

Andrew J Gentles

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

22,281
citations

147801

31
h-index

161849

54
g-index

64
all docs

64
docs citations

64
times ranked

30319
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust enumeration of cell subsets from tissue expression profiles. <i>Nature Methods</i> , 2015, 12, 453-457.	19.0	8,460
2	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
3	The prognostic landscape of genes and infiltrating immune cells across human cancers. <i>Nature Medicine</i> , 2015, 21, 938-945.	30.7	2,505
4	Determining cell type abundance and expression from bulk tissues with digital cytometry. <i>Nature Biotechnology</i> , 2019, 37, 773-782.	17.5	2,396
5	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
6	Association of a Leukemic Stem Cell Gene Expression Signature With Clinical Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2010, 304, 2706.	7.4	339
7	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1116-25.	7.1	307
8	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. <i>Science</i> , 2021, 372, .	12.6	297
9	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.	9.4	239
10	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. <i>Nature</i> , 2020, 580, 136-141.	27.8	203
11	Prediction of survival in diffuse large B-cell lymphoma based on the expression of 2 genes reflecting tumor and microenvironment. <i>Blood</i> , 2011, 118, 1350-1358.	1.4	175
12	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i> . <i>Genome Research</i> , 2007, 17, 992-1004.	5.5	137
13	An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. <i>Nature Communications</i> , 2015, 6, 8489.	12.8	121
14	Atlas of clinically distinct cell states and ecosystems across human solid tumors. <i>Cell</i> , 2021, 184, 5482-5496.e28.	28.9	116
15	Lymph node colonization induces tumor-immune tolerance to promote distant metastasis. <i>Cell</i> , 2022, 185, 1924-1942.e23.	28.9	111
16	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2021, 39, 1422-1437.e10.	16.8	102
17	Human AML-iPSCs Reacquire Leukemic Properties after Differentiation and Model Clonal Variation of Disease. <i>Cell Stem Cell</i> , 2017, 20, 329-344.e7.	11.1	101
18	CD93 Marks a Non-Quiescent Human Leukemia Stem Cell Population and Is Required for Development of MLL-Rearranged Acute Myeloid Leukemia. <i>Cell Stem Cell</i> , 2015, 17, 412-421.	11.1	97

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19	Active Idiotypic Vaccination Versus Control Immunotherapy for Follicular Lymphoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 1797-1803.	1.6	75
20	GFPT2-Expressing Cancer-Associated Fibroblasts Mediate Metabolic Reprogramming in Human Lung Adenocarcinoma. <i>Cancer Research</i> , 2018, 78, 3445-3457.	0.9	75
21	NSD1 inactivation defines an immune cold, DNA hypomethylated subtype in squamous cell carcinoma. <i>Scientific Reports</i> , 2017, 7, 17064.	3.3	67
22	Integrating Tumor and Stromal Gene Expression Signatures With Clinical Indices for Survival Stratification of Early-Stage Non-Small Cell Lung Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv211.	6.3	64
23	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. <i>Blood</i> , 2009, 114, 3158-3166.	1.4	52
24	Reprogramming of primary human Philadelphia chromosome-positive B cell acute lymphoblastic leukemia cells into nonleukemic macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4074-4079.	7.1	52
25	Targetable genetic alterations of TCF4 (E2-2) drive immunoglobulin expression in diffuse large B cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	51
26	Prognostic profiling of the immune cell microenvironment in Ewing's Sarcoma Family of Tumors. <i>Oncotarget</i> , 2019, 8, e1674113.	4.6	50
27	LMO2 Confers Synthetic Lethality to PARP Inhibition in DLBCL. <i>Cancer Cell</i> , 2019, 36, 237-249.e6.	16.8	50
28	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, .	7.1	50
29	Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition. <i>Blood</i> , 2015, 125, 316-326.	1.4	45
30	Maternal Anti-Dengue IgG Fucosylation Predicts Susceptibility to Dengue Disease in Infants. <i>Cell Reports</i> , 2020, 31, 107642.	6.4	44
31	Identification of cell types in multiplexed in situ images by combining protein expression and spatial information using CELESTA. <i>Nature Methods</i> , 2022, 19, 759-769.	19.0	42
32	Module Analysis Captures Pancancer Genetically and Epigenetically Deregulated Cancer Driver Genes for Smoking and Antiviral Response. <i>EBioMedicine</i> , 2018, 27, 156-166.	6.1	40
33	MYC and Twist1 cooperate to drive metastasis by eliciting crosstalk between cancer and innate immunity. <i>ELife</i> , 2020, 9, .	6.0	38
34	Identifying Network Perturbation in Cancer. <i>PLoS Computational Biology</i> , 2016, 12, e1004888.	3.2	35
35	Low BUB1 expression is an adverse prognostic marker in gastric adenocarcinoma. <i>Oncotarget</i> , 2017, 8, 76329-76339.	1.8	34
36	A human lung tumor microenvironment interactome identifies clinically relevant cell-type cross-talk. <i>Genome Biology</i> , 2020, 21, 107.	8.8	33

