Janet E Olson

List of Publications by Year
in descending order

138 papers	13,349 citations	50276 46 h-index	24258 110 g-index
143 all docs	143 docs citations	143 times ranked	17489 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
4	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
5	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	1.6	521
6	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
7	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
8	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
9	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	27.0	414
10	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
11	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
12	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
13	The continuing increase in the incidence of primary central nervous system non-Hodgkin lymphoma. Cancer, 2002, 95, 1504-1510.	4.1	296
14	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
15	Preemptive Genotyping for Personalized Medicine: Design of the Right Drug, Right Dose, Right Timeâ€”Using Genomic Data to Individualize Treatment Protocol. Mayo Clinic Proceedings, 2014, 89, 25-33.	3.0	250
16	Incorporating a Genetic Risk Score Into Coronary Heart Disease Risk Estimates. Circulation, 2016, 133, 1181-1188.	1.6	198
17	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
18	The Mayo Clinic Biobank: A Building Block for Individualized Medicine. Mayo Clinic Proceedings, 2013, 88, 952-962.	3.0	180

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19	The Contributions of Breast Density and Common Genetic Variation to Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	6.3	174
20	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
21	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
22	Postmenopausal cancer risk after self-reported endometriosis diagnosis in the Iowa Women's Health Study. Cancer, 2002, 94, 1612-1618.	4.1	128
23	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
24	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
25	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	2.9	106
26	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
27	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
28	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
29	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
30	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
31	Aspirin use and the risk of cholangiocarcinomaâ€¡. Hepatology, 2016, 64, 785-796.	7.3	84
32	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
33	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
34	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
35	Multidisciplinary model to implement pharmacogenomics at the point of care. Genetics in Medicine, 2017, 19, 421-429.	2.4	74
36	Integrating Pharmacogenomics into Clinical Practice: Promise vs Reality. American Journal of Medicine, 2016, 129, 1093-1099.e1.	1.5	67

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37	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
38	Evaluation of Germline Genetic Testing Criteria in a Hospital-Based Series of Women With Breast Cancer. Journal of Clinical Oncology, 2020, 38, 1409-1418.	1.6	64
39	Impact of demographics on human gut microbial diversity in a US Midwest population. PeerJ, 2016, 4, e1514.	2.0	61
40	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
41	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.9	55
42	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
43	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	51
44	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
45	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
46	Participant-perceived understanding and perspectives on pharmacogenomics: the Mayo Clinic RIGHT protocol (Right Drug, Right Dose, Right Time). Genetics in Medicine, 2017, 19, 819-825.	2.4	50
47	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
48	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. Journal of Clinical Oncology, 2021, 39, 2564-2573.	1.6	47
49	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
50	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
51	A Robust e-Epidemiology Tool in Phenotyping Heart Failure with Differentiation for Preserved and Reduced Ejection Fraction: the Electronic Medical Records and Genomics (eMERGE) Network. Journal of Cardiovascular Translational Research, 2015, 8, 475-483.	2.4	44
52	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. Journal of Personalized Medicine, 2018, 8, 2.	2.5	44
53	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
54	A novel housing-based socioeconomic measure predicts hospitalisation and multiple chronic conditions in a community population. Journal of Epidemiology and Community Health, 2016, 70, 286-291.	3.7	41

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55	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
56	Inferring multimodal latent topics from electronic health records. Nature Communications, 2020, 11, 2536.	12.8	40
57	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
58	Improvement in Cardiovascular Risk Prediction with Electronic Health Records. Journal of Cardiovascular Translational Research, 2016, 9, 214-222.	2.4	38
59	Individual housing-based socioeconomic status predicts risk of accidental falls among adults. Annals of Epidemiology, 2017, 27, 415-420.e2.	1.9	35
60	Cohort Profile: The Right Drug, Right Dose, Right Time: Using Genomic Data to Individualize Treatment Protocol (RIGHT Protocol). International Journal of Epidemiology, 2020, 49, 23-24k.	1.9	34
61	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
62	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	5.0	31
63	Characteristics and utilisation of the Mayo Clinic Biobank, a clinic-based prospective collection in the USA: cohort profile. BMJ Open, 2019, 9, e032707.	1.9	31
64	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
65	The Return of Actionable Variants Empirical (RAVE) Study, a Mayo Clinic Genomic Medicine Implementation Study: Design and Initial Results. Mayo Clinic Proceedings, 2018, 93, 1600-1610.	3.0	29
66	Implementation of preemptive DNA sequenceâ€“based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. Genetics in Medicine, 2022, 24, 1062-1072.	2.4	28
67	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
68	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
69	CDKN2A Germline Rare Coding Variants and Risk of Pancreatic Cancer in Minority Populations. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1364-1370.	2.5	23
70	Genetic basis of hypercholesterolemia in adults. Npj Genomic Medicine, 2021, 6, 28.	3.8	22
71	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
72	Risk of serious infection among individuals with and without low count monoclonal B-cell lymphocytosis (MBL). Leukemia, 2021, 35, 239-244.	7.2	21

