

# Andrew J Mungall

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11687123/publications.pdf>

Version: 2024-02-01

49  
papers

29,308  
citations

76326

40  
h-index

189892

50  
g-index

54  
all docs

54  
docs citations

54  
times ranked

48732  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	27.0	4,139
3	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
4	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	28.9	2,277
5	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
6	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	21.4	1,504
7	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	27.8	1,428
8	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
9	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. <i>Science</i> , 2014, 343, 189-193.	12.6	1,147
10	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
11	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	16.8	750
12	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. <i>Blood</i> , 2011, 117, 2451-2459.	1.4	556
13	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. <i>Nature Medicine</i> , 2018, 24, 103-112.	30.7	525
14	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
15	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
16	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	1.4	349
17	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	333
18	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012, 226, 7-16.	4.5	272

#	ARTICLE	IF	CITATIONS
19	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
20	Double-Hit Gene Expression Signature Defines a Distinct Subgroup of Germinal Center B-Cell-Like Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2019, 37, 190-201.	1.6	257
21	Mutations in EZH2 Cause Weaver Syndrome. <i>American Journal of Human Genetics</i> , 2012, 90, 110-118.	6.2	253
22	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	28.9	228
23	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. <i>Nature Genetics</i> , 2013, 45, 836-841.	21.4	207
24	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. <i>Blood</i> , 2019, 133, 1313-1324.	1.4	172
25	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. <i>Blood</i> , 2013, 121, 3666-3674.	1.4	139
26	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , 2012, 3, 1308-1319.	1.8	127
27	Large-scale profiling of microRNAs for The Cancer Genome Atlas. <i>Nucleic Acids Research</i> , 2016, 44, e3-e3.	14.5	125
28	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. <i>Genome Biology</i> , 2015, 16, 18.	8.8	107
29	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. <i>Cancer Cell</i> , 2016, 29, 394-406.	16.8	105
30	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. <i>Nature Communications</i> , 2018, 9, 4001.	12.8	102
31	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. <i>Cell Reports</i> , 2016, 17, 2060-2074.	6.4	90
32	Identification and Analyses of Extra-Cranial and Cranial Rhabdoid Tumor Molecular Subgroups Reveal Tumors with Cytotoxic T Cell Infiltration. <i>Cell Reports</i> , 2019, 29, 2338-2354.e7.	6.4	74
33	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. <i>Blood</i> , 2014, 123, 3914-3924.	1.4	69
34	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. <i>Blood</i> , 2012, 119, 4949-4952.	1.4	60
35	Assessment of Capture and Amplicon-Based Approaches for the Development of a Targeted Next-Generation Sequencing Pipeline to Personalize Lymphoma Management. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 203-214.	2.8	58
36	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. <i>Journal of Pathology</i> , 2013, 230, 249-260.	4.5	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. <i>Nucleic Acids Research</i> , 2019, 47, e12-e12.	14.5	50
38	MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. <i>Journal of Clinical Oncology</i> , 2017, 35, 3964-3977.	1.6	49
39	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	12.8	49
40	Recurrent genomic rearrangements in primary testicular lymphoma. <i>Journal of Pathology</i> , 2015, 236, 136-141.	4.5	47
41	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. <i>Nature Medicine</i> , 2020, 26, 577-588.	30.7	46
42	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. <i>Blood</i> , 2020, 136, 572-584.	1.4	44
43	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. <i>Oncolmmunology</i> , 2017, 6, e1321184.	4.6	23
44	Impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. <i>Blood</i> , 2021, 137, 2196-2208.	1.4	18
45	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550.	2.8	12
46	Sample Tracking Using Unique Sequence Controls. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 141-146.	2.8	10
47	Modulation of the Host Cell Transcriptome and Epigenome by <i>Fusobacterium nucleatum</i> . <i>MBio</i> , 2021, 12, e0206221.	4.1	10
48	Epigenomic programming in early fetal brain development. <i>Epigenomics</i> , 2020, 12, 1053-1070.	2.1	9
49	Characterization of the human thyroid epigenome. <i>Journal of Endocrinology</i> , 2017, 235, 153-165.	2.6	8