Jeffrey R Marks

List of Publications by Year
in descending order

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	Transition to invasive breast cancer is associated with progressive changes in the structure and composition of tumor stroma. Cell, 2022, 185, 299-310.e18.	13.5	161
2	Prediction of Upstaging in Ductal Carcinoma in Situ Based on Mammographic Radiomic Features. Radiology, 2022, 303, 54-62.	3.6	17
3	Abstract P1-22-05: Identifying predictors of invasive recurrence based on molecular profiles of DCIS lesions. Cancer Research, 2022, 82, P1-22-05-P1-22-05.	0.4	0
4	Automated Dcis Identification From Multiplex Immunohistochemistry Using Generative Adversarial Networks. , 2022, , .		1
5	Unmasking the immune microecology of ductal carcinoma in situ with deep learning. Npj Breast Cancer, 2021, 7, 19.	2.3	20
6	A new method to accurately identify single nucleotide variants using small FFPE breast samples. Briefings in Bioinformatics, 2021, 22, .	3.2	4
7	RIPK3 upregulation confers robust proliferation and collateral cystine-dependence on breast cancer recurrence. Cell Death and Differentiation, 2020, 27, 2234-2247.	5.0	35
8	The Lineage Determining Factor GRHL2 Collaborates with FOXA1 to Establish a Targetable Pathway in Endocrine Therapy-Resistant Breast Cancer. Cell Reports, 2019, 29, 889-903.e10.	2.9	40
9	Association of distant recurrence–free survival with algorithmically extracted MRI characteristics in breast cancer. Journal of Magnetic Resonance Imaging, 2019, 49, e231-e240.	1.9	16
10	Oncogenic lncRNA downregulates cancer cell antigen presentation and intrinsic tumor suppression. Nature Immunology, 2019, 20, 835-851.	7.0	277
11	LncRNAs-directed PTEN enzymatic switch governs epithelial–mesenchymal transition. Cell Research, 2019, 29, 286-304.	5.7	43
12	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. Breast Cancer Research and Treatment, 2019, 173, 455-463.	1.1	127
13	Prediction of Occult Invasive Disease in Ductal Carcinoma in Situ Using Deep Learning Features. Journal of the American College of Radiology, 2018, 15, 527-534.	0.9	56
14	LncRNA CamK-A Regulates Ca2+-Signaling-Mediated Tumor Microenvironment Remodeling. Molecular Cell, 2018, 72, 71-83.e7.	4.5	119
15	CircIRAK3 sponges miR-3607 to facilitate breast cancer metastasis. Cancer Letters, 2018, 430, 179-192.	3.2	132
16	Expression of Long Noncoding RNA *YIYA* Promotes Glycolysis in Breast Cancer. Cancer Research, 2018, 78, 4524-4532.	0.4	59
17	Intra-tumor molecular heterogeneity in breast cancer: definitions of measures and association with distant recurrence-free survival. Breast Cancer Research and Treatment, 2018, 172, 123-132.	1.1	9
18	Algorithms for prediction of the Oncotype DX recurrence score using clinicopathologic data: a review and comparison using an independent dataset. Breast Cancer Research and Treatment, 2017, 162, 1-10.	1.1	35

