

Aaron M Newman

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

29,676
citations

71061

41
h-index

74108

75
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98
docs citations

98
times ranked

37842
citing authors

#	ARTICLE	IF	CITATIONS
1	T cell characteristics associated with toxicity to immune checkpoint blockade in patients with melanoma. <i>Nature Medicine</i> , 2022, 28, 353-362.	15.2	132
2	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis. <i>Nature Communications</i> , 2022, 13, 898.	5.8	19
3	Inferring gene expression from cell-free DNA fragmentation profiles. <i>Nature Biotechnology</i> , 2022, 40, 585-597.	9.4	63
4	Landscape of innate lymphoid cells in human head and neck cancer reveals divergent NK cell states in the tumor microenvironment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
5	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021, 39, 1422-1437.e10.	7.7	102
6	Atlas of clinically distinct cell states and ecosystems across human solid tumors. <i>Cell</i> , 2021, 184, 5482-5496.e28.	13.5	116
7	Integrated spatial multiomics reveals fibroblast fate during tissue repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	76
8	Single Cell Analysis of Adult Human Hematopoietic Stem and Progenitor Cells Identifies a Novel Lymphoid Primed Multipotent Progenitor That Expands in Relapsed Acute Myeloid Leukemia. <i>Blood</i> , 2021, 138, 3259-3259.	0.6	0
9	Circulating Tumor DNA Analysis for Detection of Minimal Residual Disease After Chemoradiotherapy for Localized Esophageal Cancer. <i>Gastroenterology</i> , 2020, 158, 494-505.e6.	0.6	147
10	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. <i>Cell</i> , 2020, 183, 363-376.e13.	13.5	206
11	LEFTY1 Is a Dual-SMAD Inhibitor that Promotes Mammary Progenitor Growth and Tumorigenesis. <i>Cell Stem Cell</i> , 2020, 27, 284-299.e8.	5.2	12
12	Molecular and Immunologic Signatures are Related to Clinical Benefit from Treatment with Vocimagene Amiretrorepvec (Toca 511) and 5-Fluorocytosine (Toca FC) in Patients with Glioma. <i>Clinical Cancer Research</i> , 2020, 26, 6176-6186.	3.2	13
13	Single-cell transcriptional diversity is a hallmark of developmental potential. <i>Science</i> , 2020, 367, 405-411.	6.0	557
14	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. <i>Methods in Molecular Biology</i> , 2020, 2117, 135-157.	0.4	249
15	Abstract 3443: Atlas of clinically-distinct cell states and cellular ecosystems across human solid tumors. , 2020, , .		0
16	Abstract 5666: A noninvasive approach for early prediction of therapeutic benefit from immune checkpoint inhibition for lung cancer. , 2020, , .		0
17	Computational approaches for characterizing the tumor immune microenvironment. <i>Immunology</i> , 2019, 158, 70-84.	2.0	30
18	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. <i>Cell</i> , 2019, 178, 699-713.e19.	13.5	138

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19	Determining cell type abundance and expression from bulk tissues with digital cytometry. <i>Nature Biotechnology</i> , 2019, 37, 773-782.	9.4	2,396
20	Reply to J. Wang et al. <i>Journal of Clinical Oncology</i> , 2019, 37, 755-757.	0.8	2
21	A functional subset of CD8+ T cells during chronic exhaustion is defined by SIRP β expression. <i>Nature Communications</i> , 2019, 10, 794.	5.8	46
22	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019, 10, 5712.	5.8	27
23	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2019, 134, 655-655.	0.6	4
24	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data. , 2019, , .		2
25	Combination Approach for Detecting Different Types of Alterations in Circulating Tumor DNA in Leiomyosarcoma. <i>Clinical Cancer Research</i> , 2018, 24, 2688-2699.	3.2	45
26	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
27	Genomic feature selection by coverage design optimization. <i>Journal of Applied Statistics</i> , 2018, 45, 2658-2676.	0.6	1
28	Profiling Tumor Infiltrating Immune Cells with CIBERSORT. <i>Methods in Molecular Biology</i> , 2018, 1711, 243-259.	0.4	1,936
29	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018, 36, 2845-2853.	0.8	313
30	Method of Isolating and Transplanting the Hematopoietic Stem Cell with Its Microenvironment Which Improves Functional Hematopoietic Engraftment. <i>Journal of the American College of Surgeons</i> , 2018, 227, e224.	0.2	0
31	Complex mammalian-like haematopoietic system found in a colonial chordate. <i>Nature</i> , 2018, 564, 425-429.	13.7	60
32	Urochordata: Botryllus "Natural Chimerism and Tolerance Induction in a Colonial Chordate. , 2018, , 503-519.		0
33	Early B cell changes predict autoimmunity following combination immune checkpoint blockade. <i>Journal of Clinical Investigation</i> , 2018, 128, 715-720.	3.9	298
34	(S012) Circulating Tumor DNA Detects Residual Disease and Anticipates Tumor Progression Earlier Than CT Imaging. <i>International Journal of Radiation Oncology Biology Physics</i> , 2017, 98, E4.	0.4	0
35	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. <i>Nature</i> , 2017, 543, 723-727.	13.7	232
36	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. <i>Cancer Discovery</i> , 2017, 7, 1394-1403.	7.7	701

