Jonine D Figueroa

List of Publications by Year
in descending order

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276 papers	20,890 citations	13099 68 h-index	12946 131 g-index
302 all docs	302 docs citations	302 times ranked	26270 citing authors

#	Article	IF	Citations
1	Relation of circulating estrogens with hair relaxer and skin lightener use among postmenopausal women in Ghana. Journal of Exposure Science and Environmental Epidemiology, 2023, 33, 301-310.	3.9	3
2	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
3	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
4	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
5	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study. Breast Cancer Research, 2022, 24, 9.	5.0	4
6	OUP accepted manuscript. Neuro-Oncology, 2022, , .	1.2	0
7	Association of Genetic Ancestry With Terminal Duct Lobular Unit Involution Among Healthy Women. Journal of the National Cancer Institute, 2022, 114, 1420-1424.	6.3	4
8	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	1.7	6
9	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	3.3	2
10	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. Human Molecular Genetics, 2022, 31, 3133-3143.	2.9	11
11	Disinfection By-Products in Drinking Water and Bladder Cancer: Evaluation of Risk Modification by Common Genetic Polymorphisms in Two Caseâ€“Control Studies. Environmental Health Perspectives, 2022, 130, 57006.	6.0	5
12	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
13	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	6.3	14
14	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.	6.3	45
15	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
16	Relation of Quantitative Histologic and Radiologic Breast Tissue Composition Metrics With Invasive Breast Cancer Risk. JNCI Cancer Spectrum, 2021, 5, pkab015.	2.9	7
17	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
18	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. International Journal of Cancer, 2021, 148, 2712-2723.	5.1	33

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19	Risk factors for breast cancer development by tumor characteristics among women with benign breast disease. Breast Cancer Research, 2021, 23, 34.	5.0	14
20	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. Journal of the National Cancer Institute, 2021, 113, 1168-1176.	6.3	41
21	Tumor-Associated Stromal Cellular Density as a Predictor of Recurrence and Mortality in Breast Cancer: Results from Ethnically Diverse Study Populations. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1397-1407.	2.5	7
22	Breast cancer risk factors in relation to molecular subtypes in breast cancer patients from Kenya. Breast Cancer Research, 2021, 23, 68.	5.0	11
23	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	12.8	24
24	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
25	Risk of missing colorectal cancer with a COVID-adapted diagnostic pathway using quantitative faecal immunochemical testing. BJS Open, 2021, 5, .	1.7	4
26	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data fromâ€‰>â€‰2000 women of African-ancestry. Human Genetics, 2021, 140, 1449-1457.	3.8	4
27	Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. Npj Precision Oncology, 2021, 5, 83.	5.4	4
28	Raised cardiovascular disease mortality after central nervous system tumor diagnosis: analysis of 171,926 patients from UK and USA. Neuro-Oncology Advances, 2021, 3, vdab136.	0.7	8
29	The impact of the Covid-19 pandemic on breast cancer early detection and screening. Preventive Medicine, 2021, 151, 106585.	3.4	68
30	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. Neuro-Oncology, 2021, 23, 979-989.	1.2	10
31	The impact of measures to curb COVID-19 on patient attendance at 10 hospitals in Machakos County, Kenya. Journal of Global Health, 2021, 11, 05016.	2.7	5
32	Variation in chemotherapy prescribing rates and mortality in early breast cancer over two decades: a national data linkage study. ESMO Open, 2021, 6, 100331.	4.5	1
33	Monitoring indirect impact of COVID-19 pandemic on services for cardiovascular diseases in the UK. Heart, 2020, 106, 1890-1897.	2.9	90
34	Longer-term (â‰¥â€‰2Âyears) survival in patients with glioblastoma in population-based studies pre- and post-2005: a systematic review and meta-analysis. Scientific Reports, 2020, 10, 11622.	3.3	155
35	Breast cancer gene expression datasets do not reflect the disease at the population level. Npj Breast Cancer, 2020, 6, 39.	5.2	5
36	Polygenic risk score for the prediction of breast cancer is related to lesser terminal duct lobular unit involution of the breast. Npj Breast Cancer, 2020, 6, 41.	5.2	5

