

Rachael Natrajan

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

109 papers	9,461 citations	52 h-index	97 g-index
114 ext. papers	10,837 ext. citations	10.3 avg, IF	5.35 L-index

#	Paper	IF	Citations
109	Resistance to therapy caused by intragenic deletion in BRCA2. <i>Nature</i> , 2008 , 451, 1111-5	50.4	741
108	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , 2009 , 462, 1005-10	50.4	684
107	FGFR1 amplification drives endocrine therapy resistance and is a therapeutic target in breast cancer. <i>Cancer Research</i> , 2010 , 70, 2085-94	10.1	533
106	BRCA1 basal-like breast cancers originate from luminal epithelial progenitors and not from basal stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 403-17	18	518
105	Integrative molecular profiling of triple negative breast cancers identifies amplicon drivers and potential therapeutic targets. <i>Oncogene</i> , 2010 , 29, 2013-23	9.2	318
104	Breast cancer molecular profiling with single sample predictors: a retrospective analysis. <i>Lancet Oncology</i> , 2010 , 11, 339-49	21.7	274
103	ECatenin pathway activation in breast cancer is associated with triple-negative phenotype but not with CTNNB1 mutation. <i>Modern Pathology</i> , 2011 , 24, 209-31	9.8	264
102	Functionally recurrent rearrangements of the MAST kinase and Notch gene families in breast cancer. <i>Nature Medicine</i> , 2011 , 17, 1646-51	50.5	262
101	Identification of a disease-defining gene fusion in epithelioid hemangioendothelioma. <i>Science Translational Medicine</i> , 2011 , 3, 98ra82	17.5	252
100	Genome-wide profiling of genetic synthetic lethality identifies CDK12 as a novel determinant of PARP1/2 inhibitor sensitivity. <i>Cancer Research</i> , 2014 , 74, 287-97	10.1	212
99	PTEN deficiency in endometrioid endometrial adenocarcinomas predicts sensitivity to PARP inhibitors. <i>Science Translational Medicine</i> , 2010 , 2, 53ra75	17.5	190
98	The molecular underpinning of lobular histological growth pattern: a genome-wide transcriptomic analysis of invasive lobular carcinomas and grade- and molecular subtype-matched invasive ductal carcinomas of no special type. <i>Journal of Pathology</i> , 2010 , 220, 45-57	9.4	184
97	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. <i>Genome Research</i> , 2014 , 24, 1854-68	9.7	168
96	Molecular analysis reveals a genetic basis for the phenotypic diversity of metaplastic breast carcinomas. <i>Journal of Pathology</i> , 2010 , 220, 562-73	9.4	165
95	Tiling path genomic profiling of grade 3 invasive ductal breast cancers. <i>Clinical Cancer Research</i> , 2009 , 15, 2711-22	12.9	138
94	FGFR signaling promotes the growth of triple-negative and basal-like breast cancer cell lines both in vitro and in vivo. <i>Clinical Cancer Research</i> , 2011 , 17, 5275-86	12.9	138
93	An integrative genomic and transcriptomic analysis reveals molecular pathways and networks regulated by copy number aberrations in basal-like, HER2 and luminal cancers. <i>Breast Cancer Research and Treatment</i> , 2010 , 121, 575-89	4.4	132

