Jonine D Figueroa

List of Publications by Citations

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	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
249	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
248	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
247	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, 250-63	9.7	513
246	Gene expression signature of cigarette smoking and its role in lung adenocarcinoma development and survival. *PLoS ONE*, **2008**, 3, e1651	3.7	470
245	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
244	Detectable clonal mosaicism and its relationship to aging and cancer. *Nature Genetics*, **2012**, 44, 651-8	36.3	409
243	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408
242	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
241	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
240	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
239	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
238	Epidemiology of Bladder Cancer: A Systematic Review and Contemporary Update of Risk Factors in 2018. *European Urology*, **2018**, 74, 784-795	10.2	265
237	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
236	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
235	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. *JAMA Oncology*, **2016**, 2, 1295-1302	13.4	189
234	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186

233	Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. *American Journal of Human Genetics*, **2013**, 92, 489-503	11	167
232	Polymorphisms in GSTT1, GSTZ1, and CYP2E1, disinfection by-products, and risk of bladder cancer in Spain. *Environmental Health Perspectives*, **2010**, 118, 1545-50	8.4	162
231	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. *Human Molecular Genetics*, **2012**, 21, 5373-84	5.6	143
230	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
229	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2011**, 20, 3289-303	5.6	140
228	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *Journal of Clinical Oncology*, **2012**, 30, 4308-16	2.2	134
227	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
226	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. *PLoS Genetics*, **2013**, 9, e1003284	6	112
225	Large-scale evaluation of candidate genes identifies associations between VEGF polymorphisms and bladder cancer risk. *PLoS Genetics*, **2007**, 3, e29	6	109
224	Breast cancer in Sub-Saharan Africa: opportunities for prevention. *Breast Cancer Research and Treatment*, **2014**, 144, 467-78	4.4	108
223	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
222	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. *Journal of the National Cancer Institute*, **2015**, 107, djv279	9.7	107
221	Genetic variation in the base excision repair pathway and bladder cancer risk. *Human Genetics*, **2007**, 121, 233-42	6.3	107
220	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. *Nature Genetics*, **2016**, 48, 1330-1338	36.3	104
219	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, 1052-67	24.4	104
218	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
217	Genome-wide association study identifies multiple loci associated with bladder cancer risk. *Human Molecular Genetics*, **2014**, 23, 1387-98	5.6	101
216	Pathway analysis of breast cancer genome-wide association study highlights three pathways and one canonical signaling cascade. *Cancer Research*, **2010**, 70, 4453-9	10.1	100

215	Polymorphisms in DNA repair genes, smoking, and bladder cancer risk: findings from the international consortium of bladder cancer. *Cancer Research*, **2009**, 69, 6857-64	10.1	94
214	GSTM1 null and NAT2 slow acetylation genotypes, smoking intensity and bladder cancer risk: results from the New England bladder cancer study and NAT2 meta-analysis. *Carcinogenesis*, **2011**, 32, 182-9	4.6	94
213	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
212	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Research*, **2012**, 72, 1795-803	10.1	93
211	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
210	Mosaic loss of chromosome Y is associated with common variation near TCL1A. *Nature Genetics*, **2016**, 48, 563-8	36.3	87
209	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. *Nature Communications*, **2014**, 5, 5303	17.4	84
208	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309	5.8	83
207	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. *Carcinogenesis*, **2007**, 28, 1788-93	4.6	83
206	Common genetic polymorphisms modify the effect of smoking on absolute risk of bladder cancer. *Cancer Research*, **2013**, 73, 2211-20	10.1	82
205	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. *Breast Cancer Research* , **2014**, 16, 3419	8.3	82
204	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. *Human Molecular Genetics*, **2011**, 20, 4282-9	5.6	82
203	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, 1046-60	11	80
202	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	11.6	80
201	An unusual suspect: an uncommon human-specific synonymous coding variant within the UGT1A6 gene explains a GWAS signal and protects against bladder cancer. *Genome Biology*, **2011**, 12,	18.3	78
200	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
199	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, 6616-33	5.6	77
198	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76

