

# Christopher A Maher

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

16,850  
citations

50276

46  
h-index

71685

76  
g-index

80  
all docs

80  
docs citations

80  
times ranked

28512  
citing authors

#	ARTICLE	IF	CITATIONS
1	Loss of Long Noncoding RNA <i>NXTAR</i> in Prostate Cancer Augments Androgen Receptor Expression and Enzalutamide Resistance. <i>Cancer Research</i> , 2022, 82, 155-168.	0.9	29
2	DANSR: A Tool for the Detection of Annotated and Novel Small RNAs. <i>Non-coding RNA</i> , 2022, 8, 9.	2.6	0
3	LINC00355 regulates p27KIP expression by binding to MENIN to induce proliferation in late-stage relapse breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 49.	5.2	4
4	ctDNA MRD Detection and Personalized Oncogenomic Analysis in Oligometastatic Colorectal Cancer From Plasma and Urine. <i>JCO Precision Oncology</i> , 2021, 5, 378-388.	3.0	26
5	Targeted Therapy to $\alpha$ 23 Integrin Reduces Chemoresistance in Breast Cancer Bone Metastases. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1183-1198.	4.1	13
6	Long, Noncoding RNA Dysregulation in Glioblastoma. <i>Cancers</i> , 2021, 13, 1604.	3.7	18
7	Long noncoding RNAs in cancer metastasis. <i>Nature Reviews Cancer</i> , 2021, 21, 446-460.	28.4	342
8	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	6.2	15
9	Sclerosing epithelioid mesenchymal neoplasm of the pancreas—A proposed new entity. <i>Modern Pathology</i> , 2020, 33, 456-467.	5.5	10
10	SV-HotSpot: detection and visualization of hotspots targeted by structural variants associated with gene expression. <i>Scientific Reports</i> , 2020, 10, 15890.	3.3	3
11	The DNA methylation landscape of advanced prostate cancer. <i>Nature Genetics</i> , 2020, 52, 778-789.	21.4	198
12	Pan-cancer proteogenomic analysis reveals long and circular noncoding RNAs encoding peptides. <i>NAR Cancer</i> , 2020, 2, zcaa015.	3.1	18
13	Long non-coding RNA RAMS11 promotes metastatic colorectal cancer progression. <i>Nature Communications</i> , 2020, 11, 2156.	12.8	83
14	The clonal evolution of metastatic colorectal cancer. <i>Science Advances</i> , 2020, 6, eaay9691.	10.3	41
15	Cell-Free DNA Alterations in the <i>AR</i> Enhancer and Locus Predict Resistance to AR-Directed Therapy in Patients With Metastatic Prostate Cancer. <i>JCO Precision Oncology</i> , 2020, 4, 680-713.	3.0	20
16	Long non-coding RNA LCAL62 / LINC00261 is associated with lung adenocarcinoma prognosis. <i>Heliyon</i> , 2020, 6, e03521.	3.2	13
17	Heparin-based hydrogel scaffolding alters the transcriptomic profile and increases the chemoresistance of MDA-MB-231 triple-negative breast cancer cells. <i>Biomaterials Science</i> , 2020, 8, 2786-2796.	5.4	15
18	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334