92	PPM1D is a potential therapeutic target in ovarian clear cell carcinomas. <i>Clinical Cancer Research</i> , 2009 , 15, 2269-80	12.9	128
91	SF3B1 mutations constitute a novel therapeutic target in breast cancer. <i>Journal of Pathology</i> , 2015 , 235, 571-80	9.4	124
90	Adenoid cystic carcinomas constitute a genomically distinct subgroup of triple-negative and basal-like breast cancers. <i>Journal of Pathology</i> , 2012 , 226, 84-96	9.4	122
89	Mucinous carcinoma of the breast is genomically distinct from invasive ductal carcinomas of no special type. <i>Journal of Pathology</i> , 2010 , 222, 282-98	9.4	120
88	Down-regulation of the miRNA master regulators Drosha and Dicer is associated with specific subgroups of breast cancer. <i>European Journal of Cancer</i> , 2011 , 47, 138-50	7.5	117
87	Functional viability profiles of breast cancer. <i>Cancer Discovery</i> , 2011 , 1, 260-73	24.4	117
86	Genomic analysis of the HER2/TOP2A amplicon in breast cancer and breast cancer cell lines. <i>Laboratory Investigation</i> , 2008 , 88, 491-503	5.9	116
85	Genomic and mutational profiling of ductal carcinomas in situ and matched adjacent invasive breast cancers reveals intra-tumour genetic heterogeneity and clonal selection. <i>Journal of Pathology</i> , 2012 , 227, 42-52	9.4	115
84	Microarray-based class discovery for molecular classification of breast cancer: analysis of interobserver agreement. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 662-73	9.7	105
83	Genomic landscape of adenoid cystic carcinoma of the breast. <i>Journal of Pathology</i> , 2015 , 237, 179-89	9.4	101
82	Genomic analysis reveals the molecular heterogeneity of ovarian clear cell carcinomas. <i>Clinical Cancer Research</i> , 2011 , 17, 1521-34	12.9	100
81	The Landscape of Somatic Genetic Alterations in Metaplastic Breast Carcinomas. <i>Clinical Cancer Research</i> , 2017 , 23, 3859-3870	12.9	92
80	Array CGH using whole genome amplification of fresh-frozen and formalin-fixed, paraffin-embedded tumor DNA. <i>Genomics</i> , 2006 , 87, 298-306	4.3	87
79	Integrated functional, gene expression and genomic analysis for the identification of cancer targets. <i>PLoS ONE</i> , 2009 , 4, e5120	3.7	85
78	Intra-tumor genetic heterogeneity and alternative driver genetic alterations in breast cancers with heterogeneous HER2 gene amplification. <i>Genome Biology</i> , 2015 , 16, 107	18.3	83
77	Large-Scale Profiling of Kinase Dependencies in Cancer Cell Lines. <i>Cell Reports</i> , 2016 , 14, 2490-501	10.6	77
76	Chromogenic and fluorescent in situ hybridization in breast cancer. <i>Human Pathology</i> , 2007 , 38, 1105-22	3.7	77
75	Unlocking pathology archives for molecular genetic studies: a reliable method to generate probes for chromogenic and fluorescent in situ hybridization. <i>Laboratory Investigation</i> , 2006 , 86, 398-408	5.9	76

