

# Jeffrey R Marks

## List of Publications by Year in descending order

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76  
papers

8,474  
citations

71061

41  
h-index

91828

69  
g-index

77  
all docs

77  
docs citations

77  
times ranked

13045  
citing authors

#	ARTICLE	IF	CITATIONS
1	Oncogenic pathway signatures in human cancers as a guide to targeted therapies. <i>Nature</i> , 2006, 439, 353-357.	13.7	1,815
2	Young Age at Diagnosis Correlates With Worse Prognosis and Defines a Subset of Breast Cancers With Shared Patterns of Gene Expression. <i>Journal of Clinical Oncology</i> , 2008, 26, 3324-3330.	0.8	695
3	BRCA2 mutations in primary breast and ovarian cancers. <i>Nature Genetics</i> , 1996, 13, 238-240.	9.4	319
4	Artificial neural networks improve the accuracy of cancer survival prediction. , 1997, 79, 857-862.		301
5	Oncogenic lncRNA downregulates cancer cell antigen presentation and intrinsic tumor suppression. <i>Nature Immunology</i> , 2019, 20, 835-851.	7.0	277
6	Patterns of Gene Expression That Characterize Long-term Survival in Advanced Stage Serous Ovarian Cancers. <i>Clinical Cancer Research</i> , 2005, 11, 3686-3696.	3.2	246
7	Oncogenic properties of PPM1D located within a breast cancer amplification epicenter at 17q23. <i>Nature Genetics</i> , 2002, 31, 133-134.	9.4	235
8	Glutamine Synthetase Is a Genetic Determinant of Cell Type-Specific Glutamine Independence in Breast Epithelia. <i>PLoS Genetics</i> , 2011, 7, e1002229.	1.5	232
9	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. <i>Cancer Cell</i> , 2003, 3, 297-302.	7.7	229
10	Identification of a New Subclass of Alu DNA Repeats Which Can Function as Estrogen Receptor-dependent Transcriptional Enhancers. <i>Journal of Biological Chemistry</i> , 1995, 270, 22777-22782.	1.6	205
11	The LINK-A lncRNA interacts with PtdIns(3,4,5)P3 to hyperactivate AKT and confer resistance to AKT inhibitors. <i>Nature Cell Biology</i> , 2017, 19, 238-251.	4.6	201
12	JAK2-binding long noncoding RNA promotes breast cancer brain metastasis. <i>Journal of Clinical Investigation</i> , 2017, 127, 4498-4515.	3.9	177
13	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
14	A joint analysis of metabolomics and genetics of breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 415.	2.2	161
15	Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma. <i>Cell</i> , 2022, 185, 299-310.e18.	13.5	161
16	Combined cDNA Array Comparative Genomic Hybridization and Serial Analysis of Gene Expression Analysis of Breast Tumor Progression. <i>Cancer Research</i> , 2006, 66, 4065-4078.	0.4	159
17	The p53 tumor suppressor gene frequently is altered in gynecologic cancers. <i>American Journal of Obstetrics and Gynecology</i> , 1994, 170, 246-252.	0.7	157
18	lncRNA wires up Hippo and Hedgehog signaling to reprogramme glucose metabolism. <i>EMBO Journal</i> , 2017, 36, 3325-3335.	3.5	139