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37	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
38	Distinguishing between direct and indirect consequences of covid-19. BMJ, The, 2020, 369, m2377.	6.0	12
39	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
40	Distinct temporal trends in breast cancer incidence from 1997 to 2016 by molecular subtypes: a population-based study of Scottish cancer registry data. British Journal of Cancer, 2020, 123, 852-859.	6.4	30
41	Reproductive factors and risk of breast cancer by tumor subtypes among Ghanaian women: A populationâ€based caseâ€“control study. International Journal of Cancer, 2020, 147, 1535-1547.	5.1	28
42	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
43	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14
44	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. BMC Bioinformatics, 2020, 21, 30.	2.6	32
45	Abstract 2320: Evaluating a polygenic risk score for breast cancer in women of African ancestry. , 2020, , .		1
46	Abstract 4613: Cross-ancestry genome-wide association study identifies six new loci for breast cancer in women of African and european ancestry. , 2020, , .		1
47	Abstract 4636: Breast cancer age-specific incidence rates among Ghanaian women by breast cancer risk factors: A study using census and population-based case-control study data. , 2020, , .		0
48	Abstract 4638: Associations of fecal microbial profiles with non-malignant breast disease and breast cancer in the Ghana Breast Health Study. , 2020, , .		0
49	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
50	Involution of Breast Lobules, Mammographic Breast Density and Prognosis Among Tamoxifen-Treated Estrogen Receptor-Positive Breast Cancer Patients. Journal of Clinical Medicine, 2019, 8, 1868.	2.4	9
51	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
52	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. PLoS ONE, 2019, 14, e0215347.	2.5	14
53	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.	5.5	51
54	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52

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55	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
56	The relationship between terminal duct lobular unit features and mammographic density among Chinese breast cancer patients. International Journal of Cancer, 2019, 145, 70-77.	5.1	9
57	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
58	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	21.4	7
59	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
60	Abstract 622: Reproductive factors and breast cancer risk to women in Ghana, West Africa. , 2019, , .		0
61	Abstract LB-178: Performance of breast cancer polygenic risk score (PRS) in a Ghanaian population. , 2019, , .		1
62	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
63	Serum insulinâ€like growth factor (IGF)â€I and IGF binding proteinâ€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. International Journal of Cancer, 2018, 143, 496-507.	5.1	8
64	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	5.1	19
65	Skin lighteners and hair relaxers as risk factors for breast cancer: results from the Ghana breast health study. Carcinogenesis, 2018, 39, 571-579.	2.8	24
66	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.	1.9	88
67	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.	3.3	51
68	The Relation of Type 2 Diabetes and Breast Cancer Incidence in Asian, Hispanic and African American Populationsâ€”A Review. Canadian Journal of Diabetes, 2018, 42, 100-105.	0.8	9
69	Epidemiology of Bladder Cancer: A Systematic Review and Contemporary Update of Risk Factors in 2018. European Urology, 2018, 74, 784-795.	1.9	530
70	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
71	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.	5.0	58
72	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75

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73	Design considerations for identifying breast cancer risk factors in a populationâ€based study in Africa. International Journal of Cancer, 2017, 140, 2667-2677.	5.1	30
74	Factors contributing to delays in diagnosis of breast cancers in Ghana, West Africa. Breast Cancer Research and Treatment, 2017, 162, 105-114.	2.5	49
75	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
76	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
77	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. Carcinogenesis, 2017, 38, 1167-1179.	2.8	18
78	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
79	Age-related terminal duct lobular unit involution in benign tissues from Chinese breast cancer patients with luminal and triple-negative tumors. Breast Cancer Research, 2017, 19, 61.	5.0	16
80	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. International Journal of Cancer, 2017, 140, 825-832.	5.1	9
81	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
82	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
83	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
84	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	1.8	14
85	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
86	Abstract 5290: Racial variation in terminal duct lobular unit (TDLU) involution in Chinese and Polish breast cancer patients. , 2017, , .		0
87	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.	1.8	31
88	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.	8.4	118
89	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
90	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174

