

Martin Peifer

List of Publications by Citations

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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.

89 papers	9,349 citations	45 h-index	94 g-index
94 ext. papers	11,446 ext. citations	13.4 avg, IF	4.87 L-index

#	Paper	IF	Citations
89	Comprehensive genomic profiles of small cell lung cancer. <i>Nature</i> , 2015 , 524, 47-53	50.4	1061
88	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <i>Nature Genetics</i> , 2012 , 44, 1104-10	36.3	919
87	Frequent and focal FGFR1 amplification associates with therapeutically tractable FGFR1 dependency in squamous cell lung cancer. <i>Science Translational Medicine</i> , 2010 , 2, 62ra93	17.5	646
86	PTEN loss contributes to erlotinib resistance in EGFR-mutant lung cancer by activation of Akt and EGFR. <i>Cancer Research</i> , 2009 , 69, 3256-61	10.1	411
85	Mutations in the DDR2 kinase gene identify a novel therapeutic target in squamous cell lung cancer. <i>Cancer Discovery</i> , 2011 , 1, 78-89	24.4	389
84	Telomerase activation by genomic rearrangements in high-risk neuroblastoma. <i>Nature</i> , 2015 , 526, 700-4	50.4	347
83	MYC Drives Progression of Small Cell Lung Cancer to a Variant Neuroendocrine Subtype with Vulnerability to Aurora Kinase Inhibition. <i>Cancer Cell</i> , 2017 , 31, 270-285	24.3	231
82	Identifying genotype-dependent efficacy of single and combined PI3K- and MAPK-pathway inhibition in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 18351-6	11.5	226
81	Pan-cancer analysis of somatic copy-number alterations implicates IRS4 and IGF2 in enhancer hijacking. <i>Nature Genetics</i> , 2017 , 49, 65-74	36.3	220
80	Testing for directed influences among neural signals using partial directed coherence. <i>Journal of Neuroscience Methods</i> , 2006 , 152, 210-9	3	218
79	Comparison of RNA-seq and microarray-based models for clinical endpoint prediction. <i>Genome Biology</i> , 2015 , 16, 133	18.3	212
78	Predicting drug susceptibility of non-small cell lung cancers based on genetic lesions. <i>Journal of Clinical Investigation</i> , 2009 , 119, 1727-40	15.9	205
77	Mutational dynamics between primary and relapse neuroblastomas. <i>Nature Genetics</i> , 2015 , 47, 872-7	36.3	191
76	Differential protein stability and ALK inhibitor sensitivity of EML4-ALK fusion variants. <i>Clinical Cancer Research</i> , 2012 , 18, 4682-90	12.9	191
75	A crucial requirement for Hedgehog signaling in small cell lung cancer. <i>Nature Medicine</i> , 2011 , 17, 1504-8	50.5	188
74	Frequent mutations in chromatin-remodelling genes in pulmonary carcinoids. <i>Nature Communications</i> , 2014 , 5, 3518	17.4	173
73	CD74-NRG1 fusions in lung adenocarcinoma. <i>Cancer Discovery</i> , 2014 , 4, 415-22	24.4	173

