Andrew J Gentles

List of Publications by Year
in descending order

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	*NSD1* mutations deregulate transcription and DNA methylation of bivalent developmental genes in Sotos syndrome. Human Molecular Genetics, 2022, 31, 2164-2184.	2.9	11
2	Lymph node colonization induces tumor-immune tolerance to promote distant metastasis. Cell, 2022, 185, 1924-1942.e23.	28.9	111
3	Identification of cell types in multiplexed in situ images by combining protein expression and spatial information using CELESTA. Nature Methods, 2022, 19, 759-769.	19.0	42
4	Abstract CT142: GD2.Ox40.CD28.z CAR T cell trial in neuroblastoma and osteosarcoma. Cancer Research, 2022, 82, CT142-CT142.	0.9	1
5	Prognostic Gene Expression, Stemness and Immune Microenvironment in Pediatric Tumors. Cancers, 2021, 13, 854.	3.7	10
6	Transient rest restores functionality in exhausted CAR-T cells through epigenetic remodeling. Science, 2021, 372, .	12.6	297
7	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, .	7.1	50
8	High-grade serous ovarian tumor cells modulate NK cell function to create an immune-tolerant microenvironment. Cell Reports, 2021, 36, 109632.	6.4	26
9	HGAL inhibits lymphoma dissemination by interacting with multiple Cytoskeletal proteins. Blood Advances, 2021, 5, 5072-5085.	5.2	2
10	The landscape of tumor cell states and ecosystems in diffuse large B cell lymphoma. Cancer Cell, 2021, 39, 1422-1437.e10.	16.8	102
11	Atlas of clinically distinct cell states and ecosystems across human solid tumors. Cell, 2021, 184, 5482-5496.e28.	28.9	116
12	Clonal architecture predicts clinical outcomes and drug sensitivity in acute myeloid leukemia. Nature Communications, 2021, 12, 7244.	12.8	29
13	Maternal Anti-Dengue IgG Fucosylation Predicts Susceptibility to Dengue Disease in Infants. Cell Reports, 2020, 31, 107642.	6.4	44
14	A human lung tumor microenvironment interactome identifies clinically relevant cell-type cross-talk. Genome Biology, 2020, 21, 107.	8.8	33
15	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	27.8	203
16	MYC and Twist1 cooperate to drive metastasis by eliciting crosstalk between cancer and innate immunity. ELife, 2020, 9, .	6.0	38
17	Targetable genetic alterations of *TCF4* (*E2-2*) drive immunoglobulin expression in diffuse large B cell lymphoma. Science Translational Medicine, 2019, 11, .	12.4	51
18	Prognostic profiling of the immune cell microenvironment in EwingÂ´s Sarcoma Family of Tumors. OncoImmunology, 2019, 8, e1674113.	4.6	50

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19	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
20	LMO2 Confers Synthetic Lethality to PARP Inhibition in DLBCL. Cancer Cell, 2019, 36, 237-249.e6.	16.8	50
21	Determining cell type abundance and expression from bulk tissues with digital cytometry. Nature Biotechnology, 2019, 37, 773-782.	17.5	2,396
22	Data mining for mutation-specific targets in acute myeloid leukemia. Leukemia, 2019, 33, 826-843.	7.2	23
23	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
24	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
25	Module Analysis Captures Pancancer Genetically and Epigenetically Deregulated Cancer Driver Genes for Smoking and Antiviral Response. EBioMedicine, 2018, 27, 156-166.	6.1	40
26	Brd4 regulates the expression of essential autophagy genes and Keap1 in AML cells. Oncotarget, 2018, 9, 11665-11676.	1.8	14
27	*GFPT2*-Expressing Cancer-Associated Fibroblasts Mediate Metabolic Reprogramming in Human Lung Adenocarcinoma. Cancer Research, 2018, 78, 3445-3457.	0.9	75
28	Human AML-iPSCs Reacquire Leukemic Properties after Differentiation and Model Clonal Variation of Disease. Cell Stem Cell, 2017, 20, 329-344.e7.	11.1	101
29	NSD1 inactivation defines an immune cold, DNA hypomethylated subtype in squamous cell carcinoma. Scientific Reports, 2017, 7, 17064.	3.3	67
30	Role of *KEAP1*/*NRF2* and *TP53* Mutations in Lung Squamous Cell Carcinoma Development and Radiation Resistance. Cancer Discovery, 2017, 7, 86-101.	9.4	239
31	Data normalization considerations for digital tumor dissection. Genome Biology, 2017, 18, 128.	8.8	25
32	Low BUB1 expression is an adverse prognostic marker in gastric adenocarcinoma. Oncotarget, 2017, 8, 76329-76339.	1.8	34
33	Identifying Network Perturbation in Cancer. PLoS Computational Biology, 2016, 12, e1004888.	3.2	35
34	Pathophysiological significance and therapeutic targeting of germinal center kinase in diffuse large B-cell lymphoma. Blood, 2016, 128, 239-248.	1.4	17
35	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
36	Sparse expression bases in cancer reveal tumor drivers. Nucleic Acids Research, 2015, 43, 1332-1344.	14.5	27

