Aaron M Newman

List of Publications by Year
in descending order

87 papers	29,676 citations	70961 41 h-index	74018 75 g-index
98 all docs	98 docs citations	98 times ranked	37842 citing authors

#	Article	IF	Citations
1	Robust enumeration of cell subsets from tissue expression profiles. Nature Methods, 2015, 12, 453-457.	9.0	8,460
2	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
3	The prognostic landscape of genes and infiltrating immune cells across human cancers. Nature Medicine, 2015, 21, 938-945.	15.2	2,505
4	Determining cell type abundance and expression from bulk tissues with digital cytometry. Nature Biotechnology, 2019, 37, 773-782.	9.4	2,396
5	Profiling Tumor Infiltrating Immune Cells with CIBERSORT. Methods in Molecular Biology, 2018, 1711, 243-259.	0.4	1,936
6	An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. Nature Medicine, 2014, 20, 548-554.	15.2	1,771
7	Integrated digital error suppression for improved detection of circulating tumor DNA. Nature Biotechnology, 2016, 34, 547-555.	9.4	837
8	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. Cancer Discovery, 2017, 7, 1394-1403.	7.7	701
9	Single-cell transcriptional diversity is a hallmark of developmental potential. Science, 2020, 367, 405-411.	6.0	557
10	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. BMC Bioinformatics, 2011, 12, 436.	1.2	541
11	Identification and isolation of a dermal lineage with intrinsic fibrogenic potential. Science, 2015, 348, aaa2151.	6.0	520
12	Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients. Nature Communications, 2016, 7, 11815.	5.8	520
13	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. Science Translational Medicine, 2016, 8, 364ra155.	5.8	348
14	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2018, 36, 2845-2853.	0.8	313
15	Early B cell changes predict autoimmunity following combination immune checkpoint blockade. Journal of Clinical Investigation, 2018, 128, 715-720.	3.9	298
16	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. Methods in Molecular Biology, 2020, 2117, 135-157.	0.4	249
17	Role of *KEAP1*/*NRF2* and *TP53* Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. Cancer Discovery, 2017, 7, 86-101.	7.7	239
18	Systems-level analysis of age-related macular degeneration reveals global biomarkers and phenotype-specific functional networks. Genome Medicine, 2012, 4, 16.	3.6	234

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19	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. Nature, 2017, 543, 723-727.	13.7	232
20	FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution. Bioinformatics, 2014, 30, 3390-3393.	1.8	212
21	The genome sequence of the colonial chordate, Botryllus schlosseri. ELife, 2013, 2, e00569.	2.8	209
22	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. Cell, 2020, 183, 363-376.e13.	13.5	206
23	InÂVivo Clonal Analysis Reveals Lineage-Restricted Progenitor Characteristics in Mammalian Kidney Development, Maintenance, and Regeneration. Cell Reports, 2014, 7, 1270-1283.	2.9	199
24	Lab-Specific Gene Expression Signatures in Pluripotent Stem Cells. Cell Stem Cell, 2010, 7, 258-262.	5.2	195
25	Circulating Tumor DNA Analysis for Detection of Minimal Residual Disease After Chemoradiotherapy for Localized Esophageal Cancer. Gastroenterology, 2020, 158, 494-505.e6.	0.6	147
26	XSTREAM: A practical algorithm for identification and architecture modeling of tandem repeats in protein sequences. BMC Bioinformatics, 2007, 8, 382.	1.2	145
27	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. Cell, 2019, 178, 699-713.e19.	13.5	138
28	T cell characteristics associated with toxicity to immune checkpoint blockade in patients with melanoma. Nature Medicine, 2022, 28, 353-362.	15.2	132
29	Atlas of clinically distinct cell states and ecosystems across human solid tumors. Cell, 2021, 184, 5482-5496.e28.	13.5	116
30	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. Cancer Cell, 2021, 39, 1422-1437.e10.	7.7	102
31	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. BMC Bioinformatics, 2010, 11, 117.	1.2	92
32	Identification of a Colonial Chordate Histocompatibility Gene. Science, 2013, 341, 384-387.	6.0	91
33	Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging. PLoS ONE, 2015, 10, e0133627.	1.1	90
34	Integrated spatial multiomics reveals fibroblast fate during tissue repair. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	76
35	Potential clinical utility of ultrasensitive circulating tumor DNA detection with CAPP-Seq. Expert Review of Molecular Diagnostics, 2015, 15, 715-719.	1.5	75
36	Identification of tumorigenic cells and therapeutic targets in pancreatic neuroendocrine tumors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4464-4469.	3.3	70

