Andrew Mungall

List of Publications by Year
in descending order

286 papers	151,859 citations	1463 107 h-index	663 255 g-index
309 all docs	309 docs citations	309 times ranked	138681 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
3	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
4	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
5	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
6	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
7	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
8	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
9	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
10	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
11	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
12	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
13	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
14	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
15	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
16	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
17	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
18	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318

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19	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
20	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
21	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
22	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
23	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
24	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
25	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
26	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
27	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
28	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
29	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	27.8	1,448
30	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
31	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
32	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
33	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
34	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	27.8	1,158
35	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	12.6	1,147
36	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040

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37	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
38	The whole-genome landscape of medulloblastoma subtypes. Nature, 2017, 547, 311-317.	27.8	787
39	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
40	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
41	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
42	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
43	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
44	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
45	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
46	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
47	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
48	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.	1.4	556
49	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	27.8	545
50	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
51	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. Nature Medicine, 2018, 24, 103-112.	30.7	525
52	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
53	Mutations in a gene encoding a novel protein tyrosine phosphatase cause progressive myoclonus epilepsy. Nature Genetics, 1998, 20, 171-174.	21.4	499
54	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482

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55	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
56	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
57	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
58	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
59	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
60	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
61	Assembling the 20 Gb white spruce (Picea glauca) genome from whole-genome shotgun sequencing data. Bioinformatics, 2013, 29, 1492-1497.	4.1	356
62	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
63	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
64	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
65	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. Nature, 2017, 549, 227-232.	27.8	321
66	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
67	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
68	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. Nature Genetics, 2016, 48, 758-767.	21.4	287
69	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
70	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
71	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
72	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270

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73	Comparison of human genetic and sequence-based physical maps. Nature, 2001, 409, 951-953.	27.8	267
74	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
75	Complete MHC Haplotype Sequencing for Common Disease Gene Mapping. Genome Research, 2004, 14, 1176-1187.	5.5	260
76	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.	1.6	257
77	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	21.4	255
78	Mutations in EZH2 Cause Weaver Syndrome. American Journal of Human Genetics, 2012, 90, 110-118.	6.2	253
79	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
80	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	16.8	244
81	Quiescent Sox2+ Cells Drive Hierarchical Growth and Relapse in Sonic Hedgehog Subgroup Medulloblastoma. Cancer Cell, 2014, 26, 33-47.	16.8	241
82	The genetic basis and cell of origin of mixed phenotype acute leukaemia. Nature, 2018, 562, 373-379.	27.8	236
83	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
84	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. Nature Genetics, 2017, 49, 856-865.	21.4	220
85	Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. Nature Communications, 2016, 7, 13331.	12.8	218
86	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. Nature Genetics, 2013, 45, 836-841.	21.4	207
87	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
88	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
89	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. PLoS Medicine, 2016, 13, e1002197.	8.4	185
90	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177

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91	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. Blood, 2019, 133, 1313-1324.	1.4	172
92	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. Genome Biology, 2019, 20, 210.	8.8	171
93	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. Nature Genetics, 2008, 40, 971-976.	21.4	169
94	The Evolution of the DLK1-DIO3 Imprinted Domain in Mammals. PLoS Biology, 2008, 6, e135.	5.6	162
95	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	28.9	162
96	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. Clinical Cancer Research, 2017, 23, 7521-7530.	7.0	144
97	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. Blood, 2013, 121, 3666-3674.	1.4	139
98	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
99	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	1.8	127
100	Cyclin D3 is a target gene of t(6;14)(p21.1;q32.3) of mature B-cell malignancies. Blood, 2001, 98, 2837-2844.	1.4	125
101	Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3.	14.5	125
102	The E3 ubiquitin ligase UBR5 is recurrently mutated in mantle cell lymphoma. Blood, 2013, 121, 3161-3164.	1.4	124
103	NRG1 Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in KRAS Wild-Type Pancreatic Ductal Adenocarcinoma. Clinical Cancer Research, 2019, 25, 4674-4681.	7.0	121
104	Altered Gene Expression along the Glycolysisâ€“Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. Clinical Cancer Research, 2020, 26, 135-146.	7.0	121
105	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
106	Spatial heterogeneity in medulloblastoma. Nature Genetics, 2017, 49, 780-788.	21.4	112
107	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. Genome Biology, 2015, 16, 18.	8.8	107
108	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. Cancer Cell, 2016, 29, 394-406.	16.8	105