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37	Mutations in early follicular lymphoma progenitors are associated with suppressed antigen presentation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1116-25.	7.1	307
38	The prognostic landscape of genes and infiltrating immune cells across human cancers. Nature Medicine, 2015, 21, 938-945.	30.7	2,505
39	Reprogramming of primary human Philadelphia chromosome-positive B cell acute lymphoblastic leukemia cells into nonleukemic macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 4074-4079.	7.1	52
40	Robust enumeration of cell subsets from tissue expression profiles. Nature Methods, 2015, 12, 453-457.	19.0	8,460
41	Mutant WT1 is associated with DNA hypermethylation of PRC2 targets in AML and responds to EZH2 inhibition. Blood, 2015, 125, 316-326.	1.4	45
42	An LSC epigenetic signature is largely mutation independent and implicates the HOXA cluster in AML pathogenesis. Nature Communications, 2015, 6, 8489.	12.8	121
43	Integrating Tumor and Stromal Gene Expression Signatures With Clinical Indices for Survival Stratification of Early-Stage Non–Small Cell Lung Cancer. Journal of the National Cancer Institute, 2015, 107, djv211.	6.3	64
44	CD93 Marks a Non-Quiescent Human Leukemia Stem Cell Population and Is Required for Development of MLL-Rearranged Acute Myeloid Leukemia. Cell Stem Cell, 2015, 17, 412-421.	11.1	97
45	Active Idiotypic Vaccination Versus Control Immunotherapy for Follicular Lymphoma. Journal of Clinical Oncology, 2014, 32, 1797-1803.	1.6	75
46	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
47	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
48	Germinal Center Kinase Regulates The Proliferation and Survival Of Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 643-643.	1.4	0
49	Systematic Deconvolution of Hematolymphoid Tumor Transcriptomes Reveals Infiltrating Immune Cell Signatures Related to Survival.. Blood, 2012, 120, 2390-2390.	1.4	3
50	Hierarchy in Somatic Mutations Arising During Genomic Evolution and Progression of Follicular Lymphoma. Blood, 2012, 120, 148-148.	1.4	0
51	Prediction of survival in diffuse large B-cell lymphoma based on the expression of 2 genes reflecting tumor and microenvironment. Blood, 2011, 118, 1350-1358.	1.4	175
52	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
53	Association of a Leukemic Stem Cell Gene Expression Signature With Clinical Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2010, 304, 2706.	7.4	339
54	A Bayesian nonparametric method for model evaluation: application to genetic studies. Journal of Nonparametric Statistics, 2009, 21, 379-396.	0.9	2

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55	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. Blood, 2009, 114, 3158-3166.	1.4	52
56	Evolutionary dynamics of transposable elements in the short-tailed opossum <i>Monodelphis domestica</i>. Genome Research, 2007, 17, 992-1004.	5.5	137