197	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. *Carcinogenesis*, **2008**, 29, 1955-62	4.6	76
196	The role of genetic breast cancer susceptibility variants as prognostic factors. *Human Molecular Genetics*, **2012**, 21, 3926-39	5.6	75
195	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
194	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. *Breast Cancer Research*, **2010**, 12, R110	8.3	74
193	Common genetic variants in the PSCA gene influence gene expression and bladder cancer risk. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 4974-9	11.5	69
192	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. *PLoS Genetics*, **2016**, 12, e1006493	6	67
191	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2011**, 20, 4693-706	5.6	66
190	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. *Cancer Research*, **2016**, 76, 5103-14	10.1	66
189	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	65
188	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
187	Longer-term (≥2 years) survival in patients with glioblastoma in population-based studies pre- and post-2005: a systematic review and meta-analysis. *Scientific Reports*, **2020**, 10, 11622	4.9	60
186	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
185	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. *American Journal of Human Genetics*, **2015**, 96, 5-20	11	59
184	Tumor intrinsic subtype is reflected in cancer-adjacent tissue. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 406-14	4	58
183	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. *Human Molecular Genetics*, **2012**, 21, 1918-30	5.6	58
182	DNA hypermethylation of ESR1 and PGR in breast cancer: pathologic and epidemiologic associations. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 3036-43	4	56
181	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. *International Journal of Epidemiology*, **2018**, 47, 526-536	7.8	53
180	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53

179	Terminal duct lobular unit involution of the normal breast: implications for breast cancer etiology. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	52
178	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
177	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.1	51
176	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
175	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. *Journal of Medical Genetics*, **2012**, 49, 601-8	5.8	49
174	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	3.7	49
173	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111	5.6	48
172	Relationship of mammographic density and gene expression: analysis of normal breast tissue surrounding breast cancer. *Clinical Cancer Research*, **2013**, 19, 4972-4982	12.9	48
171	Expression of TGF-beta signaling factors in invasive breast cancers: relationships with age at diagnosis and tumor characteristics. *Breast Cancer Research and Treatment*, **2010**, 121, 727-35	4.4	45
170	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. *Breast Cancer Research*, **2016**, 18, 104	8.3	44
169	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. *EBioMedicine*, **2015**, 2, 681-9	8.8	44
168	A single nucleotide polymorphism tags variation in the arylamine N-acetyltransferase 2 phenotype in populations of European background. *Pharmacogenetics and Genomics*, **2011**, 21, 231-6	1.9	44
167	Assessment of automated image analysis of breast cancer tissue microarrays for epidemiologic studies. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 992-9	4	43
166	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	11	43
165	Cytoplasmic estrogen receptor in breast cancer. *Clinical Cancer Research*, **2012**, 18, 118-26	12.9	42
164	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. *Journal of Medical Genetics*, **2011**, 48, 477-84	5.8	42
163	Relationship between crown-like structures and sex-steroid hormones in breast adipose tissue and serum among postmenopausal breast cancer patients. *Breast Cancer Research*, **2017**, 19, 8	8.3	41
162	TGF-β signaling pathway and breast cancer susceptibility. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 1112-9	4	40

