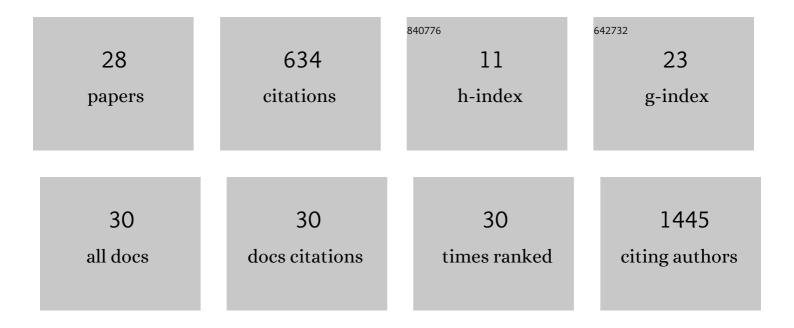
## Jason P Sinnwell

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8121517/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Penalized mediation models for multivariate data. Genetic Epidemiology, 2022, 46, 32-50.	1.3	2
2	Estrogen receptor beta repurposes EZH2 to suppress oncogenic NFκB/p65 signaling in triple negative breast cancer. Npj Breast Cancer, 2022, 8, 20.	5.2	9
3	Biomarkers for Predicting Abiraterone Treatment Outcome and Selecting Alternative Therapies in Castrationâ€Resistant Prostate Cancer. Clinical Pharmacology and Therapeutics, 2022, 111, 1296-1306.	4.7	6
4	Polygenic risk for prostate cancer: Decreasing relative risk with age but little impact on absolute risk. American Journal of Human Genetics, 2022, 109, 900-908.	6.2	10
5	Prevalence of heavy chain MGUS by race and family history risk groups using a high-sensitivity screening method. Blood Advances, 2022, 6, 3746-3750.	5.2	2
6	Body mass index associated with monoclonal gammopathy of undetermined significance (MGUS) progression in Olmsted County, Minnesota. Blood Cancer Journal, 2022, 12, 67.	6.2	13
7	Luminal androgen receptor breast cancer subtype and investigation of the microenvironment and neoadjuvant chemotherapy response. NAR Cancer, 2022, 4, .	3.1	10
8	Impact of Personalized Genetic Breast Cancer Risk Estimation With Polygenic Risk Scores on Preventive Endocrine Therapy Intention and Uptake. Cancer Prevention Research, 2021, 14, 175-184.	1.5	11
9	A clinical calculator to predict disease outcomes in women with triple-negative breast cancer. Breast Cancer Research and Treatment, 2021, 185, 557-566.	2.5	19
10	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. PLoS ONE, 2021, 16, e0249305.	2.5	5
11	Patient-Derived Xenograft Engraftment and Breast Cancer Outcomes in a Prospective Neoadjuvant Study (BEAUTY). Clinical Cancer Research, 2021, 27, 4696-4699.	7.0	7
12	Characteristics and Spatially Defined Immune (micro)landscapes of Early-stage PD-L1–positive Triple-negative Breast Cancer. Clinical Cancer Research, 2021, 27, 5628-5637.	7.0	32
13	A clinical calculator to predict disease outcomes in women with hormone receptor-positive advanced breast cancer treated with first-line endocrine therapy. Breast Cancer Research and Treatment, 2021, 189, 15-23.	2.5	6
14	Nine-gene pharmacogenomics profile service: The Mayo Clinic experience. Pharmacogenomics Journal, 2021, , .	2.0	13
15	Penalized variance components for association of multiple genes with traits. Genetic Epidemiology, 2020, 44, 665-675.	1.3	1
16	Penalized models for analysis of multiple mediators. Genetic Epidemiology, 2020, 44, 408-424.	1.3	9
17	Coinherited genetics of multiple myeloma and its precursor, monoclonal gammopathy of undetermined significance. Blood Advances, 2020, 4, 2789-2797.	5.2	20
18	Spontaneous murine tumors in the development of patient-derived xenografts: a potential pitfall. Oncotarget, 2019, 10, 3924-3930.	1.8	11

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#	Article	IF	CITATIONS
19	Discovery of a Glucocorticoid Receptor (GR) Activity Signature Using Selective GR Antagonism in ER-Negative Breast Cancer. Clinical Cancer Research, 2018, 24, 3433-3446.	7.0	49
20	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	2.6	10
21	Tumor Sequencing and Patient-Derived Xenografts in the Neoadjuvant Treatment of Breast Cancer. Journal of the National Cancer Institute, 2017, 109, .	6.3	61
22	Multivariate generalized linear model for genetic pleiotropy. Biostatistics, 2017, 20, 111-128.	1.5	9
23	Establishing and characterizing patient-derived xenografts using pre-chemotherapy percutaneous biopsy and post-chemotherapy surgical samples from a prospective neoadjuvant breast cancer study. Breast Cancer Research, 2017, 19, 130.	5.0	53
24	Determining the frequency of pathogenic germline variants from exome sequencing in patients with castrate-resistant prostate cancer. BMJ Open, 2016, 6, e010332.	1.9	32
25	Statistical Methods for Testing Genetic Pleiotropy. Genetics, 2016, 204, 483-497.	2.9	50
26	Multiplex matrix network analysis of protein complexes in the human TCR signalosome. Science Signaling, 2016, 9, rs7.	3.6	30
27	The kinship2 R Package for Pedigree Data. Human Heredity, 2014, 78, 91-93.	0.8	151
28	Does a Multiple Myeloma Polygenic Risk Score Predict Overall Survival of Myeloma Patients?. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	2