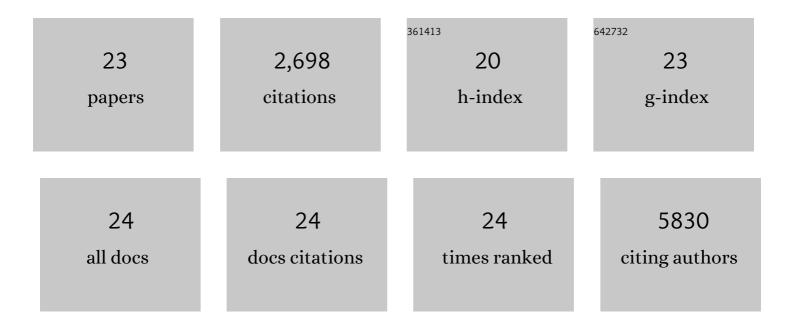
Françoise Rothé

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. Npj Breast Cancer, 2022, 8, .	5.2	8
2	Downregulation of the FTO m6A RNA demethylase promotes EMT-mediated progression of epithelial tumors and sensitivity to Wnt inhibitors. Nature Cancer, 2021, 2, 611-628.	13.2	30
3	Copy Number Aberration Analysis to Predict Response to Neoadjuvant Anti-HER2 Therapy: Results from the NeoALTTO Phase III Clinical Trial. Clinical Cancer Research, 2021, 27, 5607-5618.	7.0	5
4	Characterization of Stromal Tumor-infiltrating Lymphocytes and Genomic Alterations in Metastatic Lobular Breast Cancer. Clinical Cancer Research, 2020, 26, 6254-6265.	7.0	22
5	Tumor-Infiltrating Lymphocytes in Patients Receiving Trastuzumab/Pertuzumab-Based Chemotherapy: A TRYPHAENA Substudy. Journal of the National Cancer Institute, 2019, 111, 69-77.	6.3	60
6	ESR1 mutations in metastatic lobular breast cancer patients. Npj Breast Cancer, 2019, 5, 9.	5.2	26
7	Imprint of parity and age at first pregnancy on the genomic landscape of subsequent breast cancer. Breast Cancer Research, 2019, 21, 25.	5.0	22
8	Immune Infiltration in Invasive Lobular Breast Cancer. Journal of the National Cancer Institute, 2018, 110, 768-776.	6.3	76
9	Feasibility of developing reliable gene expression modules from FFPE derived RNA profiled on Affymetrix arrays. PLoS ONE, 2018, 13, e0203346.	2.5	4
10	Reliability of tumor-infiltrating lymphocyte and tertiary lymphoid structure assessment in human breast cancer. Modern Pathology, 2017, 30, 1204-1212.	5.5	81
11	<scp>CDK</scp> 4 phosphorylation status and a linked gene expression profile predict sensitivity to palbociclib. EMBO Molecular Medicine, 2017, 9, 1052-1066.	6.9	65
12	RNA Sequencing to Predict Response to Neoadjuvant Anti-HER2 Therapy. JAMA Oncology, 2017, 3, 227.	7.1	118
13	Genomic Characterization of Primary Invasive Lobular Breast Cancer. Journal of Clinical Oncology, 2016, 34, 1872-1881.	1.6	249
14	Tumour-educated circulating monocytes are powerful candidate biomarkers for diagnosis and disease follow-up of colorectal cancer. Gut, 2016, 65, 990-1000.	12.1	67
15	Uncovering the genomic heterogeneity of multifocal breast cancer. Journal of Pathology, 2015, 236, 457-466.	4.5	72
16	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. BMC Genomics, 2014, 15, 1008.	2.8	52
17	International study on inter-reader variability for circulating tumor cells in breast cancer. Breast Cancer Research, 2014, 16, R43.	5.0	43
18	Circulating tumor cells and response to neoadjuvant paclitaxel and HER2-targeted therapy: A sub-study from the NeoALTTO phase III trial. Breast, 2013, 22, 1060-1065.	2.2	33

#	Article	IF	CITATIONS
19	CD4+ follicular helper T cell infiltration predicts breast cancer survival. Journal of Clinical Investigation, 2013, 123, 2873-2892.	8.2	813
20	HER2-Positive Circulating Tumor Cells in Breast Cancer. PLoS ONE, 2011, 6, e15624.	2.5	176
21	DNA methylation profiling reveals a predominant immune component in breast cancers. EMBO Molecular Medicine, 2011, 3, 726-741.	6.9	210
22	Global MicroRNA Expression Profiling Identifies MiR-210 Associated with Tumor Proliferation, Invasion and Poor Clinical Outcome in Breast Cancer. PLoS ONE, 2011, 6, e20980.	2.5	214
23	Human natural Treg microRNA signature: Role of microRNAâ€31 and microRNAâ€21 in FOXP3 expression. European Journal of Immunology, 2009, 39, 1608-1618.	2.9	252