Peter T Simpson

List of Publications by Year
in descending order

118 papers	12,247 citations	38660 50 h-index	28224 105 g-index
130 all docs	130 docs citations	130 times ranked	19441 citing authors

#	Article	IF	Citations
1	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
2	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
3	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. Nature Medicine, 2017, 23, 517-525.	15.2	769
4	Molecular evolution of breast cancer. Journal of Pathology, 2005, 205, 248-254.	2.1	442
5	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
6	Metaplastic breast carcinomas are basal-like tumours. Histopathology, 2006, 49, 10-21.	1.6	288
7	Columnar Cell Lesions of the Breast: The Missing Link in Breast Cancer Progression?. American Journal of Surgical Pathology, 2005, 29, 734-746.	2.1	256
8	FGFR1 Emerges as a Potential Therapeutic Target for Lobular Breast Carcinomas. Clinical Cancer Research, 2006, 12, 6652-6662.	3.2	256
9	Invasive lobular carcinoma of the breast: morphology, biomarkers and â€™omics. Breast Cancer Research, 2015, 17, 12.	2.2	256
10	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
11	EGFR amplification and lack of activating mutations in metaplastic breast carcinomas. Journal of Pathology, 2006, 209, 445-453.	2.1	230
12	Distribution of p63, cytokeratins 5/6 and cytokeratin 14 in 51 normal and 400 neoplastic human tissue samples using TARP-4 multi-tumor tissue microarray. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2003, 443, 122-132.	1.4	220
13	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
14	Pleomorphic lobular carcinoma of the breast: role of comprehensive molecular pathology in characterization of an entity. Journal of Pathology, 2005, 207, 1-13.	2.1	172
15	Metastatic progression of breast cancer: insights from 50â€‰years of autopsies. Journal of Pathology, 2014, 232, 23-31.	2.1	161
16	Aberrant Expression of E-cadherin in Lobular Carcinomas of the Breast. American Journal of Surgical Pathology, 2008, 32, 773-783.	2.1	160
17	Molecular profiling pleomorphic lobular carcinomas of the breast: evidence for a common molecular genetic pathway with classic lobular carcinomas. Journal of Pathology, 2008, 215, 231-244.	2.1	153
18	cDNA microarray analysis of genes associated with ERBB2 (HER2/neu) overexpression in human mammary luminal epithelial cells. Oncogene, 2003, 22, 2680-2688.	2.6	152

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19	Molecular classification of breast cancer. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2014, 465, 1-14.	1.4	149
20	miR-139-5p is a regulator of metastatic pathways in breast cancer. Rna, 2013, 19, 1767-1780.	1.6	137
21	Metaplastic breast carcinomas exhibit EGFR, but not HER2, gene amplification and overexpression: immunohistochemical and chromogenic in situ hybridization analysis. Breast Cancer Research, 2005, 7, R1028-35.	2.2	134
22	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. Breast Cancer Research, 2010, 12, R46.	2.2	122
23	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
24	Gene expression profiling of tumour epithelial and stromal compartments during breast cancer progression. Breast Cancer Research and Treatment, 2012, 135, 153-165.	1.1	111
25	Calcium Channel TRPV6 as a Potential Therapeutic Target in Estrogen Receptorâ€“Negative Breast Cancer. Molecular Cancer Therapeutics, 2012, 11, 2158-2168.	1.9	109
26	MicroRNA-182-5p targets a network of genes involved in DNA repair. Rna, 2013, 19, 230-242.	1.6	108
27	The diagnosis and management of pre-invasive breast disease: Pathology of atypical lobular hyperplasia and lobular carcinoma in situ. Breast Cancer Research, 2003, 5, 258-62.	2.2	106
28	The molecular genetics of breast cancer: The contribution of comparative genomic hybridization. Pathology Research and Practice, 2005, 201, 713-725.	1.0	104
29	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
30	Subtypes of familial breast tumours revealed by expression and copy number profiling. Breast Cancer Research and Treatment, 2010, 123, 661-677.	1.1	86
31	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	5.8	86
32	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	2.4	85
33	Unlocking pathology archives for molecular genetic studies: a reliable method to generate probes for chromogenic and fluorescent in situ hybridization. Laboratory Investigation, 2006, 86, 398-408.	1.7	84
34	DNA Methylome of Familial Breast Cancer Identifies Distinct Profiles Defined by Mutation Status. American Journal of Human Genetics, 2010, 86, 420-433.	2.6	80
35	Rad51 supports triple negative breast cancer metastasis. Oncotarget, 2014, 5, 3261-3272.	0.8	80
36	Molecular Evidence for Progression of Microglandular Adenosis (MGA) to Invasive Carcinoma. American Journal of Surgical Pathology, 2009, 33, 496-504.	2.1	77