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37	Inferring gene expression from cell-free DNA fragmentation profiles. Nature Biotechnology, 2022, 40, 585-597.	9.4	63
38	Complex mammalian-like haematopoietic system found in a colonial chordate. Nature, 2018, 564, 425-429.	13.7	60
39	A proteomic approach for the identification of novel lysine methyltransferase substrates. Epigenetics and Chromatin, 2011, 4, 19.	1.8	55
40	Landscape of innate lymphoid cells in human head and neck cancer reveals divergent NK cell states in the tumor microenvironment. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	50
41	A functional subset of CD8+ T cells during chronic exhaustion is defined by SIRPÎ± expression. Nature Communications, 2019, 10, 794.	5.8	46
42	Combination Approach for Detecting Different Types of Alterations in Circulating Tumor DNA in Leiomyosarcoma. Clinical Cancer Research, 2018, 24, 2688-2699.	3.2	45
43	High-throughput genomic profiling of tumor-infiltrating leukocytes. Current Opinion in Immunology, 2016, 41, 77-84.	2.4	43
44	Efficient Selection of Biomineralizing DNA Aptamers Using Deep Sequencing and Population Clustering. ACS Nano, 2014, 8, 387-395.	7.3	33
45	Computational approaches for characterizing the tumor immune microenvironment. Immunology, 2019, 158, 70-84.	2.0	30
46	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. Nature Communications, 2019, 10, 5712.	5.8	27
47	Early prediction of clinical outcomes in resected stage II and III colorectal cancer (CRC) through deep sequencing of circulating tumor DNA (ctDNA).. Journal of Clinical Oncology, 2017, 35, 3591-3591.	0.8	27
48	Data normalization considerations for digital tumor dissection. Genome Biology, 2017, 18, 128.	3.8	25
49	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis. Nature Communications, 2022, 13, 898.	5.8	19
50	Global Analysis of Proline-Rich Tandem Repeat Proteins Reveals Broad Phylogenetic Diversity in Plant Secretomes. PLoS ONE, 2011, 6, e23167.	1.1	16
51	Targeted chromatin ligation, a robust epigenetic profiling technique for small cell numbers. Nucleic Acids Research, 2017, 45, e153-e153.	6.5	16
52	Macrophage infiltration and genetic landscape of undifferentiated uterine sarcomas. JCI Insight, 2017, 2, .	2.3	15
53	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. Clinical Cancer Research, 2020, 26, 6176-6186.	3.2	13
54	LEFTY1 Is a Dual-SMAD Inhibitor that Promotes Mammary Progenitor Growth and Tumorigenesis. Cell Stem Cell, 2020, 27, 284-299.e8.	5.2	12