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37	Role of <i>KEAP1</i> and <i>NRF2</i> and <i>TP53</i> Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. <i>Cancer Discovery</i> , 2017, 7, 86-101.	7.7	239
38	Targeted chromatin ligation, a robust epigenetic profiling technique for small cell numbers. <i>Nucleic Acids Research</i> , 2017, 45, e153-e153.	6.5	16
39	Data normalization considerations for digital tumor dissection. <i>Genome Biology</i> , 2017, 18, 128.	3.8	25
40	Macrophage infiltration and genetic landscape of undifferentiated uterine sarcomas. <i>JCI Insight</i> , 2017, 2, .	2.3	15
41	Early prediction of clinical outcomes in resected stage II and III colorectal cancer (CRC) through deep sequencing of circulating tumor DNA (ctDNA).. <i>Journal of Clinical Oncology</i> , 2017, 35, 3591-3591.	0.8	27
42	Circulating tumor DNA analysis for outcome prediction in localized esophageal cancer.. <i>Journal of Clinical Oncology</i> , 2017, 35, 4055-4055.	0.8	3
43	Analysis of circulating tumor DNA in localized lung cancer for detection of molecular residual disease and personalization of adjuvant strategies.. <i>Journal of Clinical Oncology</i> , 2017, 35, 8519-8519.	0.8	3
44	High-throughput genomic profiling of tumor-infiltrating leukocytes. <i>Current Opinion in Immunology</i> , 2016, 41, 77-84.	2.4	43
45	Noninvasive Cancer Classification Using Diverse Genomic Features in Circulating Tumor DNA. , 2016, , .		0
46	Identification of tumorigenic cells and therapeutic targets in pancreatic neuroendocrine tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4464-4469.	3.3	70
47	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. <i>Science Translational Medicine</i> , 2016, 8, 364ra155.	5.8	348
48	Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients. <i>Nature Communications</i> , 2016, 7, 11815.	5.8	520
49	Integrated digital error suppression for improved detection of circulating tumor DNA. <i>Nature Biotechnology</i> , 2016, 34, 547-555.	9.4	837
50	Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016, 128, 1089-1089.	0.6	8
51	Noninvasive Detection of Ibrutinib Resistance in Non-Hodgkin Lymphoma Using Cell-Free DNA. <i>Blood</i> , 2016, 128, 1752-1752.	0.6	8
52	Prediction of therapeutic outcomes in DLBCL from circulating tumor DNA dynamics.. <i>Journal of Clinical Oncology</i> , 2016, 34, 7511-7511.	0.8	3
53	Inter- and intra-patient heterogeneity of resistance mechanisms to the mutant EGFR selective inhibitor rociletinib.. <i>Journal of Clinical Oncology</i> , 2016, 34, 9000-9000.	0.8	2
54	Pooled mutation analysis for the NP28673 and NP28761 studies of alectinib in <i>ALK+</i> non-small-cell lung cancer (NSCLC).. <i>Journal of Clinical Oncology</i> , 2016, 34, 9061-9061.	0.8	9