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19	Diverse AR Gene Rearrangements Mediate Resistance to Androgen Receptor Inhibitors in Metastatic Prostate Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1965-1976.	7.0	55
20	Gene Fusion Discovery with INTEGRATE. <i>Methods in Molecular Biology</i> , 2020, 2079, 41-68.	0.9	2
21	Antibody profiling of patients with prostate cancer reveals differences in antibody signatures among disease stages. , 2020, 8, e001510.		9
22	Novel RB1-Loss Transcriptomic Signature Is Associated with Poor Clinical Outcomes across Cancer Types. <i>Clinical Cancer Research</i> , 2019, 25, 4290-4299.	7.0	38
23	Genomic Drivers of Poor Prognosis and Enzalutamide Resistance in Metastatic Castration-resistant Prostate Cancer. <i>European Urology</i> , 2019, 76, 562-571.	1.9	104
24	Clinical and Genomic Implications of Luminal and Basal Subtypes Across Carcinomas. <i>Clinical Cancer Research</i> , 2019, 25, 2450-2457.	7.0	52
25	Proteogenomic Analysis of Surgically Resected Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2018, 13, 1519-1529.	1.1	17
26	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. <i>Cell Reports</i> , 2018, 24, 1434-1444.e7.	6.4	73
27	Genomic Hallmarks and Structural Variation in Metastatic Prostate Cancer. <i>Cell</i> , 2018, 174, 758-769.e9.	28.9	459
28	INTEGRATE-neo: a pipeline for personalized gene fusion neoantigen discovery. <i>Bioinformatics</i> , 2017, 33, 555-557.	4.1	105
29	Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes. <i>Experimental Hematology</i> , 2017, 55, 19-33.	0.4	9
30	Genomic and transcriptomic heterogeneity in metaplastic carcinomas of the breast. <i>Npj Breast Cancer</i> , 2017, 3, 48.	5.2	63
31	Multi-institutional Analysis Shows that Low PCAT-14 Expression Associates with Poor Outcomes in Prostate Cancer. <i>European Urology</i> , 2017, 71, 257-266.	1.9	59
32	INTEGRATE-Vis: a tool for comprehensive gene fusion visualization. <i>Scientific Reports</i> , 2017, 7, 17808.	3.3	10
33	Increased breast tissue receptor activator of nuclear factor- $\kappa$ B ligand (RANKL) gene expression is associated with higher mammographic density in premenopausal women. <i>Oncotarget</i> , 2017, 8, 73787-73792.	1.8	12
34	Visualizing tumor evolution with the fishplot package for R. <i>BMC Genomics</i> , 2016, 17, 880.	2.8	131
35	Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. <i>Experimental Hematology</i> , 2016, 44, 603-613.	0.4	44
36	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1060-1071.	3.8	104

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37	INTEGRATE: gene fusion discovery using whole genome and transcriptome data. <i>Genome Research</i> , 2016, 26, 108-118.	5.5	120
38	Optimizing Cancer Genome Sequencing and Analysis. <i>Cell Systems</i> , 2015, 1, 210-223.	6.2	174
39	Genome Modeling System: A Knowledge Management Platform for Genomics. <i>PLoS Computational Biology</i> , 2015, 11, e1004274.	3.2	83
40	Pan-cancer transcriptome analysis reveals long noncoding RNAs with conserved function. <i>RNA Biology</i> , 2015, 12, 628-642.	3.1	85
41	Clonotyping for precision oncology. <i>Drug Discovery Today</i> , 2015, 20, 1464-1469.	6.4	3
42	SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. <i>Nucleic Acids Research</i> , 2014, 42, e113-e113.	14.5	17
43	Transcriptome sequencing reveals altered long intergenic non-coding RNAs in lung cancer. <i>Genome Biology</i> , 2014, 15, 429.	8.8	179
44	cDNA Hybrid Capture Improves Transcriptome Analysis on Low-Input and Archived Samples. <i>Journal of Molecular Diagnostics</i> , 2014, 16, 440-451.	2.8	40
45	Loss of Trop2 causes ErbB3 activation through a neuregulin-1-dependent mechanism in the mesenchymal subtype of HNSCC. <i>Oncotarget</i> , 2014, 5, 9281-9294.	1.8	27
46	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. <i>Cell Reports</i> , 2013, 4, 1116-1130.	6.4	539
47	Characterization of the EZH2-MMSET Histone Methyltransferase Regulatory Axis in Cancer. <i>Molecular Cell</i> , 2013, 49, 80-93.	9.7	130
48	Recurrent reciprocal RNA chimera involving YPEL5 and PPP1CB in chronic lymphocytic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3035-3040.	7.1	44
49	Transcription Factors OVOL1 and OVOL2 Induce the Mesenchymal to Epithelial Transition in Human Cancer. <i>PLoS ONE</i> , 2013, 8, e76773.	2.5	229
50	A comprehensive promoter landscape identifies a novel promoter for CD133 in restricted tissues, cancers, and stem cells. <i>Frontiers in Genetics</i> , 2013, 4, 209.	2.3	10
51	Recurrent Rearrangements in Prostate Cancer: Causes and Therapeutic Potential. <i>Current Drug Targets</i> , 2013, 14, 450-459.	2.1	18
52	Next Generation Sequencing of Prostate Cancer from a Patient Identifies a Deficiency of Methylthioadenosine Phosphorylase, an Exploitable Tumor Target. <i>Molecular Cancer Therapeutics</i> , 2012, 11, 775-783.	4.1	34
53	Whole-genome analysis informs breast cancer response to aromatase inhibition. <i>Nature</i> , 2012, 486, 353-360.	27.8	922
54	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. <i>Cell</i> , 2012, 150, 1121-1134.	28.9	1,038

