

# Jonine D Figueroa

## List of Publications by Year in descending order

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Version: 2024-02-01

276  
papers

20,890  
citations

15001

68  
h-index

14779

131  
g-index

302  
all docs

302  
docs citations

302  
times ranked

28637  
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
2	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
5	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, 250-263.	3.0	596
6	Gene Expression Signature of Cigarette Smoking and Its Role in Lung Adenocarcinoma Development and Survival. <i>PLoS ONE</i> , 2008, 3, e1651.	1.1	563
7	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	13.9	532
8	Epidemiology of Bladder Cancer: A Systematic Review and Contemporary Update of Risk Factors in 2018. <i>European Urology</i> , 2018, 74, 784-795.	0.9	530
9	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012, 44, 651-658.	9.4	519
10	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	9.4	513
11	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 978-984.	9.4	493
12	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, 371-384.	9.4	493
13	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
14	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
15	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.	9.4	357
16	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
17	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	3.4	285
18	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.	9.4	265

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19	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
20	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	2.6	201
21	Polymorphisms in <i>GSTT1</i> , <i>GSTZ1</i> , and <i>CYP2E1</i> , Disinfection By-products, and Risk of Bladder Cancer in Spain. <i>Environmental Health Perspectives</i> , 2010, 118, 1545-1550.	2.8	194
22	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.	9.4	184
23	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
24	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
25	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer-Specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316.	0.8	162
26	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.	9.4	161
27	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, 1052-1067.	7.7	157
28	Longer-term (≥2 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.	1.6	155
29	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 3289-3303.	1.4	152
30	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.	3.0	152
31	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> <i>2</i> *1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	152
32	Breast cancer in Sub-Saharan Africa: opportunities for prevention. <i>Breast Cancer Research and Treatment</i> , 2014, 144, 467-478.	1.1	149
33	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014, 23, 1387-1398.	1.4	137
34	Evidence of Gene-Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. <i>PLoS Genetics</i> , 2013, 9, e1003284.	1.5	136
35	Mosaic loss of chromosome Y is associated with common variation near <i>TCL1A</i> . <i>Nature Genetics</i> , 2016, 48, 563-568.	9.4	134
36	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125

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37	Large-Scale Evaluation of Candidate Genes Identifies Associations between VEGF Polymorphisms and Bladder Cancer Risk. <i>PLoS Genetics</i> , 2007, 3, e29.	1.5	119
38	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.	3.9	118
39	Genetic variation in the base excision repair pathway and bladder cancer risk. <i>Human Genetics</i> , 2007, 121, 233-242.	1.8	113
40	Pathway Analysis of Breast Cancer Genome-Wide Association Study Highlights Three Pathways and One Canonical Signaling Cascade. <i>Cancer Research</i> , 2010, 70, 4453-4459.	0.4	112
41	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. <i>Carcinogenesis</i> , 2011, 32, 182-189.	1.3	110
42	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014, 5, 5303.	5.8	109
43	Polymorphisms in DNA Repair Genes, Smoking, and Bladder Cancer Risk: Findings from the International Consortium of Bladder Cancer. <i>Cancer Research</i> , 2009, 69, 6857-6864.	0.4	107
44	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.4	107
45	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
46	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
47	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. <i>Human Molecular Genetics</i> , 2011, 20, 4282-4289.	1.4	100
48	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	100
49	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.4	100
50	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	3.0	99
51	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, 1046-1060.	2.6	98
52	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.	1.5	98
53	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.	2.2	97
54	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	1.5	94

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55	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
56	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	1.4	90
57	Monitoring indirect impact of COVID-19 pandemic on services for cardiovascular diseases in the UK. <i>Heart</i> , 2020, 106, 1890-1897.	1.2	90
58	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. <i>Carcinogenesis</i> , 2008, 29, 1955-1962.	1.3	88
59	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.	0.9	88
60	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. <i>Carcinogenesis</i> , 2007, 28, 1788-1793.	1.3	87
61	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
62	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. <i>Breast Cancer Research</i> , 2010, 12, R110.	2.2	82
63	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.	0.9	81
64	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	1.4	80
65	Common genetic variants in the <i>PSCA</i> gene influence gene expression and bladder cancer risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4974-4979.	3.3	79
66	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
67	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
68	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.	2.6	76
69	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
70	Tumor Intrinsic Subtype Is Reflected in Cancer-Adjacent Tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 406-414.	1.1	72
71	Associations of common variants at 1p11.2 and 14q24.1 ( <i>RAD51L1</i> ) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	1.4	71
72	Mapping of the <i>UGT1A</i> locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. <i>Human Molecular Genetics</i> , 2012, 21, 1918-1930.	1.4	71

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73	The impact of the Covid-19 pandemic on breast cancer early detection and screening. Preventive Medicine, 2021, 151, 106585.	1.6	68
74	Terminal Duct Lobular Unit Involution of the Normal Breast: Implications for Breast Cancer Etiology. Journal of the National Cancer Institute, 2014, 106, .	3.0	67
75	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
76	DNA Hypermethylation of <i>ESR1</i> and <i>PGR</i> in Breast Cancer: Pathologic and Epidemiologic Associations. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3036-3043.	1.1	60
77	A single nucleotide polymorphism tags variation in the arylamine N-acetyltransferase 2 phenotype in populations of European background. Pharmacogenetics and Genomics, 2011, 21, 231-236.	0.7	60
78	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
79	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. Journal of Medical Genetics, 2012, 49, 601-608.	1.5	58
80	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.	2.2	58
81	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	1.4	56
82	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
83	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
84	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.	2.2	56
85	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 992-999.	1.1	54
86	Cytoplasmic Estrogen Receptor in Breast Cancer. Clinical Cancer Research, 2012, 18, 118-126.	3.2	54
87	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
88	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
89	Expression of TGF- $\beta$ 2 signaling factors in invasive breast cancers: relationships with age at diagnosis and tumor characteristics. Breast Cancer Research and Treatment, 2010, 121, 727-735.	1.1	51
90	Relationship of Mammographic Density and Gene Expression: Analysis of Normal Breast Tissue Surrounding Breast Cancer. Clinical Cancer Research, 2013, 19, 4972-4982.	3.2	51