161	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
160	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285	6	38
159	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. *BMC Medicine*, **2015**, 13, 156	11.4	37
158	MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973	3.7	37
157	ERsplice variant expression in four large cohorts of human breast cancer patient tumors. *Breast Cancer Research and Treatment*, **2014**, 146, 657-67	4.4	36
156	Plasma Autoantibodies Associated with Basal-like Breast Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1332-40	4	36
155	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
154	TNF polymorphisms and prostate cancer risk. *Prostate*, **2008**, 68, 400-7	4.2	36
153	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98	5.6	35
152	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Human Molecular Genetics*, **2014**, 23, 2490-7	5.6	35
151	Common genetic variation in the sex hormone metabolic pathway and endometrial cancer risk: pathway-based evaluation of candidate genes. *Carcinogenesis*, **2010**, 31, 827-33	4.6	35
150	Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease: a nested case-control study. *Breast Cancer Research and Treatment*, **2016**, 159, 163-72	4.4	35
149	Relationship of Terminal Duct Lobular Unit Involution of the Breast with Area and Volume Mammographic Densities. *Cancer Prevention Research*, **2016**, 9, 149-58	3.2	33
148	Genome-wide interaction study of smoking and bladder cancer risk. *Carcinogenesis*, **2014**, 35, 1737-44	4.6	33
147	A versatile protein microarray platform enabling antibody profiling against denatured proteins. *Proteomics - Clinical Applications*, **2013**, 7, 378-83	3.1	33
146	Likelihood ratio test for detecting gene (G)-environment (E) interactions under an additive risk model exploiting G-E independence for case-control data. *American Journal of Epidemiology*, **2012**, 176, 1060-7	3.8	33
145	The Susan G. Komen for the Cure Tissue Bank at the IU Simon Cancer Center: a unique resource for defining the "molecular histology" of the breast. *Cancer Prevention Research*, **2012**, 5, 528-35	3.2	33
144	Large-scale pathway-based analysis of bladder cancer genome-wide association data from five studies of European background. *PLoS ONE*, **2012**, 7, e29396	3.7	33

143	Monitoring indirect impact of COVID-19 pandemic on services for cardiovascular diseases in the UK. *Heart*, **2020**, 106, 1890-1897	5.1	33
142	Sex steroid hormone levels in breast adipose tissue and serum in postmenopausal women. *Breast Cancer Research and Treatment*, **2012**, 131, 287-94	4.4	31
141	Analysis of terminal duct lobular unit involution in luminal A and basal breast cancers. *Breast Cancer Research*, **2012**, 14, R64	8.3	31
140	Cigarette smoking, body mass index, gastro-esophageal reflux disease, and non-steroidal anti-inflammatory drug use and risk of subtypes of esophageal and gastric cancers by P53 overexpression. *Cancer Causes and Control*, **2009**, 20, 361-8	2.8	31
139	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
138	Factors contributing to delays in diagnosis of breast cancers in Ghana, West Africa. *Breast Cancer Research and Treatment*, **2017**, 162, 105-114	4.4	30
137	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. *Human Molecular Genetics*, **2015**, 24, 1177-84	5.6	29
136	Alcohol consumption and survival after a breast cancer diagnosis: a literature-based meta-analysis and collaborative analysis of data for 29,239 cases. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 934-45	4	29
135	Additive interactions between susceptibility single-nucleotide polymorphisms identified in genome-wide association studies and breast cancer risk factors in the Breast and Prostate Cancer Cohort Consortium. *American Journal of Epidemiology*, **2014**, 180, 1018-27	3.8	29
134	Parity-related molecular signatures and breast cancer subtypes by estrogen receptor status. *Breast Cancer Research*, **2014**, 16, R74	8.3	29
133	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
132	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. *Human Molecular Genetics*, **2014**, 23, 1934-46	5.6	28
131	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
130	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 2222-31	4	27
129	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. *American Journal of Human Genetics*, **2015**, 97, 22-34	11	26
128	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119	8.3	26
127	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. *Hormones and Cancer*, **2014**, 5, 42-50	5	26
126	Urinary bisphenol A-glucuronide and postmenopausal breast cancer in Poland. *Cancer Causes and Control*, **2014**, 25, 1587-93	2.8	26