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73	Does a family history of cancer increase the risk for postmenopausal endometrial carcinoma?. , 1999, 85, 2444-2449.		20
74	SNP-SNP interaction analysis of NF-Î²B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
75	Personalizing Aspirin Use for Targeted Breast Cancer Chemoprevention in Postmenopausal Women. Mayo Clinic Proceedings, 2016, 91, 71-80.	3.0	20
76	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	5.0	19
77	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
78	Developing a Process for Returning Medically Actionable Genomic Variants to Latino Patients in a Federally Qualified Health Center. Public Health Genomics, 2018, 21, 77-84.	1.0	19
79	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
80	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
81	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
82	Ascertainment of Delirium Status Using Natural Language Processing From Electronic Health Records. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 524-530.	3.6	18
83	Zoledronic acid for treatment of osteopenia and osteoporosis in women with primary breast cancer undergoing adjuvant aromatase inhibitor therapy: a 5-year follow-up. Supportive Care in Cancer, 2016, 24, 1219-1226.	2.2	16
84	Design of a randomized controlled trial of disclosing genomic risk of coronary heart disease: the Myocardial Infarction Genes (MI-GENES) study. BMC Medical Genomics, 2015, 8, 51.	1.5	15
85	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
86	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	5.0	15
87	Effects of Heterozygous Variants in the Leptin-Melanocortin Pathway on Roux-en-Y Gastric Bypass Outcomes: a 15-Year Caseâ€“Control Study. Obesity Surgery, 2022, 32, 2632-2640.	2.1	15
88	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
89	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
90	Longitudinal cohorts for harnessing the electronic health record for disease prediction in a US population. BMJ Open, 2021, 11, e044353.	1.9	14

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91	Assessing the stability of biobank donor preferences regarding sample use: evidence supporting the value of dynamic consent. European Journal of Human Genetics, 2020, 28, 1168-1177.	2.8	13
92	QT prolongation in patients with index evaluation for seizure or epilepsy is predictive of all-cause mortality. Heart Rhythm, 2022, 19, 578-584.	0.7	13
93	Association between an individual housing-based socioeconomic index and inconsistent self-reporting of health conditions: a prospective cohort study in the Mayo Clinic Biobank. BMJ Open, 2018, 8, e020054.	1.9	12
94	An assessment of patient perspectives on pharmacogenomics educational materials. Pharmacogenomics, 2020, 21, 347-358.	1.3	11
95	Genetic Predictors of Chemotherapy-Induced Peripheral Neuropathy from Paclitaxel, Carboplatin and Oxaliplatin: NCCTG/Alliance N08C1, N08CA and N08CB Study. Cancers, 2021, 13, 1084.	3.7	11
96	Variability in assigning pathogenicity to incidental findings: insights from LDLR sequence linked to the electronic health record in 1013 individuals. European Journal of Human Genetics, 2017, 25, 410-415.	2.8	10
97	Polygenic risk score and risk of monoclonal B-cell lymphocytosis in caucasians and risk of chronic lymphocytic leukemia (CLL) in African Americans. Leukemia, 2022, 36, 119-125.	7.2	10
98	A hybrid model to identify fall occurrence from electronic health records. International Journal of Medical Informatics, 2022, 162, 104736.	3.3	10
99	How well do whole exome sequencing results correlate with medical findings? A study of 89 Mayo Clinic Biobank samples. Frontiers in Genetics, 2015, 6, 244.	2.3	9
100	Association between Alcohol Consumption, Folate Intake, and Risk of Pancreatic Cancer: A Case-Control Study. Nutrients, 2017, 9, 0448.	4.1	9
101	Association of Genetic Variants at TRPC6 With Chemotherapy-Related Heart Failure. Frontiers in Cardiovascular Medicine, 2020, 7, 142.	2.4	9
102	Association of mitochondrial DNA copy number with self-rated health status. The Application of Clinical Genetics, 2018, Volume 11, 121-127.	3.0	8
103	Real-World Experiences With Yoga on Cancer-Related Symptoms in Women With Breast Cancer. Global Advances in Health and Medicine, 2021, 10, 216495612098414.	1.6	8
104	Perception of Genetic Risk Among Genetic Counselors. Journal of Genetic Counseling, 2000, 9, 47-59.	1.6	7
105	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
106	Understanding the Patterns of Multimorbidity. Mayo Clinic Proceedings, 2018, 93, 824-825.	3.0	7
107	Managing the Unimaginable: Biobank Participant Views on Reconsent for Whole Genome Sequencing of Stored Biospecimens. Biopreservation and Biobanking, 2019, 17, 296-302.	1.0	7
108	Challenges in returning results in a genomic medicine implementation study: the Return of Actionable Variants Empirical (RAVE) study. Npj Genomic Medicine, 2020, 5, 19.	3.8	7

