27, 1429-1435	2.8	15
165	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
164	Circulating insulin-like growth factor-I, insulin-like growth factor binding protein-3 and terminal duct lobular unit involution of the breast: a cross-sectional study of women with benign breast disease. <i>Breast Cancer Research</i> , 2016 , 18, 24	8.3	15
163	Ages at menarche- and menopause-related genetic variants in relation to terminal duct lobular unit involution in normal breast tissue. <i>Breast Cancer Research and Treatment</i> , 2016 , 158, 341-50	4.4	5
162	Relationship of Terminal Duct Lobular Unit Involution of the Breast with Area and Volume Mammographic Densities. <i>Cancer Prevention Research</i> , 2016 , 9, 149-58	3.2	33

161	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016 , 2, 138-53	5.3	16
160	Response. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	
159	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. <i>Human Molecular Genetics</i> , 2016 , 25, 1203-14	5.6	20
158	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
157	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
156	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , 2016 , 114, 298-304	8.7	5
155	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. <i>Human Genetics</i> , 2016 , 135, 137-54	6.3	6
154	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
153	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. <i>PLoS Genetics</i> , 2016 , 12, e1006493	6.4	67
152	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
151	Pathway analysis of bladder cancer genome-wide association study identifies novel pathways involved in bladder cancer development. <i>Genes and Cancer</i> , 2016 , 7, 229-239	2.9	11
150	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016 , 7, 80140-80163	3.3	21
149	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016 , 13, e1002105	11.6	80
148	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016 , 11, e0160316	3.7	11
147	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
146	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016 , 18, 98	8.3	26
145	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
144	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

143	Relation of Serum Estrogen Metabolites with Terminal Duct Lobular Unit Involution Among Women Undergoing Diagnostic Image-Guided Breast Biopsy. <i>Hormones and Cancer</i> , 2016 , 7, 305-315	5	9
142	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016 , 18, 22	8.3	31
141	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016 , 27, 679-93	2.8	15
140	Mosaic loss of chromosome Y is associated with common variation near TCL1A. <i>Nature Genetics</i> , 2016 , 48, 563-8	36.3	87
139	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
138	Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease: a nested case-control study. <i>Breast Cancer Research and Treatment</i> , 2016 , 159, 163-72	4.4	35
137	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
136	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015 , 36, 256-71	4.6	12
135	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
134	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. <i>British Journal of Cancer</i> , 2015 , 112, 61-8	8.7	23
133	A robust association test for detecting genetic variants with heterogeneous effects. <i>Biostatistics</i> , 2015 , 16, 5-16	3.7	1
132	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015 , 97, 22-34	11	26
131	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
130	Tumor intrinsic subtype is reflected in cancer-adjacent tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 406-14	4	58
129	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. <i>Breast Cancer Research</i> , 2015 , 17, 18	8.3	17
128	Integrated analysis of DNA methylation, immunohistochemistry and mRNA expression, data identifies a methylation expression index (MEI) robustly associated with survival of ER-positive breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2015 , 150, 457-466	4.4	6
127	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015 , 97, 576-92	11	649
126	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

125	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	23
124	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015 , 13, 156	11.4	37
123	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
122	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. <i>Human Molecular Genetics</i> , 2015 , 24, 1177-84	5.6	29
121	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
120	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24
119	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015 , 107, djv279	9.7	107
118	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , 2015 , 70, 758-762 ^{2,4}		
117	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015 , 6, 37979-94	3.3	19
116	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
115	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , 2015 , 96, 487-97	11	77
114	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2015 , 1, 18-32	5.3	18
113	Plasma Autoantibodies Associated with Basal-like Breast Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1332-40	4	36
112	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015 , 2, 681-9	8.8	44
111	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
110	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015 , 96, 5-20	11	59
109	Abstract 4682: Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease 2015 ,		2
108	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. <i>Oncotarget</i> , 2015 , 6, 7390-407	3.3	14

107	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014 , 35, 1737-44	4.6	33
106	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46,450 cases and 42,461 controls from the breast cancer association consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 1934-46	5.6	28
105	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014 , 23, 1387-98	5.6	101
104	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. <i>Genetic Epidemiology</i> , 2014 , 38, 84-93	2.6	24
103	Prolactin receptor expression and breast cancer: relationships with tumor characteristics among pre- and post-menopausal women in a population-based case-control study from Poland. <i>Hormones and Cancer</i> , 2014 , 5, 42-50	5	26
102	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. <i>Cancer Research</i> , 2014 , 74, 5808-18	10.1	19
101	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014 , 5, 5303	17.4	84
100	Alcohol consumption and survival after a breast cancer diagnosis: a literature-based meta-analysis and collaborative analysis of data for 29,239 cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 934-45	4	29
99	Urinary bisphenol A-glucuronide and postmenopausal breast cancer in Poland. <i>Cancer Causes and Control</i> , 2014 , 25, 1587-93	2.8	26
98	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. <i>British Journal of Cancer</i> , 2014 , 110, 1088-100	8.7	20
97	ERβ splice variant expression in four large cohorts of human breast cancer patient tumors. <i>Breast Cancer Research and Treatment</i> , 2014 , 146, 657-67	4.4	36
96	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
95	Breast cancer in Sub-Saharan Africa: opportunities for prevention. <i>Breast Cancer Research and Treatment</i> , 2014 , 144, 467-78	4.4	108
94	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
93	Benign breast tissue composition in breast cancer patients: association with risk factors, clinical variables, and gene expression. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 2810-8	4	19
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10	Tracking Excess Deaths (TRACKED) ¶An interactive online tool to monitor excess deaths associated with the COVID-19 pandemic in the United Kingdom. <i>Wellcome Open Research</i> , 5, 168	4.8	1
9	The 4C Initiative (Clinical Care for Cardiovascular disease in the COVID-19 pandemic) ¶monitoring the indirect impact of the coronavirus pandemic on services for cardiovascular diseases in the UK		1
8	Relation of Quantitative Histologic and Radiologic Breast Tissue Composition Metrics with Invasive Breast Cancer Risk		1
7	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
6	Distinct temporal trends in breast cancer incidence from 1997 to 2016 by molecular subtypes: A population-based study of Scottish cancer registry data		1
5	TRACKing Excess Deaths (TRACKED) ¶An interactive online tool to monitor excess deaths associated with COVID-19 pandemic in the United Kingdom		1
4	Tracking Excess Deaths (TRACKED) ¶An interactive online tool to monitor excess deaths associated with the COVID-19 pandemic in the United Kingdom. <i>Wellcome Open Research</i> , 5, 168	4.8	
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2	Trends in excess cancer and cardiovascular deaths in Scotland during the COVID-19 pandemic 30 December ¶20 April suggest underestimation of COVID-19 related deaths		7
1	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2