Jonine D Figueroa

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/4837608/publications.pdf

Version: 2024-02-01

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	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
5	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, 250-263.	6.3	596
6	Gene Expression Signature of Cigarette Smoking and Its Role in Lung Adenocarcinoma Development and Survival. PLoS ONE, 2008, 3, e1651.	2.5	563
7	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
8	Epidemiology of Bladder Cancer: A Systematic Review and Contemporary Update of Risk Factors in 2018. European Urology, 2018, 74, 784-795.	1.9	530
9	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	21.4	519
10	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
11	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 2010, 42, 978-984.	21.4	493
12	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
13	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
14	Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
15	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
16	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
17	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	7.1	285
18	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

#	Article	IF	Citations
19	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
20	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.	6.2	201
21	Polymorphisms in GSTT1 , GSTZ1 , and CYP2E1 , Disinfection By-products, and Risk of Bladder Cancer in Spain. Environmental Health Perspectives, 2010, 118, 1545-1550.	6.0	194
22	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
23	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
24	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, 5373-5384.	2.9	168
25	CHEK2*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€“Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	1.6	162
26	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
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. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
28	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
29	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, 3289-3303.	2.9	152
30	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
31	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
32	Breast cancer in Sub-Saharan Africa: opportunities for prevention. Breast Cancer Research and Treatment, 2014, 144, 467-478.	2.5	149
33	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	2.9	137
34	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
35	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
36	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

#	Article	IF	Citations
37	Large-Scale Evaluation of Candidate Genes Identifies Associations between VEGF Polymorphisms and Bladder Cancer Risk. PLoS Genetics, 2007, 3, e29.	3.5	119
38	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
39	Genetic variation in the base excision repair pathway and bladder cancer risk. Human Genetics, 2007, 121, 233-242.	3.8	113
40	Pathway Analysis of Breast Cancer Genome-Wide Association Study Highlights Three Pathways and One Canonical Signaling Cascade. Cancer Research, 2010, 70, 4453-4459.	0.9	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. Carcinogenesis, 2011, 32, 182-189.	2.8	110
42	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	12.8	109
43	Polymorphisms in DNA Repair Genes, Smoking, and Bladder Cancer Risk: Findings from the International Consortium of Bladder Cancer. Cancer Research, 2009, 69, 6857-6864.	0.9	107
44	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.9	107
45	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
46	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	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. Human Molecular Genetics, 2011, 20, 4282-4289.	2.9	100
48	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
49	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
50	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
51	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, 1046-1060.	6.2	98
52	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
53	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
54	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

#	Article	IF	Citations
55	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	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. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
57	Monitoring indirect impact of COVID-19 pandemic on services for cardiovascular diseases in the UK. Heart, 2020, 106, 1890-1897.	2.9	90
58	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. Carcinogenesis, 2008, 29, 1955-1962.	2.8	88
59	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
60	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. Carcinogenesis, 2007, 28, 1788-1793.	2.8	87
61	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	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. Breast Cancer Research, 2010, 12, R110.	5.0	82
63	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
64	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
65	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, 4974-4979.	7.1	79
66	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
67	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
68	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
69	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
70	Tumor Intrinsic Subtype Is Reflected in Cancer-Adjacent Tissue. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 406-414.	2.5	72
71	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
72	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. Human Molecular Genetics, 2012, 21, 1918-1930.	2.9	71

#	Article	IF	Citations
73	The impact of the Covid-19 pandemic on breast cancer early detection and screening. Preventive Medicine, 2021, 151, 106585.	3.4	68
74	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
75	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
76	DNA Hypermethylation ofESR1andPGRin Breast Cancer: Pathologic and Epidemiologic Associations. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3036-3043.	2.5	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.	1.5	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.	6.2	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.	3.2	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.	5.0	58
81	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
82	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
83	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	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.	5.0	56
85	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 992-999.	2.5	54
86	Cytoplasmic Estrogen Receptor in Breast Cancer. Clinical Cancer Research, 2012, 18, 118-126.	7.0	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.	2.9	53
88	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
89	Expression of TGF-Î² signaling factors in invasive breast cancers: relationships with age at diagnosis and tumor characteristics. Breast Cancer Research and Treatment, 2010, 121, 727-735.	2.5	51
90	Relationship of Mammographic Density and Gene Expression: Analysis of Normal Breast Tissue Surrounding Breast Cancer. Clinical Cancer Research, 2013, 19, 4972-4982.	7.0	51