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19	CircRNA RAK3 sponges miR-3607 to facilitate breast cancer metastasis. <i>Cancer Letters</i> , 2018, 430, 179-192.	3.2	132
20	The p53 tumor suppressor gene frequently is altered in gynecologic cancers. <i>American Journal of Obstetrics and Gynecology</i> , 1994, 170, 246-252.	0.7	130
21	Frequent IGF2/H19 Domain Epigenetic Alterations and Elevated IGF2 Expression in Epithelial Ovarian Cancer. <i>Molecular Cancer Research</i> , 2006, 4, 283-292.	1.5	130
22	Multivariate machine learning models for prediction of pathologic response to neoadjuvant therapy in breast cancer using MRI features: a study using an independent validation set. <i>Breast Cancer Research and Treatment</i> , 2019, 173, 455-463.	1.1	127
23	LncRNA CamK-A Regulates Ca <sup>2+</sup> -Signaling-Mediated Tumor Microenvironment Remodeling. <i>Molecular Cell</i> , 2018, 72, 71-83.e7.	4.5	119
24	Overexpression of p53 and HER-2/neu Proteins as Prognostic Markers in Early Stage Breast Cancer. <i>Annals of Surgery</i> , 1994, 219, 332-341.	2.1	97
25	Gene Expression Patterns That Characterize Advanced Stage Serous Ovarian Cancers. <i>Journal of the Society for Gynecologic Investigation</i> , 2004, 11, 51-59.	1.9	93
26	p53 overexpression in advanced-stage endometrial adenocarcinoma. <i>American Journal of Obstetrics and Gynecology</i> , 1996, 175, 1246-1252.	0.7	88
27	High insulin-like growth factor-2 (IGF-2) gene expression is an independent predictor of poor survival for patients with advanced stage serous epithelial ovarian cancer. <i>Gynecologic Oncology</i> , 2005, 96, 355-361.	0.6	84
28	Glycosylation of KEAP1 links nutrient sensing to redox stress signaling. <i>EMBO Journal</i> , 2017, 36, 2233-2250.	3.5	82
29	Age-Specific Differences in Oncogenic Pathway Deregulation Seen in Human Breast Tumors. <i>PLoS ONE</i> , 2008, 3, e1373.	1.1	81
30	Prediction of optimal versus suboptimal cytorreduction of advanced-stage serous ovarian cancer with the use of microarrays. <i>American Journal of Obstetrics and Gynecology</i> , 2004, 190, 910-923.	0.7	80
31	Ovarian cancer tumor infiltrating T-regulatory (Treg) cells are associated with a metastatic phenotype. <i>Gynecologic Oncology</i> , 2010, 116, 556-562.	0.6	71
32	High throughput detection of M6P/IGF2R intronic hypermethylation and LOH in ovarian cancer. <i>Nucleic Acids Research</i> , 2006, 34, 555-563.	6.5	68
33	Microarray Analysis of Early Stage Serous Ovarian Cancers Shows Profiles Predictive of Favorable Outcome. <i>Clinical Cancer Research</i> , 2009, 15, 2448-2455.	3.2	67
34	Circulating Cancer-Associated Macrophage-Like Cells Differentiate Malignant Breast Cancer and Benign Breast Conditions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1037-1042.	1.1	61
35	Expression of Long Noncoding RNA YIYA Promotes Glycolysis in Breast Cancer. <i>Cancer Research</i> , 2018, 78, 4524-4532.	0.4	59
36	Outcomes of Active Surveillance for Ductal Carcinoma in Situ: A Computational Risk Analysis. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv372.	3.0	57

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37	Prediction of Occult Invasive Disease in Ductal Carcinoma in Situ Using Deep Learning Features. <i>Journal of the American College of Radiology</i> , 2018, 15, 527-534.	0.9	56
38	Analysis of tumor environmental response and oncogenic pathway activation identifies distinct basal and luminal features in HER2-related breast tumor subtypes. <i>Breast Cancer Research</i> , 2011, 13, R62.	2.2	54
39	Isolation and initial characterization of the BRCA2 promoter. <i>Oncogene</i> , 1999, 18, 6000-6012.	2.6	53
40	Inactivation of the <i>MAL</i> Gene in Breast Cancer Is a Common Event That Predicts Benefit from Adjuvant Chemotherapy. <i>Molecular Cancer Research</i> , 2009, 7, 199-209.	1.5	50
41	Predicting response to adjuvant and radiation therapy in patients with early stage breast carcinoma. , 1998, 82, 874-877.		46
42	Expression signatures of TP53 mutations in serous ovarian cancers. <i>BMC Cancer</i> , 2010, 10, 237.	1.1	46
43	Expression profiling of in vivo ductal carcinoma in situ progression models identified B cell lymphoma-9 as a molecular driver of breast cancer invasion. <i>Breast Cancer Research</i> , 2015, 17, 128.	2.2	43
44	LncRNAs-directed PTEN enzymatic switch governs epithelial-mesenchymal transition. <i>Cell Research</i> , 2019, 29, 286-304.	5.7	43
45	Loss of Expression of the p16 Tumor Suppressor Gene Is More Frequent in Advanced Ovarian Cancers Lacking p53 Mutations. <i>Gynecologic Oncology</i> , 2001, 83, 491-500.	0.6	42
46	The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. <i>Cell Reports</i> , 2019, 29, 889-903.e10.	2.9	40
47	Managing hereditary ovarian cancer risk. , 1999, 86, 2517-2524.		36
48	Prognostic significance of the number of lymph nodes examined in patients with lymph node-negative breast carcinoma. <i>Cancer</i> , 2001, 91, 2258-2262.	2.0	35
49	Algorithms for prediction of the Oncotype DX recurrence score using clinicopathologic data: a review and comparison using an independent dataset. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 1-10.	1.1	35
50	RIPK3 upregulation confers robust proliferation and collateral cystine-dependence on breast cancer recurrence. <i>Cell Death and Differentiation</i> , 2020, 27, 2234-2247.	5.0	35
51	Isogenic Normal Basal and Luminal Mammary Epithelial Isolated by a Novel Method Show a Differential Response to Ionizing Radiation. <i>Cancer Research</i> , 2007, 67, 2990-3001.	0.4	34
52	Development of an ovarian cancer screening decision model that incorporates disease heterogeneity. <i>Cancer</i> , 2011, 117, 545-553.	2.0	30
53	Prognostic significance of differential expression of angiogenic genes in women with high-grade serous ovarian carcinoma. <i>Gynecologic Oncology</i> , 2015, 139, 23-29.	0.6	27
54	Validation of ovarian cancer gene expression signatures for survival and subtype in formalin fixed paraffin embedded tissues. <i>Gynecologic Oncology</i> , 2013, 129, 159-164.	0.6	24