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19	The LINK-A lncRNA interacts with PtdIns(3,4,5)P3 toÂhyperactivate AKTÂand confer resistance to AKTÂinhibitors. Nature Cell Biology, 2017, 19, 238-251.	4.6	201
20	Can algorithmically assessed MRI features predict which patients with a preoperative diagnosis of ductal carcinoma in situ are upstaged to invasive breast cancer?. Journal of Magnetic Resonance Imaging, 2017, 46, 1332-1340.	1.9	19
21	Can Occult Invasive Disease in Ductal Carcinoma In Situ Be Predicted Using Computer-extracted Mammographic Features?. Academic Radiology, 2017, 24, 1139-1147.	1.3	18
22	Lnc<scp>RNA</scp> wires up Hippo and Hedgehog signaling to reprogramme glucose metabolism. EMBO Journal, 2017, 36, 3325-3335.	3.5	139
23	Glycosylation of <scp>KEAP</scp>1 links nutrient sensing to redox stress signaling. EMBO Journal, 2017, 36, 2233-2250.	3.5	82
24	JAK2-binding long noncoding RNA promotes breast cancer brain metastasis. Journal of Clinical Investigation, 2017, 127, 4498-4515.	3.9	177
25	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
26	Circulating Cancer-Associated Macrophage-Like Cells Differentiate Malignant Breast Cancer and Benign Breast Conditions. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1037-1042.	1.1	61
27	Integrative analyses reveal signaling pathways underlying familial breast cancer susceptibility. Molecular Systems Biology, 2016, 12, 860.	3.2	14
28	Outcomes of Active Surveillance for Ductal Carcinoma in Situ: A Computational Risk Analysis. Journal of the National Cancer Institute, 2016, 108, djv372.	3.0	57
29	Expression profiling of in vivo ductal carcinoma in situ progression models identified B cell lymphoma-9 as a molecular driver of breast cancer invasion. Breast Cancer Research, 2015, 17, 128.	2.2	43
30	Construction and Analysis of the NCI-EDRN Breast Cancer Reference Set for Circulating Markers of Disease. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 435-441.	1.1	13
31	Common variants at the<i>CHEK2</i>gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
32	Prognostic significance of differential expression of angiogenic genes in women with high-grade serous ovarian carcinoma. Gynecologic Oncology, 2015, 139, 23-29.	0.6	27
33	A joint analysis of metabolomics and genetics of breast cancer. Breast Cancer Research, 2014, 16, 415.	2.2	161
34	Validation of ovarian cancer gene expression signatures for survival and subtype in formalin fixed paraffin embedded tissues. Gynecologic Oncology, 2013, 129, 159-164.	0.6	24
35	Analysis of tumor environmental response and oncogenic pathway activation identifies distinct basal and luminal features in HER2-related breast tumor subtypes. Breast Cancer Research, 2011, 13, R62.	2.2	54
36	Development of an ovarian cancer screening decision model that incorporates disease heterogeneity. Cancer, 2011, 117, 545-553.	2.0	30

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37	Glutamine Synthetase Is a Genetic Determinant of Cell Type–Specific Glutamine Independence in Breast Epithelia. PLoS Genetics, 2011, 7, e1002229.	1.5	232
38	Expression signatures of TP53 mutations in serous ovarian cancers. BMC Cancer, 2010, 10, 237.	1.1	46
39	Ovarian cancer tumor infiltrating T-regulatory (Treg) cells are associated with a metastatic phenotype. Gynecologic Oncology, 2010, 116, 556-562.	0.6	71
40	Microarray Analysis of Early Stage Serous Ovarian Cancers Shows Profiles Predictive of Favorable Outcome. Clinical Cancer Research, 2009, 15, 2448-2455.	3.2	67
41	Inactivation of the <i>MAL</i> Gene in Breast Cancer Is a Common Event That Predicts Benefit from Adjuvant Chemotherapy. Molecular Cancer Research, 2009, 7, 199-209.	1.5	50
42	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. Breast Cancer Research and Treatment, 2009, 118, 635-43.	1.1	10
43	Young Age at Diagnosis Correlates With Worse Prognosis and Defines a Subset of Breast Cancers With Shared Patterns of Gene Expression. Journal of Clinical Oncology, 2008, 26, 3324-3330.	0.8	695
44	Age-Specific Differences in Oncogenic Pathway Deregulation Seen in Human Breast Tumors. PLoS ONE, 2008, 3, e1373.	1.1	81
45	Isogenic Normal Basal and Luminal Mammary Epithelial Isolated by a Novel Method Show a Differential Response to Ionizing Radiation. Cancer Research, 2007, 67, 2990-3001.	0.4	34
46	Decision Fusion of Circulating Markers for Breast Cancer Detection in Premenopausal Women. , 2007, , .		3
47	Regulation of the metastasis suppressor gene MKK4 in ovarian cancer. Gynecologic Oncology, 2007, 105, 312-320.	0.6	21
48	Oncogenic pathway signatures in human cancers as a guide to targeted therapies. Nature, 2006, 439, 353-357.	13.7	1,815
49	High throughput detection of M6P/IGF2R intronic hypermethylation and LOH in ovarian cancer. Nucleic Acids Research, 2006, 34, 555-563.	6.5	68
50	Frequent IGF2/H19 Domain Epigenetic Alterations and Elevated IGF2 Expression in Epithelial Ovarian Cancer. Molecular Cancer Research, 2006, 4, 283-292.	1.5	130
51	Combined cDNA Array Comparative Genomic Hybridization and Serial Analysis of Gene Expression Analysis of Breast Tumor Progression. Cancer Research, 2006, 66, 4065-4078.	0.4	159
52	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. Gynecologic Oncology, 2005, 96, 355-361.	0.6	84
53	Patterns of Gene Expression That Characterize Long-term Survival in Advanced Stage Serous Ovarian Cancers. Clinical Cancer Research, 2005, 11, 3686-3696.	3.2	246
54	Prediction of optimal versus suboptimal cytoreduction of advanced-stage serous ovarian cancer with the use of microarrays. American Journal of Obstetrics and Gynecology, 2004, 190, 910-923.	0.7	80