#	Article	IF	Citations
91	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	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. Scientific Reports, 2018, 8, 6574.	3.3	51
93	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
94	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.	2.5	51
95	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
96	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	2.8	50
97	TGF-Î² Signaling Pathway and Breast Cancer Susceptibility. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1112-1119.	2.5	49
98	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
99	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
100	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
101	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	3.2	47
102	The Susan G. Komen for the Cure Tissue Bank at the IU Simon Cancer Center: A Unique Resource for Defining the â€œMolecular Histologyâ€•of the Breast. Cancer Prevention Research, 2012, 5, 528-535.	1.5	47
103	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
104	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
105	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
106	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
107	TNF polymorphisms and prostate cancer risk. Prostate, 2008, 68, 400-407.	2.3	42
108	Common genetic variation in the sex hormone metabolic pathway and endometrial cancer risk: pathway-based evaluation of candidate genes. Carcinogenesis, 2010, 31, 827-833.	2.8	42

#	Article	IF	Citations
109	Plasma Autoantibodies Associated with Basal-like Breast Cancers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1332-1340.	2.5	42
110	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
111	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
112	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
113	Analysis of terminal duct lobular unit involution in luminal A and basal breast cancers. Breast Cancer Research, 2012, 14, R64.	5.0	39
114	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
115	ERÎ² splice variant expression in four large cohorts of human breast cancer patient tumors. Breast Cancer Research and Treatment, 2014, 146, 657-667.	2.5	39
116	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
117	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
118	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
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. Human Molecular Genetics, 2016, 25, 1203-1214.	2.9	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. American Journal of Epidemiology, 2012, 176, 1060-1067.	3.4	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. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	2.5	37
122	Urinary bisphenol A-glucuronide and postmenopausal breast cancer in Poland. Cancer Causes and Control, 2014, 25, 1587-1593.	1.8	37
123	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
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. American Journal of Epidemiology, 2014, 180, 1018-1027.	3.4	36
125	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. PLoS ONE, 2012, 7, e29396.	2.5	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. Cancer Causes and Control, 2009, 20, 361-368.	1.8	35

#	Article	IF	Citations
127	A versatile protein microarray platform enabling antibody profiling against denatured proteins. Proteomics - Clinical Applications, 2013, 7, 378-383.	1.6	34
128	Parity-related molecular signatures and breast cancer subtypes by estrogen receptor status. Breast Cancer Research, 2014, 16, R74.	5.0	34
129	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. Journal of the National Cancer Institute, 2015, 107, djv223.	6.3	34
130	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
131	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
132	Sex steroid hormone levels in breast adipose tissue and serum in postmenopausal women. Breast Cancer Research and Treatment, 2012, 131, 287-294.	2.5	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. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
134	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
135	Genetic variation in hormone metabolizing genes and risk of testicular germ cell tumors. Cancer Causes and Control, 2008, 19, 917-929.	1.8	31
136	Effect modification of endocrine disruptors and testicular germ cell tumour risk by hormoneâ€metabolizing genes. Journal of Developmental and Physical Disabilities, 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. Oncotarget, 2016, 7, 80140-80163.	1.8	31
138	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
139	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
140	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
141	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
142	Polymorphic variants in PTGS2 and prostate cancer risk: results from two large nested case-control studies. Carcinogenesis, 2007, 29, 568-572.	2.8	29
143	Prolactin serum levels and breast cancer: relationships with risk factors and tumour characteristics among pre- and postmenopausal women in a population-based caseâ€“control study from Poland. British Journal of Cancer, 2010, 103, 1097-1102.	6.4	29
144	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

#	Article	IF	Citations
145	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
146	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
147	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
148	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€“Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
149	Quantitative assessment of miR34a as an independent prognostic marker in breast cancer. British Journal of Cancer, 2015, 112, 61-68.	6.4	27
150	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genomeâ€“wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	3.1	26
151	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
152	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
153	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, 3008-3013.	5.1	24
154	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.9	24
155	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
156	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
157	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
158	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	12.8	24
159	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
160	Estrogen receptor and progesterone receptor expression in normal terminal duct lobular units surrounding invasive breast cancer. Breast Cancer Research and Treatment, 2013, 137, 837-847.	2.5	21
161	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	6.4	21
162	Benign Breast Tissue Composition in Breast Cancer Patients: Association with Risk Factors, Clinical Variables, and Gene Expression. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2810-2818.	2.5	21