72	Heterogeneous Mechanisms of Primary and Acquired Resistance to Third-Generation EGFR Inhibitors. <i>Clinical Cancer Research</i> , 2016 , 22, 4837-4847	12.9	168
71	Chemogenomic profiling provides insights into the limited activity of irreversible EGFR Inhibitors in tumor cells expressing the T790M EGFR resistance mutation. <i>Cancer Research</i> , 2010 , 70, 868-74	10.1	165
70	Integrative genomic profiling of large-cell neuroendocrine carcinomas reveals distinct subtypes of high-grade neuroendocrine lung tumors. <i>Nature Communications</i> , 2018 , 9, 1048	17.4	152
69	ALK mutations conferring differential resistance to structurally diverse ALK inhibitors. <i>Clinical Cancer Research</i> , 2011 , 17, 7394-401	12.9	147
68	Tumor VEGF:VEGFR2 autocrine feed-forward loop triggers angiogenesis in lung cancer. <i>Journal of Clinical Investigation</i> , 2013 , 123, 1732-40	15.9	142
67	A framework for identification of actionable cancer genome dependencies in small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 17034-9	11.5	138
66	Targeted expression of mutated ALK induces neuroblastoma in transgenic mice. <i>Science Translational Medicine</i> , 2012 , 4, 141ra91	17.5	119
65	Clonal dynamics towards the development of venetoclax resistance in chronic lymphocytic leukemia. <i>Nature Communications</i> , 2018 , 9, 727	17.4	116
64	A mechanistic classification of clinical phenotypes in neuroblastoma. <i>Science</i> , 2018 , 362, 1165-1170	33.3	115
63	High expression levels of total IGF-1R and sensitivity of NSCLC cells in vitro to an anti-IGF-1R antibody (R1507). <i>PLoS ONE</i> , 2009 , 4, e7273	3.7	109
62	Small Cell Lung Cancer: Can Recent Advances in Biology and Molecular Biology Be Translated into Improved Outcomes?. <i>Journal of Thoracic Oncology</i> , 2016 , 11, 453-74	8.9	106
61	Genomic and Functional Fidelity of Small Cell Lung Cancer Patient-Derived Xenografts. <i>Cancer Discovery</i> , 2018 , 8, 600-615	24.4	96
60	Benchmarking of mutation diagnostics in clinical lung cancer specimens. <i>PLoS ONE</i> , 2011 , 6, e19601	3.7	95
59	K-ras Mutation Subtypes in NSCLC and Associated Co-occurring Mutations in Other Oncogenic Pathways. <i>Journal of Thoracic Oncology</i> , 2019 , 14, 606-616	8.9	84
58	Cell-autonomous and non-cell-autonomous mechanisms of transformation by amplified FGFR1 in lung cancer. <i>Cancer Discovery</i> , 2014 , 4, 246-57	24.4	82
57	Parameter estimation in ordinary differential equations for biochemical processes using the method of multiple shooting. <i>IET Systems Biology</i> , 2007 , 1, 78-88	1.4	75
56	Genomic Amplification of (PD-L1) in Small-Cell Lung Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 1220-1226	6.9	74
55	Implementation of Amplicon Parallel Sequencing Leads to Improvement of Diagnosis and Therapy of Lung Cancer Patients. <i>Journal of Thoracic Oncology</i> , 2015 , 10, 1049-57	8.9	72

54	UBQLN4 Represses Homologous Recombination and Is Overexpressed in Aggressive Tumors. <i>Cell</i> , 2019 , 176, 505-519.e22	56.2	68
53	Hybrid optimization method with general switching strategy for parameter estimation. <i>BMC Systems Biology</i> , 2008 , 2, 26	3.5	65
52	Deficiency Is Associated with Sensitivity to PARP1- and ATR Inhibitors in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017 , 77, 3040-3056	10.1	59
51	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021 , 184, 2239-2254.e39	56.2	57
50	Transcription-induced mutational strand bias and its effect on substitution rates in human genes. <i>Molecular Biology and Evolution</i> , 2009 , 26, 131-42	8.3	52
49	Actionable perturbations of damage responses by TCL1/ATM and epigenetic lesions form the basis of T-PLL. <i>Nature Communications</i> , 2018 , 9, 697	17.4	51
48	Activating ERBB2/HER2 mutations indicate susceptibility to pan-HER inhibitors in Lynch and Lynch-like colorectal cancer. <i>Gut</i> , 2016 , 65, 1296-305	19.2	49
47	Mutational analysis of pulmonary tumours with neuroendocrine features using targeted massive parallel sequencing: a comparison of a neglected tumour group. <i>British Journal of Cancer</i> , 2015 , 113, 1704-11	8.7	48
46	Identification and Targeting of Long-Term Tumor-Propagating Cells in Small Cell Lung Cancer. <i>Cell Reports</i> , 2016 , 16, 644-56	10.6	48
45	Amplification of N-Myc is associated with a T-cell-poor microenvironment in metastatic neuroblastoma restraining interferon pathway activity and chemokine expression. <i>Oncotmunology</i> , 2017 , 6, e1320626	7.2	47
44	Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	41
43	Identification of novel fusion genes in lung cancer using breakpoint assembly of transcriptome sequencing data. <i>Genome Biology</i> , 2015 , 16, 7	18.3	39
42	Targeted next-generation sequencing of DNA regions proximal to a conserved GXGXXG signaling motif enables systematic discovery of tyrosine kinase fusions in cancer. <i>Nucleic Acids Research</i> , 2010 , 38, 6985-96	20.1	36
41	Mechanisms of Primary Drug Resistance in -Amplified Lung Cancer. <i>Clinical Cancer Research</i> , 2017 , 23, 5527-5536	12.9	35
40	Genomic and transcriptomic heterogeneity of colorectal tumours arising in Lynch syndrome. <i>Journal of Pathology</i> , 2017 , 243, 242-254	9.4	35
39	Systematic Kinase Inhibitor Profiling Identifies CDK9 as a Synthetic Lethal Target in NUT Midline Carcinoma. <i>Cell Reports</i> , 2017 , 20, 2833-2845	10.6	34
38	Dissecting intratumour heterogeneity of nodal B-cell lymphomas at the transcriptional, genetic and drug-response levels. <i>Nature Cell Biology</i> , 2020 , 22, 896-906	23.4	30
37	Two mouse models reveal an actionable PARP1 dependence in aggressive chronic lymphocytic leukemia. <i>Nature Communications</i> , 2017 , 8, 153	17.4	29