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55	Integrated digital error suppression for noninvasive detection of circulating tumor DNA in NSCLC.. Journal of Clinical Oncology, 2016, 34, e20500-e20500.	0.8	1
56	Noninvasive molecular subtyping and risk stratification of DLBCL.. Journal of Clinical Oncology, 2016, 34, 7554-7554.	0.8	2
57	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	0.6	0
58	Noninvasive Detection of BCL2, BCL6, and MYC Translocations in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2930-2930.	0.6	8
59	Absence of Evidence Implicating Hematopoietic Stem Cells As Common Progenitors for DLBCL Mutations. Blood, 2016, 128, 4107-4107.	0.6	1
60	The prognostic landscape of genes and infiltrating immune cells across human cancers. Nature Medicine, 2015, 21, 938-945.	15.2	2,505
61	Potential clinical utility of ultrasensitive circulating tumor DNA detection with CAPP-Seq. Expert Review of Molecular Diagnostics, 2015, 15, 715-719.	1.5	75
62	Identification and isolation of a dermal lineage with intrinsic fibrogenic potential. Science, 2015, 348, aaa2151.	6.0	520
63	Robust enumeration of cell subsets from tissue expression profiles. Nature Methods, 2015, 12, 453-457.	9.0	8,460
64	Noninvasive Genotyping and Assessment of Treatment Response in Diffuse Large B Cell Lymphoma. Blood, 2015, 126, 114-114.	0.6	10
65	Dynamic Noninvasive Genomic Monitoring for Outcome Prediction in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 130-130.	0.6	9
66	Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging. PLoS ONE, 2015, 10, e0133627.	1.1	90
67	Pre-treatment circulating tumor DNA as a biomarker for disease burden in diffuse large B cell lymphoma (DLBCL).. Journal of Clinical Oncology, 2015, 33, 8539-8539.	0.8	0
68	Abstract PR09: The prognostic landscape of genes and infiltrating immune cells across human cancers. Cancer Research, 2015, 75, PR09-PR09.	0.4	3
69	An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. Nature Medicine, 2014, 20, 548-554.	15.2	1,771
70	FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution. Bioinformatics, 2014, 30, 3390-3393.	1.8	212
71	Efficient Selection of Biomining DNA Aptamers Using Deep Sequencing and Population Clustering. ACS Nano, 2014, 8, 387-395.	7.3	33
72	InÂVivo Clonal Analysis Reveals Lineage-Restricted Progenitor Characteristics in Mammalian Kidney Development, Maintenance, and Regeneration. Cell Reports, 2014, 7, 1270-1283.	2.9	199

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73	Identifying Stem Cell Gene Expression Patterns and Phenotypic Networks with AutoSOME. <i>Methods in Molecular Biology</i> , 2014, 1150, 115-130.	0.4	1
74	Noninvasive and ultrasensitive quantitation of circulating tumor DNA by hybrid capture and deep sequencing. <i>Journal of Clinical Oncology</i> , 2014, 32, 11016-11016.	0.8	0
75	Identification of a Colonial Chordate Histocompatibility Gene. <i>Science</i> , 2013, 341, 384-387.	6.0	91
76	The genome sequence of the colonial chordate, <i>Botryllus schlosseri</i> . <i>ELife</i> , 2013, 2, e00569.	2.8	209
77	Systems-level analysis of age-related macular degeneration reveals global biomarkers and phenotype-specific functional networks. <i>Genome Medicine</i> , 2012, 4, 16.	3.6	234
78	Exploring Stem Cell Gene Expression Signatures using AutoSOME Cluster Analysis. , 2012, , 44-70.		1
79	Genome-Wide Characterization of Human Hematopoietic Progenitor Cell Heterogeneity by Expression Profiling of Single Cells: A Pilot Study. <i>Blood</i> , 2012, 120, 1231-1231.	0.6	0
80	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival. <i>Blood</i> , 2012, 120, 2390-2390.	0.6	3
81	The Diffuse Large B-Cell Lymphoma Infiltrating Macrophage Transcriptome Signature Is Enriched for Both M1 and M2 Genes and Provides an Excellent Platform for Functional Validation of Macrophage Biology in DLBCL. <i>Blood</i> , 2012, 120, 790-790.	0.6	1
82	Global Analysis of Proline-Rich Tandem Repeat Proteins Reveals Broad Phylogenetic Diversity in Plant Secretomes. <i>PLoS ONE</i> , 2011, 6, e23167.	1.1	16
83	A proteomic approach for the identification of novel lysine methyltransferase substrates. <i>Epigenetics and Chromatin</i> , 2011, 4, 19.	1.8	55
84	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011, 12, 436.	1.2	541
85	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. <i>BMC Bioinformatics</i> , 2010, 11, 117.	1.2	92
86	Lab-Specific Gene Expression Signatures in Pluripotent Stem Cells. <i>Cell Stem Cell</i> , 2010, 7, 258-262.	5.2	195
87	XSTREAM: A practical algorithm for identification and architecture modeling of tandem repeats in protein sequences. <i>BMC Bioinformatics</i> , 2007, 8, 382.	1.2	145