Andrew J Mungall

List of Publications by Year
in descending order

49	29,308	76196	189595
papers	citations	40 h-index	50 g-index

54	54	54	48732
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
2	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
3	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
4	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
5	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
6	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	9.4	1,504
7	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	13.7	1,428
8	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
9	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	6.0	1,147
10	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
11	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
12	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. Blood, 2011, 117, 2451-2459.	0.6	556
13	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. Nature Medicine, 2018, 24, 103-112.	15.2	525
14	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
15	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
16	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	0.6	349
17	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
18	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	2.1	272

#	Article	IF	Citations
19	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
20	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. Journal of Clinical Oncology, 2019, 37, 190-201.	0.8	257
21	Mutations in EZH2 Cause Weaver Syndrome. American Journal of Human Genetics, 2012, 90, 110-118.	2.6	253
22	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
23	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	9.4	207
24	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	0.6	172
25	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. Blood, 2013, 121, 3666-3674.	0.6	139
26	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	0.8	127
27	Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3.	6.5	125
28	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. Genome Biology, 2015, 16, 18.	3.8	107
29	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406.	7.7	105
30	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	5.8	102
31	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. Cell Reports, 2016, 17, 2060-2074.	2.9	90
32	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. Cell Reports, 2019, 29, 2338-2354.e7.	2.9	74
33	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924.	0.6	69
34	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. Blood, 2012, 119, 4949-4952.	0.6	60
35	Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. Journal of Molecular Diagnostics, 2018, 20, 203-214.	1.2	58
36	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260.	2.1	57

#	Article	IF	Citations
37	Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 2019, 47, e12-e12.	6.5	50
38	MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. Journal of Clinical Oncology, 2017, 35, 3964-3977.	0.8	49
39	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	5.8	49
40	Recurrent genomic rearrangements in primary testicular lymphoma. Journal of Pathology, 2015, 236, 136-141.	2.1	47
41	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588.	15.2	46
42	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. Blood, 2020, 136, 572-584.	0.6	44
43	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. OncoImmunology, 2017, 6, e1321184.	2.1	23
44	Impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. Blood, 2021, 137, 2196-2208.	0.6	18
45	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	1.2	12
46	Sample Tracking Using Unique Sequence Controls. Journal of Molecular Diagnostics, 2020, 22, 141-146.	1.2	10
47	Modulation of the Host Cell Transcriptome and Epigenome by Fusobacterium nucleatum. MBio, 2021, 12, e0206221.	1.8	10
48	Epigenomic programming in early fetal brain development. Epigenomics, 2020, 12, 1053-1070.	1.0	9
49	Characterization of the human thyroid epigenome. Journal of Endocrinology, 2017, 235, 153-165.	1.2	8