36	Somatic copy number alterations by whole-exome sequencing implicates YWHAZ and PTK2 in castration-resistant prostate cancer. <i>Journal of Pathology</i> , 2013 , 231, 505-16	9.4	28
35	The evolutionary history of 2,658 cancers		28
34	yyIncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. <i>Cell Stem Cell</i> , 2019 , 24, 318-327.e8	18	27
33	Label-Free Protein-RNA Interactome Analysis Identifies Khsp Signaling Downstream of the p38/Mk2 Kinase Complex as a Critical Modulator of Cell Cycle Progression. <i>PLoS ONE</i> , 2015 , 10, e0125745	3.7	26
32	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
31	Copy-number analysis and inference of subclonal populations in cancer genomes using Sclust. <i>Nature Protocols</i> , 2018 , 13, 1488-1501	18.8	24
30	Exponential decay of GC content detected by strand-symmetric substitution rates influences the evolution of isochore structure. <i>Molecular Biology and Evolution</i> , 2008 , 25, 362-74	8.3	22
29	Testing for phase synchronization. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2007 , 366, 382-390	2.3	22
28	Active Akt signaling triggers CLL toward Richter transformation via overactivation of Notch1. <i>Blood</i> , 2021 , 137, 646-660	2.2	22
27	Systematic screen for tyrosine kinase rearrangements identifies a novel C6orf204-PDGFRB fusion in a patient with recurrent T-ALL and an associated myeloproliferative neoplasm. <i>Genes Chromosomes and Cancer</i> , 2012 , 51, 54-65	5	21
26	Comprehensive Analysis of Disease-Related Genes in Chronic Lymphocytic Leukemia by Multiplex PCR-Based Next Generation Sequencing. <i>PLoS ONE</i> , 2015 , 10, e0129544	3.7	21
25	Analysis of compound synergy in high-throughput cellular screens by population-based lifetime modeling. <i>PLoS ONE</i> , 2010 , 5, e8919	3.7	19
24	Non-parametric identification of non-linear oscillating systems. <i>Journal of Sound and Vibration</i> , 2003 , 267, 1157-1167	3.9	16
23	Unbiased compound-protein interface mapping and prediction of chemoresistance loci through forward genetics in haploid stem cells. <i>Oncotarget</i> , 2018 , 9, 9838-9851	3.3	13
22	Integrative Analysis of Pleomorphic Dermal Sarcomas Reveals Fibroblastic Differentiation and Susceptibility to Immunotherapy. <i>Clinical Cancer Research</i> , 2020 , 26, 5638-5645	12.9	11
21	Acquisition of the recurrent Gly101Val mutation in confers resistance to venetoclax in patients with progressive chronic lymphocytic leukemia (). <i>Haematologica</i> , 2019 , 104, e540	6.6	11
20	Deep Learning Predicts HPV Association in Oropharyngeal Squamous Cell Carcinomas and Identifies Patients with a Favorable Prognosis Using Regular H&E Stains. <i>Clinical Cancer Research</i> , 2021 , 27, 1131-1138	12.9	11
19	Deep learning for sensitive detection of Helicobacter Pylori in gastric biopsies. <i>BMC Gastroenterology</i> , 2020 , 20, 417	3	10

