

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	Relation of circulating estrogens with hair relaxer and skin lightener use among postmenopausal women in Ghana. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2023, 33, 301-310.	1.8	3
2	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	2.0	6
3	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
4	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
5	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study. <i>Breast Cancer Research</i> , 2022, 24, 9.	2.2	4
6	OUP accepted manuscript. <i>Neuro-Oncology</i> , 2022, , .	0.6	0
7	Association of Genetic Ancestry With Terminal Duct Lobular Unit Involution Among Healthy Women. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1420-1424.	3.0	4
8	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.	0.7	6
9	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	1.6	2
10	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. <i>Human Molecular Genetics</i> , 2022, 31, 3133-3143.	1.4	11
11	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.	2.8	5
12	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	3.6	19
13	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1706-1719.	3.0	14
14	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
15	CYP3A7*1C allele: linking premenopausal oestrogen and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	2.9	5
16	Relation of Quantitative Histologic and Radiologic Breast Tissue Composition Metrics With Invasive Breast Cancer Risk. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkab015.	1.4	7
17	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
18	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

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19	Risk factors for breast cancer development by tumor characteristics among women with benign breast disease. <i>Breast Cancer Research</i> , 2021, 23, 34.	2.2	14
20	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
21	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.	1.1	7
22	Breast cancer risk factors in relation to molecular subtypes in breast cancer patients from Kenya. <i>Breast Cancer Research</i> , 2021, 23, 68.	2.2	11
23	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	5.8	24
24	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	2.6	6
25	Risk of missing colorectal cancer with a COVID-adapted diagnostic pathway using quantitative faecal immunochemical testing. <i>BJS Open</i> , 2021, 5, .	0.7	4
26	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.	1.8	4
27	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.	2.3	4
28	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.	0.4	8
29	The impact of the Covid-19 pandemic on breast cancer early detection and screening. <i>Preventive Medicine</i> , 2021, 151, 106585.	1.6	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. <i>Neuro-Oncology</i> , 2021, 23, 979-989.	0.6	10
31	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.	1.2	5
32	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.	2.0	1
33	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
34	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
35	Breast cancer gene expression datasets do not reflect the disease at the population level. <i>Npj Breast Cancer</i> , 2020, 6, 39.	2.3	5
36	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.	2.3	5

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37	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
38	Distinguishing between direct and indirect consequences of covid-19. <i>BMJ, The</i> , 2020, 369, m2377.	3.0	12
39	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	1.6	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. <i>British Journal of Cancer</i> , 2020, 123, 852-859.	2.9	30
41	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
42	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
43	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.	1.1	14
44	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
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. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
50	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, 1868.	1.0	9
51	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5
52	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. <i>PLoS ONE</i> , 2019, 14, e0215347.	1.1	14
53	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
54	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52

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55	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019, 21, 144.	2.2	24
56	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.	2.3	9
57	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
58	Reply to "Mosaic loss of chromosome Y in leukocytes matters". <i>Nature Genetics</i> , 2019, 51, 7-9.	9.4	7
59	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
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 <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	1.1	19
63	Serum insulin-like growth factor (IGF) and IGF binding protein 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.	2.3	8
64	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.	2.3	19
65	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.	1.3	24
66	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
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. <i>Scientific Reports</i> , 2018, 8, 6574.	1.6	51
68	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.	0.4	9
69	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
70	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
71	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.	2.2	58
72	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75

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73	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
74	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
75	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
76	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
77	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. <i>Carcinogenesis</i> , 2017, 38, 1167-1179.	1.3	18
78	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017, 141, 1830-1840.	2.3	20
79	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.	2.2	16
80	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.	2.3	9
81	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
82	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
83	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
84	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.	0.8	14
85	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	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. <i>Oncotarget</i> , 2016, 7, 80140-80163.	0.8	31
88	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
89	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
90	<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

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91	Patient survival and tumor characteristics associated with CHEK2:p.1157T → findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
92	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
93	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
94	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.	4.9	13
95	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
96	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, 679-693.	0.8	21
97	Mosaic loss of chromosome Y is associated with common variation near TCL1A. <i>Nature Genetics</i> , 2016, 48, 563-568.	9.4	134
98	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
99	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
100	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.	2.6	59
101	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
102	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.	1.6	2
103	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
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. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
105	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
106	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
107	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
108	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.	1.6	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. <i>Breast Cancer Research</i> , 2016, 18, 104.	2.2	56
110	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.	0.8	18
111	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> <i>2</i> *110delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	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. <i>Breast Cancer Research</i> , 2016, 18, 24.	2.2	18
113	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, 341-350.	1.1	5
114	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
115	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, 138-153.	1.3	19
116	Response. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv441.	3.0	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. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	1.4	38
118	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
119	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
120	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , 2016, 114, 298-304.	2.9	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. <i>Human Genetics</i> , 2016, 135, 137-154.	1.8	8
122	<i>BRCA2</i> 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
123	No clinical utility of <i>KRAS</i> variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
124	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
125	<i>RAD51B</i> in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
126	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.	0.6	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.	2.2	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.	3.0	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.	0.2	0
131	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
132	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
133	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	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.	1.3	24
135	Plasma Autoantibodies Associated with Basal-like Breast Cancers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1332-1340.	1.1	42
136	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
137	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	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.	2.6	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.	1.3	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.	9.4	513
141	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. British Journal of Cancer, 2015, 112, 61-68.	2.9	27
142	A robust association test for detecting genetic variants with heterogeneous effects. Biostatistics, 2015, 16, 5-16.	0.9	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.	2.6	37
144	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56

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145	Tumor Intrinsic Subtype Is Reflected in Cancer-Adjacent Tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 406-414.	1.1	72
146	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.	2.2	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. <i>Breast Cancer Research and Treatment</i> , 2015, 150, 457-466.	1.1	7
148	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
149	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
150	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
151	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
152	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
153	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
154	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
155	Abstract 4682: Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease. , 2015, , .		2
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