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37	Heritable DNA methylation marks associated with susceptibility to breast cancer. Nature Communications, 2018, 9, 867.	5.8	76
38	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	9.4	75
39	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	2.1	73
40	A fine-scale dissection of the DNA double-strand break repair machinery and its implications for breast cancer therapy. Nucleic Acids Research, 2014, 42, 6106-6127.	6.5	72
41	Meta-analysis of the global gene expression profile of triple-negative breast cancer identifies genes for the prognostication and treatment of aggressive breast cancer. Oncogenesis, 2014, 3, e100-e100.	2.1	70
42	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
43	Distribution and significance of 14-3-3Ïƒ, a novel myoepithelial marker, in normal, benign, and malignant breast tissue. Journal of Pathology, 2004, 202, 274-285.	2.1	67
44	Mammographic and ultrasound features of invasive lobular carcinoma of the breast. Journal of Medical Imaging and Radiation Oncology, 2014, 58, 1-10.	0.9	67
45	Treatment of Triple-Negative Breast Cancer Using Anti-EGFRâ€“Directed Radioimmunotherapy Combined with Radiosensitizing Chemotherapy and PARP Inhibitor. Journal of Nuclear Medicine, 2013, 54, 913-921.	2.8	66
46	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	0.6	64
47	Invasive lobular carcinoma of the breast: the increasing importance of this special subtype. Breast Cancer Research, 2021, 23, 6.	2.2	64
48	Gene expression profiling of formalinâ€fixed, paraffinâ€embedded familial breast tumours using the whole genomeâ€DASL assay. Journal of Pathology, 2010, 221, 452-461.	2.1	62
49	Runx2 Is a Novel Regulator of Mammary Epithelial Cell Fate in Development and Breast Cancer. Cancer Research, 2014, 74, 5277-5286.	0.4	60
50	Heregulin-HER3-HER2 signaling promotes matrix metalloproteinase-dependent blood-brain-barrier transendothelial migration of human breast cancer cell lines. Oncotarget, 2015, 6, 3932-3946.	0.8	60
51	In Vitro Analysis of Breast Cancer Cell Line Tumourspheres and Primary Human Breast Epithelia Mammospheres Demonstrates Inter- and Intrasphere Heterogeneity. PLoS ONE, 2013, 8, e64388.	1.1	55
52	Thrombospondin-4 expression is activated during the stromal response to invasive breast cancer. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2013, 463, 535-545.	1.4	54
53	Mutations in EGFR, BRAF and RAS are rare in triple-negative and basal-like breast cancers from Caucasian women. Breast Cancer Research and Treatment, 2014, 143, 385-392.	1.1	54
54	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	2.3	51