18	Mixing properties of the Rössler system and consequences for coherence and synchronization analysis. <i>Physical Review E</i> , 2005 , 72, 026213	2.4	10
17	On studentising and blocklength selection for the bootstrap on time series. <i>Biometrical Journal</i> , 2005 , 47, 346-57	1.5	8
16	ATM activity in T cells is critical for immune surveillance of lymphoma in vivo. <i>Leukemia</i> , 2020 , 34, 771-786	6.7	8
15	An Autochthonous Mouse Model of Myd88- and BCL2-Driven Diffuse Large B-cell Lymphoma Reveals Actionable Molecular Vulnerabilities. <i>Blood Cancer Discovery</i> , 2021 , 2, 70-91	7	7
14	Tumor VEGF:VEGFR2 autocrine feed-forward loop triggers angiogenesis in lung cancer. <i>Journal of Clinical Investigation</i> , 2013 , 123, 3183-3183	15.9	7
13	Chromothripsis followed by circular recombination drives oncogene amplification in human cancer. <i>Nature Genetics</i> , 2021 , 53, 1673-1685	36.3	7
12	Variations in substitution rate in human and mouse genomes. <i>Physical Review Letters</i> , 2004 , 93, 208102	7.4	6
11	Is there an acceleration of the CpG transition rate during the mammalian radiation?. <i>Bioinformatics</i> , 2008 , 24, 2157-64	7.2	5
10	CGARS: cancer genome analysis by rank sums. <i>Bioinformatics</i> , 2014 , 30, 1295-6	7.2	4
9	BISTABILITY AND SELF-OSCILLATIONS IN CELL CYCLE CONTROL. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2006 , 16, 1057-1066	2	4
8	CaMuS: simultaneous fitting and de novo imputation of cancer mutational signature. <i>Scientific Reports</i> , 2020 , 10, 19316	4.9	3
7	Loss of TP53 mediates suppression of Macrophage Effector Function via Extracellular Vesicles and PDL1 towards Resistance against Chemoimmunotherapy in B-cell malignancies		2
6	Clonal dynamics of BRAF-driven drug resistance in EGFR-mutant lung cancer.. <i>Npj Precision Oncology</i> , 2021 , 5, 102	9.8	2
5	iRODS metadata management for a cancer genome analysis workflow. <i>BMC Bioinformatics</i> , 2019 , 20, 29	3.6	1
4	COSINE: A web server for clonal and subclonal structure inference and evolution in cancer genomics. <i>Zoological Research</i> , 2022 , 43, 75-77	3.4	1
3	Variant profiling of colorectal adenomas from three patients of two families with MSH3-related adenomatous polyposis. <i>PLoS ONE</i> , 2021 , 16, e0259185	3.7	1
2	A Novel Autochthonous Mouse Model Serves As a Preclinical Evaluation Platform and Explores Dual BTK and BCL2 Inhibition for Activated B Cell-like Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2021 , 138, 712-712	2.2	
1	Clonal Evolution of a Mutation in PTPRA As a Potential Cause for Resistance Against Anti-CD19 Directed Chimeric Antigen Receptor T-Cell (CAR-T) Therapy with CTL019 in DLBCL Patients. <i>Blood</i> , 2018 , 132, 4119-4119	2.2	