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55	Common variants at the <i>CHEK2</i> gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
56	Regulation of the metastasis suppressor gene MKK4 in ovarian cancer. <i>Gynecologic Oncology</i> , 2007, 105, 312-320.	0.6	21
57	Unmasking the immune microecology of ductal carcinoma in situ with deep learning. <i>Npj Breast Cancer</i> , 2021, 7, 19.	2.3	20
58	Can algorithmically assessed MRI features predict which patients with a preoperative diagnosis of ductal carcinoma in situ are upstaged to invasive breast cancer?. <i>Journal of Magnetic Resonance Imaging</i> , 2017, 46, 1332-1340.	1.9	19
59	Can Occult Invasive Disease in Ductal Carcinoma In Situ Be Predicted Using Computer-extracted Mammographic Features?. <i>Academic Radiology</i> , 2017, 24, 1139-1147.	1.3	18
60	Prediction of Upstaging in Ductal Carcinoma in Situ Based on Mammographic Radiomic Features. <i>Radiology</i> , 2022, 303, 54-62.	3.6	17
61	Association of distant recurrence-free survival with algorithmically extracted MRI characteristics in breast cancer. <i>Journal of Magnetic Resonance Imaging</i> , 2019, 49, e231-e240.	1.9	16
62	Integrative analyses reveal signaling pathways underlying familial breast cancer susceptibility. <i>Molecular Systems Biology</i> , 2016, 12, 860.	3.2	14
63	Construction and Analysis of the NCI-EDRN Breast Cancer Reference Set for Circulating Markers of Disease. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 435-441.	1.1	13
64	TAFII70 Isoform-Specific Growth Suppression Correlates With Its Ability to Complex With the GADD45a Protein. <i>Molecular Cancer Research</i> , 2004, 2, 442-452.	1.5	12
65	Proliferation index in various stages of breast cancer determined by ki-67 immunostaining. <i>Journal of Surgical Oncology</i> , 1991, 48, 11-20.	0.8	11
66	Novel tumor sampling strategies to enable microarray gene expression signatures in breast cancer: a study to determine feasibility and reproducibility in the context of clinical care. <i>Breast Cancer Research and Treatment</i> , 2009, 118, 635-43.	1.1	10
67	Intra-tumor molecular heterogeneity in breast cancer: definitions of measures and association with distant recurrence-free survival. <i>Breast Cancer Research and Treatment</i> , 2018, 172, 123-132.	1.1	9
68	Managing hereditary ovarian cancer risk. <i>Cancer</i> , 1999, 86, 1697-1704.	2.0	9
69	Determination of Proliferation Index By MIB-1 Immunostaining in Early Stage Breast Cancer Using Quantitative Image Analysis. <i>Breast Journal</i> , 1995, 1, 362-371.	0.4	6
70	A new method to accurately identify single nucleotide variants using small FFPE breast samples. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
71	p53 in Human Cancer. , 1995, , 77-110.		4
72	Decision Fusion of Circulating Markers for Breast Cancer Detection in Premenopausal Women. , 2007, , .		3

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73	Relative promoter activity in human mammary epithelial cells assayed by transient expression. <i>In Vitro Cellular &amp; Developmental Biology</i> , 1992, 28, 730-734.	1.0	1
74	Prognostic significance of the number of lymph nodes examined in patients with lymph node-negative breast carcinoma. <i>Cancer</i> , 2001, 91, 2258-2262.	2.0	1
75	Automated Dcis Identification From Multiplex Immunohistochemistry Using Generative Adversarial Networks. , 2022, , .		1
76	Abstract P1-22-05: Identifying predictors of invasive recurrence based on molecular profiles of DCIS lesions. <i>Cancer Research</i> , 2022, 82, P1-22-05-P1-22-05.	0.4	0