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91	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015, 13, 156.	2.3	51
92	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.	1.6	51
93	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.	2.9	51
94	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.	1.1	51
95	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
96	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	1.3	50
97	TGF- $\beta$ 2 Signaling Pathway and Breast Cancer Susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1112-1119.	1.1	49
98	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
99	Factors contributing to delays in diagnosis of breast cancers in Ghana, West Africa. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 105-114.	1.1	49
100	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, 163-172.	1.1	48
101	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. <i>Journal of Medical Genetics</i> , 2011, 48, 477-484.	1.5	47
102	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. <i>Cancer Prevention Research</i> , 2012, 5, 528-535.	0.7	47
103	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
104	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.	3.0	45
105	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
106	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	43
107	<i>TNF</i> polymorphisms and prostate cancer risk. <i>Prostate</i> , 2008, 68, 400-407.	1.2	42
108	Common genetic variation in the sex hormone metabolic pathway and endometrial cancer risk: pathway-based evaluation of candidate genes. <i>Carcinogenesis</i> , 2010, 31, 827-833.	1.3	42

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109	Plasma Autoantibodies Associated with Basal-like Breast Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1332-1340.	1.1	42
110	Relationship of Terminal Duct Lobular Unit Involution of the Breast with Area and Volume Mammographic Densities. <i>Cancer Prevention Research</i> , 2016, 9, 149-158.	0.7	42
111	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	3.0	41
112	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
113	Analysis of terminal duct lobular unit involution in luminal A and basal breast cancers. <i>Breast Cancer Research</i> , 2012, 14, R64.	2.2	39
114	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
115	ER $\beta$ splice variant expression in four large cohorts of human breast cancer patient tumors. <i>Breast Cancer Research and Treatment</i> , 2014, 146, 657-667.	1.1	39
116	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.	2.2	39
117	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. <i>Human Molecular Genetics</i> , 2015, 24, 1177-1184.	1.4	38
118	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, 285-298.	1.4	38
119	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, 1203-1214.	1.4	38
120	Likelihood Ratio Test for Detecting Gene (G)-Environment (E) Interactions Under an Additive Risk Model Exploiting G-E Independence for Case-Control Data. <i>American Journal of Epidemiology</i> , 2012, 176, 1060-1067.	1.6	37
121	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, 934-945.	1.1	37
122	Urinary bisphenol A-glucuronide and postmenopausal breast cancer in Poland. <i>Cancer Causes and Control</i> , 2014, 25, 1587-1593.	0.8	37
123	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.	2.6	37
124	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. <i>American Journal of Epidemiology</i> , 2014, 180, 1018-1027.	1.6	36
125	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. <i>PLoS ONE</i> , 2012, 7, e29396.	1.1	36
126	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. <i>Cancer Causes and Control</i> , 2009, 20, 361-368.	0.8	35



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127	A versatile protein microarray platform enabling antibody profiling against denatured proteins. <i>Proteomics - Clinical Applications</i> , 2013, 7, 378-383.	0.8	34
128	Parity-related molecular signatures and breast cancer subtypes by estrogen receptor status. <i>Breast Cancer Research</i> , 2014, 16, R74.	2.2	34
129	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv223.	3.0	34
130	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.	1.4	33
131	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.	2.3	33
132	Sex steroid hormone levels in breast adipose tissue and serum in postmenopausal women. <i>Breast Cancer Research and Treatment</i> , 2012, 131, 287-294.	1.1	32
133	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, 1934-1946.	1.4	32
134	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. <i>BMC Bioinformatics</i> , 2020, 21, 30.	1.2	32
135	Genetic variation in hormone metabolizing genes and risk of testicular germ cell tumors. <i>Cancer Causes and Control</i> , 2008, 19, 917-929.	0.8	31
136	Effect modification of endocrine disruptors and testicular germ cell tumour risk by hormone-metabolizing genes. <i>Journal of Developmental and Physical Disabilities</i> , 2010, 33, 588-596.	3.6	31
137	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.	0.8	31
138	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.	2.2	31
139	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.	2.3	30
140	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.	2.9	30
141	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
142	Polymorphic variants in PTGS2 and prostate cancer risk: results from two large nested case-control studies. <i>Carcinogenesis</i> , 2007, 29, 568-572.	1.3	29
143	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. <i>British Journal of Cancer</i> , 2010, 103, 1097-1102.	2.9	29
144	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.	4.9	29

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145	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Gene-Environment Interactions. <i>Genetic Epidemiology</i> , 2014, 38, 84-93.	0.6	28
146	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
147	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.	2.3	28
148	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor-Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	1.1	27
149	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. <i>British Journal of Cancer</i> , 2015, 112, 61-68.	2.9	27
150	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. <i>Endocrine-Related Cancer</i> , 2013, 20, 875-887.	1.6	26
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