74	Characterization of the genomic features and expressed fusion genes in micropapillary carcinomas of the breast. <i>Journal of Pathology</i> , 2014 , 232, 553-65	9.4	75
73	Loss of 16q in high grade breast cancer is associated with estrogen receptor status: Evidence for progression in tumors with a luminal phenotype?. <i>Genes Chromosomes and Cancer</i> , 2009 , 48, 351-65	5	74
72	Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology-Genomic Integration Analysis. <i>PLoS Medicine</i> , 2016 , 13, e1001961	11.6	74
71	Is acinic cell carcinoma a variant of secretory carcinoma? A FISH study using ETV6Split apartS probes. <i>Histopathology</i> , 2008 , 52, 840-6	7.3	69
70	ESR1 gene amplification in breast cancer: a common phenomenon?. <i>Nature Genetics</i> , 2008 , 40, 809-10; author reply 810-2	36.3	66
69	Immunophenotypic and genomic characterization of papillary carcinomas of the breast. <i>Journal of Pathology</i> , 2012 , 226, 427-441	9.4	65
68	Mixed micropapillary-ductal carcinomas of the breast: a genomic and immunohistochemical analysis of morphologically distinct components. <i>Journal of Pathology</i> , 2009 , 218, 301-15	9.4	65
67	Infant High-Grade Gliomas Comprise Multiple Subgroups Characterized by Novel Targetable Gene Fusions and Favorable Outcomes. <i>Cancer Discovery</i> , 2020 , 10, 942-963	24.4	65
66	Phase I Trial of First-in-Class ATR Inhibitor M6620 (VX-970) as Monotherapy or in Combination With Carboplatin in Patients With Advanced Solid Tumors. <i>Journal of Clinical Oncology</i> , 2020 , 38, 3195-3204	2.2	63
65	Enhanced RAD21 cohesin expression confers poor prognosis and resistance to chemotherapy in high grade luminal, basal and HER2 breast cancers. <i>Breast Cancer Research</i> , 2011 , 13, R9	8.3	62
64	Getting it right: designing microarray (and not Smicroawry\$ comparative genomic hybridization studies for cancer research. <i>Laboratory Investigation</i> , 2007 , 87, 737-54	5.9	62
63	Metaplastic breast carcinomas display genomic and transcriptomic heterogeneity [corrected].. <i>Modern Pathology</i> , 2015 , 28, 340-51	9.8	56
62	Genomic profiling of histological special types of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013 , 142, 257-69	4.4	55
61	Synthetic Lethal Targeting of ARID1A-Mutant Ovarian Clear Cell Tumors with Dasatinib. <i>Molecular Cancer Therapeutics</i> , 2016 , 15, 1472-84	6.1	54
60	Cross-platform pathway-based analysis identifies markers of response to the PARP inhibitor olaparib. <i>Breast Cancer Research and Treatment</i> , 2012 , 135, 505-17	4.4	54
59	PPM1D gene amplification and overexpression in breast cancer: a qRT-PCR and chromogenic in situ hybridization study. <i>Modern Pathology</i> , 2010 , 23, 1334-45	9.8	54
58	Loss of heterozygosity at 2q37 in sporadic WilmsStumor: putative role for miR-562. <i>Clinical Cancer Research</i> , 2009 , 15, 5985-92	12.9	53
57	E-Cadherin/ROS1 Inhibitor Synthetic Lethality in Breast Cancer. <i>Cancer Discovery</i> , 2018 , 8, 498-515	24.4	51

56	Functional characterization of the 19q12 amplicon in grade III breast cancers. <i>Breast Cancer Research</i> , 2012 , 14, R53	8.3	51
55	APRIN is a cell cycle specific BRCA2-interacting protein required for genome integrity and a predictor of outcome after chemotherapy in breast cancer. <i>EMBO Journal</i> , 2012 , 31, 1160-76	13	51
54	An ecological measure of immune-cancer colocalization as a prognostic factor for breast cancer. <i>Breast Cancer Research</i> , 2015 , 17, 131	8.3	50
53	Genomic and immunohistochemical analysis of adenosquamous carcinoma of the breast. <i>Modern Pathology</i> , 2010 , 23, 951-60	9.8	47
52	CD44 is overexpressed in basal-like breast cancers but is not a driver of 11p13 amplification. <i>Breast Cancer Research and Treatment</i> , 2010 , 120, 95-109	4.4	47
51	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. <i>Nature Genetics</i> , 2020 , 52, 187-197	36.3	47
50	Amplification and overexpression of CACNA1E correlates with relapse in favorable histology WilmsS tumors. <i>Clinical Cancer Research</i> , 2006 , 12, 7284-93	12.9	45
49	A whole-genome massively parallel sequencing analysis of BRCA1 mutant oestrogen receptor-negative and -positive breast cancers. <i>Journal of Pathology</i> , 2012 , 227, 29-41	9.4	44
48	Molecular profiling reveals frequent gain of MYCN and anaplasia-specific loss of 4q and 14q in Wilms tumor. <i>Genes Chromosomes and Cancer</i> , 2011 , 50, 982-95	5	44
47	Molecular evidence in support of the neoplastic and precursor nature of microglandular adenosis. <i>Histopathology</i> , 2012 , 60, E115-30	7.3	42
46	Microglandular adenosis or microglandular adenoma? A molecular genetic analysis of a case associated with atypia and invasive carcinoma. <i>Histopathology</i> , 2009 , 55, 732-43	7.3	42
45	Prognostic classification of relapsing favorable histology Wilms tumor using cDNA microarray expression profiling and support vector machines. <i>Genes Chromosomes and Cancer</i> , 2004 , 41, 65-79	5	42
44	Integrative genomic and transcriptomic characterization of papillary carcinomas of the breast. <i>Molecular Oncology</i> , 2014 , 8, 1588-602	7.9	38
43	Genomic and transcriptomic heterogeneity in metaplastic carcinomas of the breast. <i>Npj Breast Cancer</i> , 2017 , 3, 48	7.8	38
42	Blastemal expression of type I insulin-like growth factor receptor in WilmsStumors is driven by increased copy number and correlates with relapse. <i>Cancer Research</i> , 2006 , 66, 11148-55	10.1	38
41	Evaluation of CDK12 Protein Expression as a Potential Novel Biomarker for DNA Damage Response-Targeted Therapies in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2018 , 17, 306-315	6.1	37
40	Mutation profiling of adenoid cystic carcinomas from multiple anatomical sites identifies mutations in the RAS pathway, but no KIT mutations. <i>Histopathology</i> , 2013 , 62, 543-50	7.3	33
39	Identification of gene fusion transcripts by transcriptome sequencing in BRCA1-mutated breast cancers and cell lines. <i>BMC Medical Genomics</i> , 2011 , 4, 75	3.7	33