#	Article	IF	Citations
163	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
164	Nonsteroidal antiâ€inflammatory drugs and other analgesic use and bladder cancer in northern New England. International Journal of Cancer, 2013, 132, 162-173.	5.1	20
165	SNP-SNP interaction analysis of NF-ÎºB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
166	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
167	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
168	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
169	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
170	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
171	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
172	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
173	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.	5.0	18
174	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
175	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
176	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
177	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. Carcinogenesis, 2017, 38, 1167-1179.	2.8	18
178	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
179	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
180	The associations between a polygenic score, reproductive and menstrual risk factors and breast cancer risk. Breast Cancer Research and Treatment, 2013, 140, 427-434.	2.5	15

#	Article	IF	Citations
181	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, 927-936.	2.5	15
182	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
183	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
184	Quantitative analysis of TDLUs using adaptive morphological shape techniques. Proceedings of SPIE, 2013, 8676, .	0.8	14
185	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
186	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
187	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. PLoS ONE, 2019, 14, e0215347.	2.5	14
188	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
189	Risk factors for breast cancer development by tumor characteristics among women with benign breast disease. Breast Cancer Research, 2021, 23, 34.	5.0	14
190	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
191	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
192	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
193	The oral microbiome and breast cancer and nonâ€malignant breast disease, and its relationship with the fecal microbiome in the Ghana Breast Health Study. International Journal of Cancer, 0, , .	5.1	13
194	Large-scale genotyping identifies a new locus at 22q13.2 associated with female breast size. Journal of Medical Genetics, 2013, 50, 666-673.	3.2	12
195	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
196	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
197	Distinguishing between direct and indirect consequences of covid-19. BMJ, The, 2020, 369, m2377.	6.0	12
198	Breast cancer susceptibility associated with rs1219648 (fibroblast growth factor receptor 2) and postmenopausal hormone therapy use in a population-based United States study. Menopause, 2013, 20, 354-358.	2.0	12

#	Article	IF	Citations
199	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
200	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2013, 132, 2044-2055.	5.1	11
201	Breast cancer risk factors in relation to molecular subtypes in breast cancer patients from Kenya. Breast Cancer Research, 2021, 23, 68.	5.0	11
202	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
203	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
204	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
205	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
206	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
207	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
208	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
209	Emerging Concepts in Breast Cancer Risk Prediction. Current Obstetrics and Gynecology Reports, 2013, 2, 43-52.	0.8	8
210	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
211	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
212	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
213	Reproductive windows, genetic loci, and breast cancer risk. Annals of Epidemiology, 2014, 24, 376-382.	1.9	7
214	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
215	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
216	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	21.4	7

#	Article	IF	Citations
217	Relation of Quantitative Histologic and Radiologic Breast Tissue Composition Metrics With Invasive Breast Cancer Risk. JNCI Cancer Spectrum, 2021, 5, pkab015.	2.9	7
218	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
219	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
220	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
221	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
222	Fine mapping of 14q24.1 breast cancer susceptibility locus. Human Genetics, 2012, 131, 479-490.	3.8	5
223	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
224	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
225	Breast cancer gene expression datasets do not reflect the disease at the population level. Npj Breast Cancer, 2020, 6, 39.	5.2	5
226	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
227	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
228	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
229	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
230	Risk of missing colorectal cancer with a COVID-adapted diagnostic pathway using quantitative faecal immunochemical testing. BJS Open, 2021, 5, .	1.7	4
231	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
232	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
233	Analysis of cancer diagnoses from 2015-2019 within Machakos County, Kenya, support establishment of Cancer Centre in 2019 likely changing referral patterns. Wellcome Open Research, 0, 5, 290.	1.8	4
234	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study. Breast Cancer Research, 2022, 24, 9.	5.0	4

