

Aaron M Newman

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.

83
papers

15,247
citations

34
h-index

98
g-index

98
ext. papers

23,477
ext. citations

14.5
avg, IF

6.38
L-index

#	Paper	IF	Citations
83	Robust enumeration of cell subsets from tissue expression profiles. <i>Nature Methods</i> , 2015 , 12, 453-7	21.6	3934
82	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
81	The prognostic landscape of genes and infiltrating immune cells across human cancers. <i>Nature Medicine</i> , 2015 , 21, 938-945	50.5	1541
80	An ultrasensitive method for quantitating circulating tumor DNA with broad patient coverage. <i>Nature Medicine</i> , 2014 , 20, 548-54	50.5	1363
79	Determining cell type abundance and expression from bulk tissues with digital cytometry. <i>Nature Biotechnology</i> , 2019 , 37, 773-782	44.5	761
78	Profiling Tumor Infiltrating Immune Cells with CIBERSORT. <i>Methods in Molecular Biology</i> , 2018 , 1711, 243-259	1.4	692
77	Integrated digital error suppression for improved detection of circulating tumor DNA. <i>Nature Biotechnology</i> , 2016 , 34, 547-555	44.5	589
76	Circulating tumour DNA profiling reveals heterogeneity of EGFR inhibitor resistance mechanisms in lung cancer patients. <i>Nature Communications</i> , 2016 , 7, 11815	17.4	409
75	Early Detection of Molecular Residual Disease in Localized Lung Cancer by Circulating Tumor DNA Profiling. <i>Cancer Discovery</i> , 2017 , 7, 1394-1403	24.4	384
74	Skin fibrosis. Identification and isolation of a dermal lineage with intrinsic fibrogenic potential. <i>Science</i> , 2015 , 348, aaa2151	33.3	362
73	clusterMaker: a multi-algorithm clustering plugin for Cytoscape. <i>BMC Bioinformatics</i> , 2011 , 12, 436	3.6	337
72	Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. <i>Science Translational Medicine</i> , 2016 , 8, 364ra155	17.5	231
71	Early B cell changes predict autoimmunity following combination immune checkpoint blockade. <i>Journal of Clinical Investigation</i> , 2018 , 128, 715-720	15.9	186
70	The genome sequence of the colonial chordate, <i>Botryllus schlosseri</i> . <i>ELife</i> , 2013 , 2, e00569	8.9	175
69	Lab-specific gene expression signatures in pluripotent stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 258-62	18	171
68	Circulating Tumor DNA Measurements As Early Outcome Predictors in Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2018 , 36, 2845-2853	2.2	164
67	Antigen presentation profiling reveals recognition of lymphoma immunoglobulin neoantigens. <i>Nature</i> , 2017 , 543, 723-727	50.4	161