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55	ID4 controls mammary stem cells and marks breast cancers with a stem cell-like phenotype. Nature Communications, 2015, 6, 6548.	5.8	49
56	Pleomorphic lobular carcinoma of the breast: molecular pathology and clinical impact. Future Oncology, 2009, 5, 233-243.	1.1	48
57	Microarray-based comparative genomic hybridisation of breast cancer patients receiving neoadjuvant chemotherapy. British Journal of Cancer, 2007, 96, 341-351.	2.9	47
58	Molecular signatures in breast cancer. Methods, 2017, 131, 135-146.	1.9	47
59	Kinome profiling reveals breast cancer heterogeneity and identifies targeted therapeutic opportunities for triple negative breast cancer. Oncotarget, 2014, 5, 3145-3158.	0.8	42
60	Personalised pathway analysis reveals association between DNA repair pathway dysregulation and chromosomal instability in sporadic breast cancer. Molecular Oncology, 2016, 10, 179-193.	2.1	36
61	Expression of <scp>MAGE</scp>â€A and <scp>NY</scp>â€<scp>ESO</scp>â€1 cancer/testis antigens is enriched in tripleâ€negative invasive breast cancers. Histopathology, 2018, 73, 68-80.	1.6	34
62	Expression Profiling of Archival Tumors for Long-term Health Studies. Clinical Cancer Research, 2012, 18, 6136-6146.	3.2	32
63	An epithelial to mesenchymal transition programme does not usually drive the phenotype of invasive lobular carcinomas. Journal of Pathology, 2016, 238, 489-494.	2.1	32
64	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	2.1	31
65	Breast cancer metastasis to gynaecological organs: a clinicoâ€pathological and molecular profiling study. Journal of Pathology: Clinical Research, 2019, 5, 25-39.	1.3	31
66	LobSig is a multigene predictor of outcome in invasive lobular carcinoma. Npj Breast Cancer, 2019, 5, 18.	2.3	28
67	Multidimensional phenotyping of breast cancer cell lines to guide preclinical research. Breast Cancer Research and Treatment, 2018, 167, 289-301.	1.1	27
68	Using the MCF10A/MCF10CA1a Breast Cancer Progression Cell Line Model to Investigate the Effect of Active, Mutant Forms of EGFR in Breast Cancer Development and Treatment Using Gefitinib. PLoS ONE, 2015, 10, e0125232.	1.1	27
69	Evaluating the repair of DNA derived from formalin-fixed paraffin-embedded tissues prior to genomic profiling by SNPâ€“CGH analysis. Laboratory Investigation, 2013, 93, 701-710.	1.7	26
70	Novel highly specific antiâ€periostin antibodies uncover the functional importance of the fascilin 1â€1 domain and highlight preferential expression of periostin in aggressive breast cancer. International Journal of Cancer, 2016, 138, 1959-1970.	2.3	26
71	Mutational mechanisms of amplifications revealed by analysis of clustered rearrangements in breast cancers. Annals of Oncology, 2018, 29, 2223-2231.	0.6	26
72	Metaplastic breast cancers frequently express immune checkpoint markers FOXP3 and PD-L1. British Journal of Cancer, 2020, 123, 1665-1672.	2.9	26

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73	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
74	TGFÎ² isoforms and receptors mRNA expression in breast tumours: prognostic value and clinical implications. BMC Cancer, 2015, 15, 1010.	1.1	25
75	Understanding the functional impact of copy number alterations in breast cancer using a network modeling approach. Molecular BioSystems, 2016, 12, 963-972.	2.9	25
76	Diff-Quik Cytology Smears from Endobronchial Ultrasound Transbronchial Needle Aspiration Lymph Node Specimens as a Source of DNA for Next-Generation Sequencing Instead of Cell Blocks. Respiration, 2019, 97, 525-539.	1.2	25
77	Molecular and morphological analysis of adenoid cystic carcinoma of the breast with synchronous tubular adenosis. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2009, 454, 107-114.	1.4	23
78	Thioredoxin-interacting protein is an independent risk stratifier for breast ductal carcinoma in situ. Modern Pathology, 2018, 31, 1807-1815.	2.9	23
79	Molecular classification of breast cancer: is it time to pack up our microscopes?. Pathology, 2011, 43, 1-8.	0.3	22
80	Expression and Function of the Protein Tyrosine Phosphatase Receptor J (PTPRJ) in Normal Mammary Epithelial Cells and Breast Tumors. PLoS ONE, 2012, 7, e40742.	1.1	22
81	Complex-based analysis of dysregulated cellular processes in cancer. BMC Systems Biology, 2014, 8, S1.	3.0	19
82	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
83	Breast pathology: beyond morphology. Seminars in Diagnostic Pathology, 2010, 27, 91-96.	1.0	16
84	Integrin alpha-2 and beta-1 expression increases through multiple generations of the EDW01 patient-derived xenograft model of breast cancerâ€"insight into their role in epithelial mesenchymal transition in vivo gained from an in vitro model system. Breast Cancer Research, 2020, 22, 136.	2.2	16
85	Digital spatial profiling application in breast cancer: a userâ€™s perspective. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 477, 885-890.	1.4	16
86	p63-driven Nuclear Accumulation of Î²-Catenin is Not a Frequent Event in Human Neoplasms. Pathology Research and Practice, 2003, 199, 785-793.	1.0	15
87	Molecular Aspects of Breast Cancer Metastasis to the Brain. Genetics Research International, 2011, 2011, 1-9.	2.0	14
88	Next-Generation Sequencing of Endobronchial Ultrasound Transbronchial Needle Aspiration Specimens in Lung Cancer. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 388-391.	2.5	14
89	Morphologic and Genomic Heterogeneity in the Evolution and Progression of Breast Cancer. Cancers, 2020, 12, 848.	1.7	14
90	The Genomic Landscape of Lobular Breast Cancer. Cancers, 2021, 13, 1950.	1.7	13