#	Article	IF	Citations
235	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
236	Unraveling Genes, Hormones, and Breast Cancer. Journal of the National Cancer Institute, 2012, 104, 641-642.	6.3	3
237	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
238	Breast cancer incidence and survival in Scotland by socio-economic deprivation and tumour subtype. Breast Cancer Research and Treatment, 0, , .	2.5	3
239	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
240	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
241	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2
242	Abstract 4682: Standardized measures of lobular involution and subsequent breast cancer risk among women with benign breast disease. , 2015, , .		2
243	Tracking Excess Deaths (TRACKED) â€“ an interactive online tool to monitor excess deaths associated with the COVID-19 pandemic in the United Kingdom. Wellcome Open Research, 0, 5, 168.	1.8	2
244	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
245	A robust association test for detecting genetic variants with heterogeneous effects. Biostatistics, 2015, 16, 5-16.	1.5	1
246	Large-scale evaluation of candidate genes for cancer identifies common genetic variants in vascular endothelial growth factor associated with bladder cancer risk. PLoS Genetics, 2005, preprint, e29.	3.5	1
247	Abstract 385: Tamoxifen-resistant breast cancer: DNA methylation and expression of MAGED1. , 2014, , .		1
248	Abstract LB-178: Performance of breast cancer polygenic risk score (PRS) in a Ghanaian population. , 2019, , .		1
249	Abstract 2320: Evaluating a polygenic risk score for breast cancer in women of African ancestry. , 2020, , .		1
250	Abstract 4613: Cross-ancestry genome-wide association study identifies six new loci for breast cancer in women of African and european ancestry. , 2020, , .		1
251	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
252	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, .	8.8	0

#	Article	IF	Citations
253	A novel functional variant in 8q24 is associated with regulation of prostate stem cell antigen (PSCA) gene expression and bladder cancer risk. Genome Biology, 2011, 12, .	8.8	0
254	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
255	Response. Journal of the National Cancer Institute, 2016, 108, djv441.	6.3	0
256	Abstract 2201: Pathway analysis of breast cancer genome wide association study highlights three pathways and one canonical signaling cascade. , 2010, , .		0
257	Abstract 2779: Relationship of mammographic density with breast cancer subtypes. , 2010, , .		0
258	Abstract 2783: A novel functional variant is associated with regulation of the prostate stem cell antigen (PSCA) gene and bladder cancer risk in males. , 2011, , .		0
259	Abstract LB-336: Association of variant rs2046210 at 6q25.1 (ESR1) with breast cancer risk suggests heterogeneity by E-cadherin tumor tissue expression. , 2012, , .		0
260	Abstract LB-337: Synergistic effects of twelve common genetic polymorphisms and smoking habits on absolute risk of bladder cancer. , 2012, , .		0
261	Abstract 4465: Breast cancer risk factor associations with breast tissue morphometry: results from the Komen for the CureÂ® Tissue Bank. , 2012, , .		0
262	Abstract 1658: Post-GWAS genetic and functional studies for bladder cancer: An uncommon protective synonymous coding variant within the UGT1A6 gene explains the GWAS signal and affects cellular detoxification. , 2012, , .		0
263	Abstract 3651: Parity-related molecular signatures and breast cancer heterogeneity.. , 2013, , .		0
264	Abstract 944: Translational implications of the 19q12 bladder cancer GWAS signal for aggressive bladder cancer. , 2014, , .		0
265	Abstract 874: Autoantibody biomarker discovery in basal-like breast cancer using nucleic acid programmable protein array. , 2014, , .		0
266	Abstract C11: Impact of pathologic specimen quality on classifying molecular subtypes of breast cancer: A pilot study from three hospitals in Ghana, Africa. , 2014, , .		0
267	Abstract 5570: Heterogeneity of luminal breast cancer characterized by immunohistochemical expression of basal markers. , 2015, , .		0
268	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
269	Abstract 5290: Racial variation in terminal duct lobular unit (TDLU) involution in Chinese and Polish breast cancer patients. , 2017, , .		0
270	Longer-Term (â‰¥2 Years) Survival in Patients with Glioblastoma in Population-Based Studies Pre- and Post-2005. SSRN Electronic Journal, 0, , .	0.4	0

#	Article	IF	Citations
271	Reproductive Factors and Risk of Breast Cancer by Tumour Subtypes Among Ghanaian Women: A Population-Based Case-Control Study. SSRN Electronic Journal, 0, , .	0.4	0
272	Abstract 622: Reproductive factors and breast cancer risk to women in Ghana, West Africa. , 2019, , .		0
273	Tracking Excess Deaths (TRACKED) â€“ an interactive online tool to monitor excess deaths associated with the COVID-19 pandemic in the United Kingdom. Wellcome Open Research, 0, 5, 168.	1.8	0
274	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
275	Abstract 4638: Associations of fecal microbial profiles with non-malignant breast disease and breast cancer in the Ghana Breast Health Study. , 2020, , .		0
276	OUP accepted manuscript. Neuro-Oncology, 2022, , .	1.2	0