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55	Noninvasive Genotyping and Assessment of Treatment Response in Diffuse Large B Cell Lymphoma. Blood, 2015, 126, 114-114.	0.6	10
56	Dynamic Noninvasive Genomic Monitoring for Outcome Prediction in Diffuse Large B-Cell Lymphoma. Blood, 2015, 126, 130-130.	0.6	9
57	Pooled mutation analysis for the NP28673 and NP28761 studies of alectinib in <i>ALK+</i> non-small-cell lung cancer (NSCLC).. Journal of Clinical Oncology, 2016, 34, 9061-9061.	0.8	9
58	Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 1089-1089.	0.6	8
59	Noninvasive Detection of Ibrutinib Resistance in Non-Hodgkin Lymphoma Using Cell-Free DNA. Blood, 2016, 128, 1752-1752.	0.6	8
60	Noninvasive Detection of BCL2, BCL6, and MYC Translocations in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2930-2930.	0.6	8
61	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. Blood, 2019, 134, 655-655.	0.6	4
62	Prediction of therapeutic outcomes in DLBCL from circulating tumor DNA dynamics.. Journal of Clinical Oncology, 2016, 34, 7511-7511.	0.8	3
63	Circulating tumor DNA analysis for outcome prediction in localized esophageal cancer.. Journal of Clinical Oncology, 2017, 35, 4055-4055.	0.8	3
64	Analysis of circulating tumor DNA in localized lung cancer for detection of molecular residual disease and personalization of adjuvant strategies.. Journal of Clinical Oncology, 2017, 35, 8519-8519.	0.8	3
65	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival.. Blood, 2012, 120, 2390-2390.	0.6	3
66	Abstract PR09: The prognostic landscape of genes and infiltrating immune cells across human cancers. Cancer Research, 2015, 75, PR09-PR09.	0.4	3
67	Reply to J. Wang et al. Journal of Clinical Oncology, 2019, 37, 755-757.	0.8	2
68	Inter- and intra-patient heterogeneity of resistance mechanisms to the mutant EGFR selective inhibitor rociletinib.. Journal of Clinical Oncology, 2016, 34, 9000-9000.	0.8	2
69	Noninvasive molecular subtyping and risk stratification of DLBCL.. Journal of Clinical Oncology, 2016, 34, 7554-7554.	0.8	2
70	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data. , 2019, , .		2
71	Genomic feature selection by coverage design optimization. Journal of Applied Statistics, 2018, 45, 2658-2676.	0.6	1
72	Identifying Stem Cell Gene Expression Patterns and Phenotypic Networks with AutoSOME. Methods in Molecular Biology, 2014, 1150, 115-130.	0.4	1

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73	Integrated digital error suppression for noninvasive detection of circulating tumor DNA in NSCLC.. Journal of Clinical Oncology, 2016, 34, e20500-e20500.	0.8	1
74	Exploring Stem Cell Gene Expression Signatures using AutoSOME Cluster Analysis. , 2012, , 44-70.		1
75	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. Blood, 2012, 120, 790-790.	0.6	1
76	Absence of Evidence Implicating Hematopoietic Stem Cells As Common Progenitors for DLBCL Mutations. Blood, 2016, 128, 4107-4107.	0.6	1
77	Noninvasive Cancer Classification Using Diverse Genomic Features in Circulating Tumor DNA. , 2016, , .		0
78	(S012) Circulating Tumor DNA Detects Residual Disease and Anticipates Tumor Progression Earlier Than CT Imaging. International Journal of Radiation Oncology Biology Physics, 2017, 98, E4.	0.4	0
79	Method of Isolating and Transplanting the Hematopoietic Stem Cell with Its Microenvironment Which Improves Functional Hematopoietic Engraftment. Journal of the American College of Surgeons, 2018, 227, e224.	0.2	0
80	Urochordata: Botryllus â€" Natural Chimerism and Tolerance Induction in a Colonial Chordate. , 2018, , 503-519.		0
81	Genome-Wide Characterization of Human Hematopoietic Progenitor Cell Heterogeneity by Expression Profiling of Single Cells: A Pilot Study. Blood, 2012, 120, 1231-1231.	0.6	0
82	Noninvasive and ultrasensitive quantitation of circulating tumor DNA by hybrid capture and deep sequencing.. Journal of Clinical Oncology, 2014, 32, 11016-11016.	0.8	0
83	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
84	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. Blood, 2016, 128, 915-915.	0.6	0
85	Abstract 3443: Atlas of clinically-distinct cell states and cellular ecosystems across human solid tumors. , 2020, , .		0
86	Abstract 5666: A noninvasive approach for early prediction of therapeutic benefit from immune checkpoint inhibition for lung cancer. , 2020, , .		0
87	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. Blood, 2021, 138, 3259-3259.	0.6	0