125	Polymorphic variants in PTGS2 and prostate cancer risk: results from two large nested case-control studies. *Carcinogenesis*, **2008**, 29, 568-72	4.6	26
124	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. *Breast Cancer Research*, **2016**, 18, 98	8.3	26
123	Genetic variation in hormone metabolizing genes and risk of testicular germ cell tumors. *Cancer Causes and Control*, **2008**, 19, 917-29	2.8	25
122	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	8.3	25
121	Combined quantitative measures of ER, PR, HER2, and KI67 provide more prognostic information than categorical combinations in luminal breast cancer. *Modern Pathology*, **2019**, 32, 1244-1256	9.8	24
120	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	5.6	24
119	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. *Genetic Epidemiology*, **2014**, 38, 84-93	2.6	24
118	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24
117	Prolactin serum levels and breast cancer: relationships with risk factors and tumour characteristics among pre- and postmenopausal women in a population-based case-control study from Poland. *British Journal of Cancer*, **2010**, 103, 1097-102	8.7	24
116	Effect modification of endocrine disruptors and testicular germ cell tumour risk by hormone-metabolizing genes. *Journal of Developmental and Physical Disabilities*, **2010**, 33, 588-96		24
115	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. *British Journal of Cancer*, **2015**, 112, 61-8	8.7	23
114	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	23
113	Differential urinary specific gravity as a molecular phenotype of the bladder cancer genetic association in the urea transporter gene, SLC14A1. *International Journal of Cancer*, **2013**, 133, 3008-13	7.5	22
112	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. *Oncotarget*, **2016**, 7, 80140-80163	3.3	21
111	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
110	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, 1203-14	5.6	20
109	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. *British Journal of Cancer*, **2014**, 110, 1088-100	8.7	20
108	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	4.9	19

107	The 19q12 bladder cancer GWAS signal: association with cyclin E function and aggressive disease. *Cancer Research*, **2014**, 74, 5808-18	10.1	19
106	Benign breast tissue composition in breast cancer patients: association with risk factors, clinical variables, and gene expression. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 2810-8	4	19
105	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
104	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. *Endocrine-Related Cancer*, **2013**, 20, 875-87	5.7	19
103	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2015**, 1, 18-32	5.3	18
102	Circulating sex hormones and terminal duct lobular unit involution of the normal breast. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 2765-73	4	18
101	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. *BMC Bioinformatics*, **2020**, 21, 30	3.6	18
100	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
99	Design considerations for identifying breast cancer risk factors in a population-based study in Africa. *International Journal of Cancer*, **2017**, 140, 2667-2677	7.5	17
98	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. *Breast Cancer Research*, **2015**, 17, 18	8.3	17
97	Nonsteroidal anti-inflammatory drugs and other analgesic use and bladder cancer in northern New England. *International Journal of Cancer*, **2013**, 132, 162-73	7.5	17
96	The BRCA2 c.68-7T□□A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
95	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). *Scientific Reports*, **2016**, 6, 32512	4.9	16
94	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2016**, 2, 138-53	5.3	16
93	Estrogen receptor and progesterone receptor expression in normal terminal duct lobular units surrounding invasive breast cancer. *Breast Cancer Research and Treatment*, **2013**, 137, 837-47	4.4	16
92	Genetic variation in PRL and PRLR, and relationships with serum prolactin levels and breast cancer risk: results from a population-based case-control study in Poland. *Breast Cancer Research*, **2011**, 13, R42	8.3	16
91	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
90	Smoking status, usual adult occupation, and risk of recurrent urothelial bladder carcinoma: data from The Cancer Genome Atlas (TCGA) Project. *Cancer Causes and Control*, **2016**, 27, 1429-1435	2.8	15

89	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. *Breast Cancer Research*, **2016**, 18, 24	8.3	15
88	The associations between a polygenic score, reproductive and menstrual risk factors and breast cancer risk. *Breast Cancer Research and Treatment*, **2013**, 140, 427-34	4.4	15
87	Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. *Breast Cancer Research and Treatment*, **2014**, 143, 181-7	4.4	15
86	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93	2.8	15
85	Plasma carotenoid- and retinol-weighted multi-SNP scores and risk of breast cancer in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2013**, 22, 927-36	4	14
84	Quantitative Analysis of TDLUs using Adaptive Morphological Shape Techniques. *Proceedings of SPIE*, **2013**, 8676,	1.7	14
83	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. *Oncotarget*, **2015**, 6, 7390-407	3.3	14
82	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	9.7	14
81	Skin lighteners and hair relaxers as risk factors for breast cancer: results from the Ghana breast health study. *Carcinogenesis*, **2018**, 39, 571-579	4.6	13
80	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
79	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. *Carcinogenesis*, **2015**, 36, 256-71	4.6	12
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