38	Next-generation sequencing applied to molecular diagnostics. <i>Expert Review of Molecular Diagnostics</i> , 2011 , 11, 425-44	3.8	32
37	Multifaceted dysregulation of the epidermal growth factor receptor pathway in clear cell sarcoma of the kidney. <i>Clinical Cancer Research</i> , 2007 , 13, 4360-4	12.9	31
36	Functional characterization of EMSY gene amplification in human cancers. <i>Journal of Pathology</i> , 2011 , 225, 29-42	9.4	29
35	Transcriptomic analysis of tubular carcinomas of the breast reveals similarities and differences with molecular subtype-matched ductal and lobular carcinomas. <i>Journal of Pathology</i> , 2010 , 222, 64-75	9.4	29
34	High-resolution deletion mapping of 15q13.2-q21.1 in transitional cell carcinoma of the bladder. <i>Cancer Research</i> , 2003 , 63, 7657-62	10.1	29
33	Optimised ARID1A immunohistochemistry is an accurate predictor of ARID1A mutational status in gynaecological cancers. <i>Journal of Pathology: Clinical Research</i> , 2018 , 4, 154-166	5.3	28
32	An siRNA screen identifies the GNAS locus as a driver in 20q amplified breast cancer. <i>Oncogene</i> , 2014 , 33, 2478-86	9.2	26
31	Cortactin gene amplification and expression in breast cancer: a chromogenic in situ hybridisation and immunohistochemical study. <i>Breast Cancer Research and Treatment</i> , 2010 , 124, 653-66	4.4	26
30	Three-dimensional modelling identifies novel genetic dependencies associated with breast cancer progression in the isogenic MCF10 model. <i>Journal of Pathology</i> , 2016 , 240, 315-328	9.4	24
29	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. <i>Clinical Cancer Research</i> , 2018 , 24, 4763-4770	12.9	21
28	Integrative molecular and functional profiling of ERBB2-amplified breast cancers identifies new genetic dependencies. <i>Oncogene</i> , 2014 , 33, 619-31	9.2	21
27	Hotspot SF3B1 mutations induce metabolic reprogramming and vulnerability to serine deprivation. <i>Journal of Clinical Investigation</i> , 2019 , 129, 4708-4723	15.9	21
26	Robust BRCA1-like classification of copy number profiles of samples repeated across different datasets and platforms. <i>Molecular Oncology</i> , 2015 , 9, 1274-86	7.9	20
25	Systematic analysis of tumour cell-extracellular matrix adhesion identifies independent prognostic factors in breast cancer. <i>Oncotarget</i> , 2016 , 7, 62939-62953	3.3	19
24	DNA amplifications in breast cancer: genotypic-phenotypic correlations. <i>Future Oncology</i> , 2010 , 6, 967-84.6	3.6	18
23	The importance of gene-centring microarray data [AuthorsReply]. <i>Lancet Oncology, The</i> , 2010 , 11, 720-723.1.7	1.7	18
22	Delineation of a 1Mb breakpoint region at 1p13 in Wilms tumors by fine-tiling oligonucleotide array CGH. <i>Genes Chromosomes and Cancer</i> , 2007 , 46, 607-15	5	18
21	Genomic profiling of mitochondrion-rich breast carcinoma: chromosomal changes may be relevant for mitochondria accumulation and tumour biology. <i>Breast Cancer Research and Treatment</i> , 2012 , 132, 15-28	4.4	17