66	In vivo clonal analysis reveals lineage-restricted progenitor characteristics in mammalian kidney development, maintenance, and regeneration. <i>Cell Reports</i> , 2014 , 7, 1270-83	10.6	160
65	Role of KEAP1/NRF2 and TP53 Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. <i>Cancer Discovery</i> , 2017 , 7, 86-101	24.4	159
64	Systems-level analysis of age-related macular degeneration reveals global biomarkers and phenotype-specific functional networks. <i>Genome Medicine</i> , 2012 , 4, 16	14.4	157
63	FACTERA: a practical method for the discovery of genomic rearrangements at breakpoint resolution. <i>Bioinformatics</i> , 2014 , 30, 3390-3	7.2	130
62	Single-cell transcriptional diversity is a hallmark of developmental potential. <i>Science</i> , 2020 , 367, 405-411	33.3	128
61	XSTREAM: a practical algorithm for identification and architecture modeling of tandem repeats in protein sequences. <i>BMC Bioinformatics</i> , 2007 , 8, 382	3.6	109
60	Dynamic Risk Profiling Using Serial Tumor Biomarkers for Personalized Outcome Prediction. <i>Cell</i> , 2019 , 178, 699-713.e19	56.2	84
59	AutoSOME: a clustering method for identifying gene expression modules without prior knowledge of cluster number. <i>BMC Bioinformatics</i> , 2010 , 11, 117	3.6	77
58	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. <i>Cell</i> , 2020 , 183, 363-376.e13	56.2	76
57	Circulating Tumor DNA Analysis for Detection of Minimal Residual Disease After Chemoradiotherapy for Localized Esophageal Cancer. <i>Gastroenterology</i> , 2020 , 158, 494-505.e6	13.3	71
56	Identification of a colonial chordate histocompatibility gene. <i>Science</i> , 2013 , 341, 384-7	33.3	66
55	Large-Scale and Comprehensive Immune Profiling and Functional Analysis of Normal Human Aging. <i>PLoS ONE</i> , 2015 , 10, e0133627	3.7	61
54	Profiling Cell Type Abundance and Expression in Bulk Tissues with CIBERSORTx. <i>Methods in Molecular Biology</i> , 2020 , 2117, 135-157	1.4	54
53	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, 4464-9	11.5	49
52	A proteomic approach for the identification of novel lysine methyltransferase substrates. <i>Epigenetics and Chromatin</i> , 2011 , 4, 19	5.8	47
51	Complex mammalian-like haematopoietic system found in a colonial chordate. <i>Nature</i> , 2018 , 564, 425-429	30.4	34
50	Combination Approach for Detecting Different Types of Alterations in Circulating Tumor DNA in Leiomyosarcoma. <i>Clinical Cancer Research</i> , 2018 , 24, 2688-2699	12.9	32
49	High-throughput genomic profiling of tumor-infiltrating leukocytes. <i>Current Opinion in Immunology</i> , 2016 , 41, 77-84	7.8	28

48	A functional subset of CD8 T cells during chronic exhaustion is defined by SIRP β expression. <i>Nature Communications</i> , 2019 , 10, 794	17.4	28
47	Efficient selection of biomineralizing DNA aptamers using deep sequencing and population clustering. <i>ACS Nano</i> , 2014 , 8, 387-95	16.7	24
46	Data normalization considerations for digital tumor dissection. <i>Genome Biology</i> , 2017 , 18, 128	18.3	23
45	Atlas of clinically distinct cell states and ecosystems across human solid tumors. <i>Cell</i> , 2021 , 184, 5482-5496.e2821	19.6	21
44	Computational approaches for characterizing the tumor immune microenvironment. <i>Immunology</i> , 2019 , 158, 70-84	7.8	15
43	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	2.2	15
42	Functional significance of U2AF1 S34F mutations in lung adenocarcinomas. <i>Nature Communications</i> , 2019 , 10, 5712	17.4	15
41	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021 , 39, 1422-1437.e10	24.3	15
40	Global analysis of proline-rich tandem repeat proteins reveals broad phylogenetic diversity in plant secretomes. <i>PLoS ONE</i> , 2011 , 6, e23167	3.7	14
39	Targeted chromatin ligation, a robust epigenetic profiling technique for small cell numbers. <i>Nucleic Acids Research</i> , 2017 , 45, e153	20.1	12
38	Macrophage infiltration and genetic landscape of undifferentiated uterine sarcomas. <i>JCI Insight</i> , 2017 , 2,	9.9	12
37	Noninvasive Genotyping and Assessment of Treatment Response in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2015 , 126, 114-114	2.2	9
36	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,	11.5	9
35	Pooled mutation analysis for the NP28673 and NP28761 studies of alectinib in ALK+ non-small-cell lung cancer (NSCLC).. <i>Journal of Clinical Oncology</i> , 2016 , 34, 9061-9061	2.2	8
34	Dynamic Noninvasive Genomic Monitoring for Outcome Prediction in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2015 , 126, 130-130	2.2	7
33	Development and Validation of Biopsy-Free Genotyping for Molecular Subtyping of Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016 , 128, 1089-1089	2.2	7
32	T cell characteristics associated with toxicity to immune checkpoint blockade in patients with melanoma.. <i>Nature Medicine</i> , 2022 ,	50.5	6
31	Noninvasive Detection of Ibrutinib Resistance in Non-Hodgkin Lymphoma Using Cell-Free DNA. <i>Blood</i> , 2016 , 128, 1752-1752	2.2	6