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37	Clonal architecture predicts clinical outcomes and drug sensitivity in acute myeloid leukemia. Nature Communications, 2021, 12, 7244.	12.8	29
38	Sparse expression bases in cancer reveal tumor drivers. Nucleic Acids Research, 2015, 43, 1332-1344.	14.5	27
39	High-grade serous ovarian tumor cells modulate NK cell function to create an immune-tolerant microenvironment. Cell Reports, 2021, 36, 109632.	6.4	26
40	Data normalization considerations for digital tumor dissection. Genome Biology, 2017, 18, 128.	8.8	25
41	Perfusion MRI-Based Fractional Tumor Burden Differentiates between Tumor and Treatment Effect in Recurrent Glioblastomas and Informs Clinical Decision-Making. American Journal of Neuroradiology, 2019, 40, 1649-1657.	2.4	23
42	Data mining for mutation-specific targets in acute myeloid leukemia. Leukemia, 2019, 33, 826-843.	7.2	23
43	Pathophysiological significance and therapeutic targeting of germinal center kinase in diffuse large B-cell lymphoma. Blood, 2016, 128, 239-248.	1.4	17
44	Brd4 regulates the expression of essential autophagy genes and Keap1 in AML cells. Oncotarget, 2018, 9, 11665-11676.	1.8	14
45	<i>NSD1</i> mutations deregulate transcription and DNA methylation of bivalent developmental genes in Sotos syndrome. Human Molecular Genetics, 2022, 31, 2164-2184.	2.9	11
46	Prognostic Gene Expression, Stemness and Immune Microenvironment in Pediatric Tumors. Cancers, 2021, 13, 854.	3.7	10
47	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival.. Blood, 2012, 120, 2390-2390.	1.4	3
48	A Bayesian nonparametric method for model evaluation: application to genetic studies. Journal of Nonparametric Statistics, 2009, 21, 379-396.	0.9	2
49	HGAL inhibits lymphoma dissemination by interacting with multiple Cytoskeletal proteins. Blood Advances, 2021, 5, 5072-5085.	5.2	2
50	Gene Expression Analysis Of Plasmablastic Lymphoma Identifies Down Regulation Of B Cell Receptor Signaling and Additional Unique Transcriptional Programs. Blood, 2013, 122, 3779-3779.	1.4	1
51	DNA Copy Number Gains of TCF4 (E2-2) Are Associated with Poor Outcome in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2686-2686.	1.4	1
52	Abstract CT142: GD2.Ox40.CD28.z CART cell trial in neuroblastoma and osteosarcoma. Cancer Research, 2022, 82, CT142-CT142.	0.9	1
53	Identification of LMO2 Transcriptome and Interactome in Diffuse Large B-Cell Lymphoma by Integrated Experimental and Computational Approach. Blood, 2011, 118, 438-438.	1.4	0
54	Hierarchy in Somatic Mutations Arising During Genomic Evolution and Progression of Follicular Lymphoma. Blood, 2012, 120, 148-148.	1.4	0

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55	Transdifferentiation Of Primary Human Philadelphia Chromosome-Positive B Cell Acute Lymphoblastic Leukemia Cells Into Non-Leukemic Macrophages. Blood, 2013, 122, 1430-1430.	1.4	0
56	Germinal Center Kinase Regulates The Proliferation and Survival Of Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 643-643.	1.4	0