20	From integrative genomics to therapeutic targets. <i>Cancer Research</i> , 2013 , 73, 3483-8	10.1	16
19	High-throughput detection of fusion genes in cancer using the Sequenom MassARRAY platform. <i>Laboratory Investigation</i> , 2011 , 91, 1491-501	5.9	16
18	Splicing dysregulation as a driver of breast cancer. <i>Endocrine-Related Cancer</i> , 2018 , 25, R467-R478	5.7	15
17	Non-existence of caveolin-1 gene mutations in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2012 , 131, 307-10	4.4	13
16	Preclinical evaluation of the PARP inhibitor BMN-673 for the treatment of ovarian clear cell cancer. <i>Oncotarget</i> , 2017 , 8, 6057-6066	3.3	11
15	Translational genomics of ovarian clear cell carcinoma. <i>Seminars in Cancer Biology</i> , 2020 , 61, 121-131	12.7	9
14	Utilizing Functional Genomics Screening to Identify Potentially Novel Drug Targets in Cancer Cell Spheroid Cultures. <i>Journal of Visualized Experiments</i> , 2016 ,	1.6	5
13	Real-time ex vivo perfusion of human lymph nodes invaded by cancer (REPLICANT): a feasibility study. <i>Journal of Pathology</i> , 2020 , 250, 262-274	9.4	5
12	Driver Oncogenes but Not as We Know Them: Targetable Fusion Genes in Breast Cancer. <i>Cancer Discovery</i> , 2018 , 8, 272-275	24.4	4
11	An epithelial-mesenchymal-amoeboid transition gene signature reveals subtypes of breast cancer progression and metastasis		4
10	Longitudinal analysis of a secondary BRCA2 mutation using digital droplet PCR. <i>Journal of Pathology: Clinical Research</i> , 2020 , 6, 3-11	5.3	4
9	Proteomics of REPLICANT perfusate detects changes in the metastatic lymph node microenvironment. <i>Npj Breast Cancer</i> , 2021 , 7, 24	7.8	4
8	ATARI trial: ATR inhibitor in combination with olaparib in gynecological cancers with ARID1A loss or no loss (ENGOT/GYN1/NCRI). <i>International Journal of Gynecological Cancer</i> , 2021 , 31, 1471-1475	3.5	4
7	The status of epidermal growth factor receptor in borderline ovarian tumours. <i>Oncotarget</i> , 2016 , 7, 10568-10577	9.3	3
6	Subclonal heterogeneity and evolution in breast cancer.. <i>Npj Breast Cancer</i> , 2021 , 7, 155	7.8	3
5	Breast cancer heterogeneity: parallel evolution or conscious uncoupling?. <i>Journal of Pathology</i> , 2015 , 237, 1-3	9.4	2
4	3D Functional Genomics Screens Identify CREBBP as a Targetable Driver in Aggressive Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2021 , 81, 847-859	10.1	2
3	Quantitative Assessment and Prognostic Associations of the Immune Landscape in Ovarian Clear Cell Carcinoma. <i>Cancers</i> , 2021 , 13,	6.6	1

2 Microarray-Based Comparative Genomic Hybridization135-161

- 1 Identification and Validation of Driver Kinases from Next-Generation Sequencing Data. *Methods in Molecular Biology*, **2017**, 1636, 179-195 1.4