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55	Chromothripsis and Human Disease: Piecing Together the Shattering Process. <i>Cell</i> , 2012, 148, 29-32.	28.9	141
56	Genetic and epigenetic loss of microRNA-31 leads to feed-forward expression of EZH2 in melanoma. <i>Oncotarget</i> , 2012, 3, 1011-1025.	1.8	126
57	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUIWE1 and DIAPH2 Genes in Multiple Myeloma. <i>Blood</i> , 2012, 120, 320-320.	1.4	0
58	Common Gene Rearrangements in Prostate Cancer. <i>Journal of Clinical Oncology</i> , 2011, 29, 3659-3668.	1.6	268
59	Functionally recurrent rearrangements of the MAST kinase and Notch gene families in breast cancer. <i>Nature Medicine</i> , 2011, 17, 1646-1651.	30.7	301
60	Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. <i>Nature Biotechnology</i> , 2011, 29, 742-749.	17.5	950
61	Targeting of microRNA-142-3p in dendritic cells regulates endotoxin-induced mortality. <i>Blood</i> , 2011, 117, 6172-6183.	1.4	132
62	Mechanistic Rationale for Inhibition of Poly(ADP-Ribose) Polymerase in ETS Gene Fusion-Positive Prostate Cancer. <i>Cancer Cell</i> , 2011, 19, 664-678.	16.8	397
63	Coordinated Regulation of Polycomb Group Complexes through microRNAs in Cancer. <i>Cancer Cell</i> , 2011, 20, 187-199.	16.8	191
64	ChimeraScan: a tool for identifying chimeric transcription in sequencing data. <i>Bioinformatics</i> , 2011, 27, 2903-2904.	4.1	241
65	Deep sequencing reveals distinct patterns of DNA methylation in prostate cancer. <i>Genome Research</i> , 2011, 21, 1028-1041.	5.5	166
66	A p53/miRNA-34 axis regulates Snail1-dependent cancer cell epithelial to mesenchymal transition. <i>Journal of Cell Biology</i> , 2011, 195, 417-433.	5.2	390
67	A Comparison of Single Molecule and Amplification Based Sequencing of Cancer Transcriptomes. <i>PLoS ONE</i> , 2011, 6, e17305.	2.5	48
68	Rearrangements of the RAF kinase pathway in prostate cancer, gastric cancer and melanoma. <i>Nature Medicine</i> , 2010, 16, 793-798.	30.7	436
69	A Genome-Wide Characterization of MicroRNA Genes in Maize. <i>PLoS Genetics</i> , 2009, 5, e1000716.	3.5	318
70	Chimeric transcript discovery by paired-end transcriptome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12353-12358.	7.1	302
71	Transcriptome sequencing to detect gene fusions in cancer. <i>Nature</i> , 2009, 458, 97-101.	27.8	791
72	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642

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73	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
74	miR-24 Inhibits Cell Proliferation by Targeting E2F2, MYC, and Other Cell-Cycle Genes via Binding to 3' UTR MicroRNA Recognition Elements. <i>Molecular Cell</i> , 2009, 35, 610-625.	9.7	544
75	Genomic Loss of microRNA-101 Leads to Overexpression of Histone Methyltransferase EZH2 in Cancer. <i>Science</i> , 2008, 322, 1695-1699.	12.6	995
76	Genome-wide analysis of cancer/testis gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20422-20427.	7.1	295
77	Genome-wide analysis for discovery of rice microRNAs reveals natural antisense microRNAs (nat-miRNAs). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4951-4956.	7.1	218
78	Evolution of Arabidopsis microRNA families through duplication events. <i>Genome Research</i> , 2006, 16, 510-519.	5.5	328
79	Creating genetic applications for informal science learning in multi-user virtual environments. <i>Journal of Network and Computer Applications</i> , 2002, 25, 295-308.	9.1	2