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55	Gene Expression Patterns That Characterize Advanced Stage Serous Ovarian Cancers. Journal of the Society for Gynecologic Investigation, 2004, 11, 51-59.	1.9	93
56	TAFII70 Isoform-Specific Growth Suppression Correlates With Its Ability to Complex With the GADD45a Protein. Molecular Cancer Research, 2004, 2, 442-452.	1.5	12
57	Genomic amplification and oncogenic properties of the KCNK9 potassium channel gene. Cancer Cell, 2003, 3, 297-302.	7.7	229
58	Oncogenic properties of PPM1D located within a breast cancer amplification epicenter at 17q23. Nature Genetics, 2002, 31, 133-134.	9.4	235
59	Prognostic significance of the number of lymph nodes examined in patients with lymph node-negative breast carcinoma. Cancer, 2001, 91, 2258-2262.	2.0	35
60	Loss of Expression of the p16 Tumor Suppressor Gene Is More Frequent in Advanced Ovarian Cancers Lacking p53 Mutations. Gynecologic Oncology, 2001, 83, 491-500.	0.6	42
61	Prognostic significance of the number of lymph nodes examined in patients with lymph node–negative breast carcinoma. Cancer, 2001, 91, 2258-2262.	2.0	1
62	Isolation and initial characterization of the BRCA2 promoter. Oncogene, 1999, 18, 6000-6012.	2.6	53
63	Managing hereditary ovarian cancer risk. , 1999, 86, 2517-2524.		36
64	Managing hereditary ovarian cancer risk. Cancer, 1999, 86, 1697-1704.	2.0	9
65	Predicting response to adjuvant and radiation therapy in patients with early stage breast carcinoma. , 1998, 82, 874-877.		46
66	Artificial neural networks improve the accuracy of cancer survival prediction. , 1997, 79, 857-862.		301
67	BRCA2 mutations in primary breast and ovarian cancers. Nature Genetics, 1996, 13, 238-240.	9.4	319
68	p53 overexpression in advanced-stage endometrial adenocarcinoma. American Journal of Obstetrics and Gynecology, 1996, 175, 1246-1252.	0.7	88
69	Determination of Proliferation Index By MIB-1 Immunostaining in Early Stage Breast Cancer Using Quantitative Image Analysis. Breast Journal, 1995, 1, 362-371.	0.4	6
70	Identification of a New Subclass of Alu DNA Repeats Which Can Function as Estrogen Receptor-dependent Transcriptional Enhancers. Journal of Biological Chemistry, 1995, 270, 22777-22782.	1.6	205
71	p53 in Human Cancer. , 1995, , 77-110.		4
72	The p53 tumor suppressor gene frequently is altered in gynecologic cancers. American Journal of Obstetrics and Gynecology, 1994, 170, 246-252.	0.7	157

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73	The p53 tumor suppressor gene frequently is altered in gynecologic cancers. American Journal of Obstetrics and Gynecology, 1994, 170, 246-252.	0.7	130
74	Overexpression of p53 and HER-2/neu Proteins as Prognostic Markers in Early Stage Breast Cancer. Annals of Surgery, 1994, 219, 332-341.	2.1	97
75	Relative promoter activity in human mammary epithelial cells assayed by transient expression. In Vitro Cellular & Developmental Biology, 1992, 28, 730-734.	1.0	1
76	Proliferation index in various stages of breast cancer determined by ki-67 immunostaining. Journal of Surgical Oncology, 1991, 48, 11-20.	0.8	11