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91	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
92	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.	5.0	31
93	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	7.1	285
94	Relation of Serum Estrogen Metabolites with Terminal Duct Lobular Unit Involution Among Women Undergoing Diagnostic Image-Guided Breast Biopsy. Hormones and Cancer, 2016, 7, 305-315.	4.9	13
95	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
96	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
97	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
98	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
99	Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease: a nested caseâ€“control study. Breast Cancer Research and Treatment, 2016, 159, 163-172.	2.5	48
100	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.	6.2	59
101	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.	2.9	33
102	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
103	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.	21.4	161
104	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
105	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
106	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
107	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
108	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.	3.3	19

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109	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.	5.0	56
110	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.	1.8	18
111	Age- and Tumor Subtypeâ€"Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
112	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.	5.0	18
113	Ages at menarche- and menopause-related genetic variants in relation to terminal duct lobular unit involution in normal breast tissue. Breast Cancer Research and Treatment, 2016, 158, 341-350.	2.5	5
114	Relationship of Terminal Duct Lobular Unit Involution of the Breast with Area and Volume Mammographic Densities. Cancer Prevention Research, 2016, 9, 149-158.	1.5	42
115	Highâ€throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	3.0	19
116	Response. Journal of the National Cancer Institute, 2016, 108, djv441.	6.3	0
117	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, 1203-1214.	2.9	38
118	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
119	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
120	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
121	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. Human Genetics, 2016, 135, 137-154.	3.8	8
122	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
123	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
124	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.	3.5	98
125	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
126	Pathway analysis of bladder cancer genome-wide association study identifies novel pathways involved in bladder cancer development. Genes and Cancer, 2016, 7, 229-239.	1.9	12

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127	Abstract 4283: Relationship between mammographic breast density and measures of terminal duct lobular unit involution among women diagnosed with estrogen receptor positive breast cancer. , 2016, , .		0
128	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
129	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.	6.3	152
130	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
131	SNP-SNP interaction analysis of NF-ÎºB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
132	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
133	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
134	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.	3.0	24
135	Plasma Autoantibodies Associated with Basal-like Breast Cancers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1332-1340.	2.5	42
136	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
137	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
138	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.	6.2	76
139	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, 256-271.	2.8	14
140	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
141	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. British Journal of Cancer, 2015, 112, 61-68.	6.4	27
142	A robust association test for detecting genetic variants with heterogeneous effects. Biostatistics, 2015, 16, 5-16.	1.5	1
143	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.	6.2	37
144	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56

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145	Tumor Intrinsic Subtype Is Reflected in Cancer-Adjacent Tissue. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 406-414.	2.5	72
146	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.	5.0	20
147	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. Breast Cancer Research and Treatment, 2015, 150, 457-466.	2.5	7
148	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
149	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
150	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. Journal of the National Cancer Institute, 2015, 107, djv223.	6.3	34
151	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	51
152	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
153	Genome-wide association study identified SNP on 15q24 associated with bladder cancer risk in Japanese population. Human Molecular Genetics, 2015, 24, 1177-1184.	2.9	38
154	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
155	Abstract 4682: Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease. , 2015, , .		2
156	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	1.8	15
157	Abstract 5570: Heterogeneity of luminal breast cancer characterized by immunohistochemical expression of basal markers. , 2015, , .		0
158	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
159	Terminal Duct Lobular Unit Involution of the Normal Breast: Implications for Breast Cancer Etiology. Journal of the National Cancer Institute, 2014, 106, .	6.3	67
160	Circulating Sex Hormones and Terminal Duct Lobular Unit Involution of the Normal Breast. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2765-2773.	2.5	23
161	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
162	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, 1018-1027.	3.4	36

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163	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, 6616-6633.	2.9	90
164	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
165	Parity-related molecular signatures and breast cancer subtypes by estrogen receptor status. Breast Cancer Research, 2014, 16, R74.	5.0	34
166	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
167	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
168	Reproductive windows, genetic loci, and breast cancer risk. Annals of Epidemiology, 2014, 24, 376-382.	1.9	7
169	Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. Breast Cancer Research and Treatment, 2014, 143, 181-187.	2.5	16
170	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	2.8	50
171	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, 1934-1946.	2.9	32
172	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	2.9	137
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174	Prolactin Receptor Expression and Breast Cancer: Relationships with Tumor Characteristics among Pre- and Post-menopausal Women in a Population-Based Caseâ€“Control Study from Poland. Hormones and Cancer, 2014, 5, 42-50.	4.9	29
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