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109	No Association Between Pharmacogenomics Variants and Hospital and Emergency Department Utilization: A Mayo Clinic Biobank Retrospective Study. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 229-237.	0.7	7
110	Prevalence and Overall Survival of Low Count Monoclonal B-Cell Lymphocytosis (LC-MBL): A Screening Study of 8,297 Individuals from the Mayo Clinic Biobank. Blood, 2021, 138, 2632-2632.	1.4	7
111	Inflammatory biomarkers, multi-morbidity, and biologic aging. Journal of International Medical Research, 2022, 50, 030006052211093.	1.0	7
112	Colorectal cancer outcomes after screening with the multi-target stool DNA assay: protocol for a large-scale, prospective cohort study (the Voyage study). BMJ Open Gastroenterology, 2020, 7, e000353.	2.7	6
113	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
114	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
115	An investigation of the biological basis of an interaction of abdominal fat distribution and family history of breast cancer. A nested study of sisters in the Iowa Women's Health Study (United States). Cancer Causes and Control, 2000, 11, 941-954.	1.8	5
116	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
117	Mini-Review of Laboratory Operations in Biobanking: Building Biobanking Resources for Translational Research. Frontiers in Public Health, 2020, 8, 362.	2.7	5
118	Impact of Diverse Data Sources on Computational Phenotyping. Frontiers in Genetics, 2020, 11, 556.	2.3	5
119	Real-world experiences with acupuncture among breast cancer survivors: a cross-sectional survey study. Supportive Care in Cancer, 2020, 28, 5833-5838.	2.2	5
120	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
121	N-Terminal Pro Brain Natriuretic Peptide, sST2, and Galectin-3 Levels in Breast Cancer Survivors. Journal of Clinical Medicine, 2021, 10, 3313.	2.4	5
122	Characteristics Associated With Recruitment and Re-contact in Mayo Clinic Biobank. Frontiers in Public Health, 2020, 8, 9.	2.7	4
123	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4
124	Genetic Variations and Health-Related Quality of Life (HRQOL): A Genome-Wide Study Approach. Cancers, 2021, 13, 716.	3.7	3
125	Impact of Pharmacogenomic Information on Values of Care and Quality of Life Associated with Codeine and Tramadol-Related Adverse Drug Events. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2021, 5, 35-45.	2.4	3
126	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2

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127	Does a family history of cancer increase the risk for postmenopausal endometrial carcinoma?. Cancer, 1999, 85, 2444-2449.	4.1	2
128	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
129	Long-term neurotoxicity in women with breast cancer.. Journal of Clinical Oncology, 2019, 37, e23089-e23089.	1.6	2
130	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
131	Associations of history of vaccination and hospitalization due to infection with risk of monoclonal B-cell lymphocytosis. Leukemia, 2022, , .	7.2	1
132	Validation of a population coronary disease predictive system: the CASSANDRA model. Journal of Epidemiology and Community Health, 2014, 68, 1009-1009.	3.7	0
133	Pathway to Ascertain the Role of Pharmacogenomics in Healthcare Utilization Outcomes [Response to Letter]. Pharmacogenomics and Personalized Medicine, 2021, Volume 14, 545-546.	0.7	0
134	Association between the Risk of Low/High-Count Monoclonal B-Cell Lymphocytosis (MBL) and the Chronic Lymphocytic Leukemia (CLL) Polygenic Risk Score (PRS). Blood, 2018, 132, 5538-5538.	1.4	0
135	Acupuncture: Real-world patient-reported outcomes of treatment-related symptoms in breast cancer survivors.. Journal of Clinical Oncology, 2019, 37, e23111-e23111.	1.6	0
136	N-terminal pro-brain natriuretic peptide levels after receipt of anthracycline for breast cancer.. Journal of Clinical Oncology, 2020, 38, e24103-e24103.	1.6	0
137	Relationship and Susceptibility to Serious Infections Among Monoclonal B-Cell Lymphocytosis (MBL), Monoclonal Gammopathy of Undetermined Significance (MGUS), and Clonal Hematopoiesis (CH) Premalignant Conditions. Blood, 2021, 138, 3739-3739.	1.4	0
138	Polygenic Risk Score and Risk of Chronic Lymphocytic Leukemia, Monoclonal B-Cell Lymphocytosis (MBL), and MBL Subtypes. Blood, 2020, 136, 35-36.	1.4	0