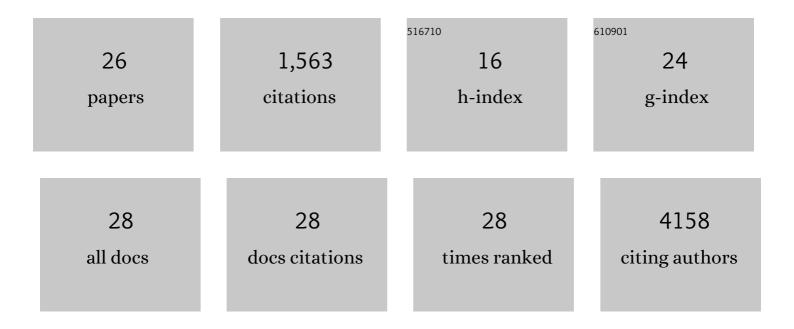
Jennifer L Caswell

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5129876/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Patient perspectives on window of opportunity clinical trials in early-stage breast cancer. Breast Cancer Research and Treatment, 2022, , 1.	2.5	0
2	Genetic and immunohistochemical profiling of small cell and large cell neuroendocrine carcinomas of the breast. Modern Pathology, 2022, 35, 1349-1361.	5.5	5
3	Breast cancer diagnosis and treatment during the COVID-19 pandemic in a nationwide, insured population. Breast Cancer Research and Treatment, 2022, 194, 475-482.	2.5	14
4	Molecular Heterogeneity and Evolution in Breast Cancer. Annual Review of Cancer Biology, 2021, 5, 79-94.	4.5	14
5	Androgen receptor agonists as breast cancer therapeutics. Nature Medicine, 2021, 27, 198-199.	30.7	7
6	Spatial proteomic characterization of HER2-positive breast tumors through neoadjuvant therapy predicts response. Nature Cancer, 2021, 2, 400-413.	13.2	41
7	Treatment and Monitoring Variability in US Metastatic Breast Cancer Care. JCO Clinical Cancer Informatics, 2021, 5, 600-614.	2.1	5
8	Performance of the IBIS/Tyrer uzick model of breast cancer risk by race and ethnicity in the Women's Health Initiative. Cancer, 2021, 127, 3742-3750.	4.1	21
9	Pathologic and molecular responses to neoadjuvant trastuzumab and/or lapatinib from a phase II randomized trial in HER2-positive breast cancer (TRIO-US B07). Nature Communications, 2020, 11, 5824.	12.8	42
10	Prevalence of Pathogenic Variants in Cancer Susceptibility Genes Among Women With Postmenopausal Breast Cancer. JAMA - Journal of the American Medical Association, 2020, 323, 995.	7.4	26
11	Using natural language processing to construct a metastatic breast cancer cohort from linked cancer registry and electronic medical records data. JAMIA Open, 2019, 2, 528-537.	2.0	40
12	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	27.8	239
13	Response to Peshkin, Isaacs, and Schwartz. Journal of the National Cancer Institute, 2019, 111, 874-874.	6.3	0
14	Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. Nature Communications, 2019, 10, 657.	12.8	43
15	Chromatin regulators mediate anthracycline sensitivity in breast cancer. Nature Medicine, 2019, 25, 1721-1727.	30.7	27
16	Cascade Genetic Testing of Relatives for Hereditary Cancer Risk: Results of an Online Initiative. Journal of the National Cancer Institute, 2019, 111, 95-98.	6.3	81
17	Racial/ethnic differences in multiple-gene sequencing results for hereditary cancer risk. Genetics in Medicine, 2018, 20, 234-239.	2.4	131
18	Pathogenic Variants in Less Familiar Cancer Susceptibility Genes: What Happens After Genetic Testing?. JCO Precision Oncology, 2018, 2, 1-10.	3.0	7

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#	Article	IF	CITATIONS
19	Change in Survival in Metastatic Breast Cancer with Treatment Advances: Meta-Analysis and Systematic Review. JNCI Cancer Spectrum, 2018, 2, pky062.	2.9	199
20	Acute, Unilateral Breast Toxicity From Gemcitabine in the Setting of Thoracic Inlet Obstruction. Journal of Oncology Practice, 2016, 12, 763-764.	2.5	1
21	Genome-wide association study identifies variants at 16p13 associated with survival in multiple myeloma patients. Nature Communications, 2015, 6, 7539.	12.8	38
22	Multiple breast cancer risk variants are associated with differential transcript isoform expression in tumors. Human Molecular Genetics, 2015, 24, 7421-7431.	2.9	24
23	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	12.8	123
24	High mammographic density in women of Ashkenazi Jewish descent. Breast Cancer Research, 2013, 15, R40.	5.0	4
25	8q24 prostate, breast, and colon cancer risk loci show tissue-specific long-range interaction with <i>MYC</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9742-9746.	7.1	353
26	Analysis of Chimpanzee History Based on Genome Sequence Alignments. PLoS Genetics, 2008, 4, e1000057.	3.5	73