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91	The Brisbane Breast Bank. Open Journal of Bioresources, 2018, 5, .	1.5	13
92	Clinicopathologic significance of nuclear HER4 and phospho-YAP(S¹²⁷) in human breast cancers and matching brain metastases. Therapeutic Advances in Medical Oncology, 2020, 12, 175883592094625.	1.4	11
93	Blood-Derived Extracellular Vesicle-Associated miR-3182 Detects Non-Small Cell Lung Cancer Patients. Cancers, 2022, 14, 257.	1.7	11
94	Epigenome erosion and SOX10 drive neural crest phenotypic mimicry in triple-negative breast cancer. Npj Breast Cancer, 2022, 8, 57.	2.3	11
95	Whole genome deep sequencing analysis of cell-free DNA in samples with low tumour content. BMC Cancer, 2022, 22, 85.	1.1	9
96	Examination of tumour histopathology and gene expression in a neu/S100A4 transgenic model of metastatic breast cancer. International Journal of Experimental Pathology, 2003, 84, 173-184.	0.6	8
97	Integrating Multi-omics Data to Dissect Mechanisms of DNA repair Dysregulation in Breast Cancer. Scientific Reports, 2016, 6, 34000.	1.6	8
98	Proteogenomic analysis of Inhibitor of Differentiation 4 (ID4) in basal-like breast cancer. Breast Cancer Research, 2020, 22, 63.	2.2	8
99	Tumor Heterogeneity in a Follicular Carcinoma of Thyroid: a Study by Comparative Genomic Hybridization. Endocrine Pathology, 2011, 22, 103-107.	5.2	7
100	Comparison of actionable events detected in cancer genomes by whole-genome sequencing, in silico whole-exome and mutation panels. ESMO Open, 2022, 7, 100540.	2.0	7
101	In Situ Carcinomaâ€"Can We Predict which Patient Will Come Back with a Recurrence?. Cancer Cell, 2007, 12, 409-411.	7.7	6
102	Application of molecular findings to the diagnosis and management of breast disease: recent advances and challenges. Human Pathology, 2011, 42, 153-165.	1.1	6
103	Characterization of Immune Cell Subsets of Tumor Infiltrating Lymphocytes in Brain Metastases. Biology, 2021, 10, 425.	1.3	6
104	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
105	Characterization of a novel breast cancer cell line derived from a metastatic bone lesion of a breast cancer patient. Breast Cancer Research and Treatment, 2018, 170, 179-188.	1.1	5
106	Gene Expression Analysis Using Filter cDNA Microarrays. , 2006, 120, 415-424.		2
107	A Comprehensive Guide to Core Needle Biopsies of the Breast. , 2016, , .		2
108	Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptorâ€"Positive Breast Cancer. JAMA Network Open, 2020, 3, e209486.	2.8	2

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109	Flipping Pathology: Our Experience at an Australian Medical School. Medical Science Educator, 2017, 27, 409-415.	0.7	1
110	Phenotypic drift in metastatic progression of breast cancer: A case report with histologically heterogeneous lesions that are clonally related. Clinical Case Reports (discontinued), 2020, 8, 2725-2731.	0.2	1
111	Genetic Alterations in Normal and Malignant Breast Tissue. , 2010, , 53-66.		1
112	214 Distinct pathological characteristics of lobular carcinoma. European Journal of Cancer, Supplement, 2010, 8, 121.	2.2	0
113	Molecular pathology of pre-invasive breast disease in the screening setting: application in diagnosis and management. Diagnostic Histopathology, 2012, 18, 64-69.	0.2	0
114	Lobular Carcinoma in Situ. , 2010, , 181-199.		0
115	Future Role of Molecular Profiling in Small Breast Samples and Personalised Medicine. , 2016, , 803-817.		0
116	Abstract PD6-05: Identifying genetic vulnerabilities in cancers driven by defects in DNA-damage response. , 2016, , .		0
117	Columnar Cell Lesions. Encyclopedia of Pathology, 2018, , 1-8.	0.0	0
118	Columnar Cell Lesions. Encyclopedia of Pathology, 2020, , 71-79.	0.0	0