30	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	12.9	6
29	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,	11.5	6
28	Inferring gene expression from cell-free DNA fragmentation profiles.. <i>Nature Biotechnology</i> , 2022 ,	44.5	5
27	An Atlas of Clinically-Distinct Tumor Cellular Ecosystems in Diffuse Large B Cell Lymphoma. <i>Blood</i> , 2019 , 134, 655-655	2.2	4
26	LEFTY1 Is a Dual-SMAD Inhibitor that Promotes Mammary Progenitor Growth and Tumorigenesis. <i>Cell Stem Cell</i> , 2020 , 27, 284-299.e8	18	4
25	Circulating tumor DNA analysis for outcome prediction in localized esophageal cancer.. <i>Journal of Clinical Oncology</i> , 2017 , 35, 4055-4055	2.2	3
24	Prediction of therapeutic outcomes in DLBCL from circulating tumor DNA dynamics.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 7511-7511	2.2	2
23	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	2.2	2
22	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	2.2	2
21	Abstract 1690: A tumor deconvolution DREAM Challenge: Inferring immune infiltration from bulk gene expression data 2019 ,		2
20	CDK19 is a Regulator of Triple-Negative Breast Cancer Growth		2
19	Integrated spatial multi-omics reveals fibroblast fate during tissue repair		2
18	Integrative molecular and clinical profiling of acral melanoma links focal amplification of 22q11.21 to metastasis.. <i>Nature Communications</i> , 2022 , 13, 898	17.4	2
17	Reply to J. Wang et al. <i>Journal of Clinical Oncology</i> , 2019 , 37, 755-757	2.2	1
16	Genomic Feature Selection by Coverage Design Optimization. <i>Journal of Applied Statistics</i> , 2018 , 45, 2658-2676		1
15	Integrated digital error suppression for noninvasive detection of circulating tumor DNA in NSCLC.. <i>Journal of Clinical Oncology</i> , 2016 , 34, e20500-e20500	2.2	1
14	Identifying stem cell gene expression patterns and phenotypic networks with AutoSOME. <i>Methods in Molecular Biology</i> , 2014 , 1150, 115-30	1.4	1
13	Noninvasive molecular subtyping and risk stratification of DLBCL.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 7554-7554	2.2	1

12	Noninvasive Detection of BCL2, BCL6, and MYC Translocations in Diffuse Large B-Cell Lymphoma. <i>Blood</i> , 2016 , 128, 2930-2930	2.2	1
11	Integrative molecular and clinical profiling of acral melanoma identifies LZTR1 as a key tumor promoter and therapeutic target		1
10	LMO2 is critical for early metastatic events in breast cancer		1
9	Urochordata: Botryllus [Natural Chimerism and Tolerance Induction in a Colonial Chordate 2018 , 503-519		
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	2.2	
7	Noninvasive and ultrasensitive quantitation of circulating tumor DNA by hybrid capture and deep sequencing.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 11016-11016	2.2	
6	Pre-treatment circulating tumor DNA as a biomarker for disease burden in diffuse large B cell lymphoma (DLBCL).. <i>Journal of Clinical Oncology</i> , 2015 , 33, 8539-8539	2.2	
5	Antigen Presentation Profiling Reveals T-Cell Recognition of Lymphoma Immunoglobulin Neoantigens. <i>Blood</i> , 2016 , 128, 915-915	2.2	
4	Absence of Evidence Implicating Hematopoietic Stem Cells As Common Progenitors for DLBCL Mutations. <i>Blood</i> , 2016 , 128, 4107-4107	2.2	
3	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	2.2	
2	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival.. <i>Blood</i> , 2012 , 120, 2390-2390	2.2	
1	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	2.2	