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109	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
110	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes. Nature Cancer, 2020, 1, 452-468.	13.2	103
111	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. Nature Communications, 2018, 9, 4001.	12.8	102
112	Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. Blood, 2019, 134, 802-813.	1.4	96
113	Lessons learned from the application of whole-genome analysis to the treatment of patients with advanced cancers. Journal of Physical Education and Sports Management, 2015, 1, a000570.	1.2	92
114	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. Cell Reports, 2016, 17, 2060-2074.	6.4	90
115	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
116	Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. Annals of Oncology, 2017, 28, 3092-3097.	1.2	83
117	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
118	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. Clinical Cancer Research, 2016, 22, 5582-5591.	7.0	82
119	Cloning and characterization of the common fragile site FRA6F harboring a replicative senescence gene and frequently deleted in human tumors. Oncogene, 2002, 21, 7266-7276.	5.9	79
120	High-resolution architecture and partner genes of MYC rearrangements in lymphoma with DLBCL morphology. Blood Advances, 2018, 2, 2755-2765.	5.2	74
121	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.	6.4	74
122	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	27.8	71
123	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. Blood, 2014, 123, 3914-3924.	1.4	69
124	Vanin genes are clustered (human 6q22-24 and mouse 10A2B1) and encode isoforms of pantetheinase ectoenzymes. Immunogenetics, 2001, 53, 296-306.	2.4	68
125	Application of a Neural Network Whole Transcriptomeâ€“Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. JAMA Network Open, 2019, 2, e192597.	5.9	67
126	Replication Timing of Human Chromosome 6. Cell Cycle, 2005, 4, 172-176.	2.6	66

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127	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013.	12.8	64
128	A somatic reference standard for cancer genome sequencing. Scientific Reports, 2016, 6, 24607.	3.3	64
129	Ocular developmental abnormalities and glaucoma associated with interstitial 6p25 duplications and deletions. Investigative Ophthalmology and Visual Science, 2002, 43, 1843-9.	3.3	63
130	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. Blood, 2012, 119, 4949-4952.	1.4	60
131	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.	2.8	58
132	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260.	4.5	57
133	Epigenetic and transcriptional determinants of the human breast. Nature Communications, 2015, 6, 6351.	12.8	56
134	The genomic and transcriptomic landscape of anaplastic thyroid cancer: implications for therapy. BMC Cancer, 2015, 15, 984.	2.6	55
135	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924.	4.1	54
136	The Organization of the Î³-Glutamyl Transferase Genes and Other Low Copy Repeats in Human Chromosomeâ€‰22q11. Genome Research, 1997, 7, 522-531.	5.5	53
137	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. Genome Research, 2019, 29, 1211-1222.	5.5	52
138	High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copyâ€neutral loss of heterozygosity and copy number alterations that target single genes. Genes Chromosomes and Cancer, 2010, 49, 669-681.	2.8	51
139	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.	14.5	50
140	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. Clinical Cancer Research, 2021, 27, 202-212.	7.0	50
141	miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. Oncotarget, 2016, 7, 25930-25948.	1.8	49
142	CSF3R mutations have a high degree of overlap with CEBPA mutations in pediatric AML. Blood, 2016, 127, 3094-3098.	1.4	49
143	MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. Journal of Clinical Oncology, 2017, 35, 3964-3977.	1.6	49
144	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49

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145	Recurrent genomic rearrangements in primary testicular lymphoma. Journal of Pathology, 2015, 236, 136-141.	4.5	47
146	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. Blood, 2016, 128, 1206-1213.	1.4	47
147	The transcriptional landscape of Shh medulloblastoma. Nature Communications, 2021, 12, 1749.	12.8	47
148	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. Nature Medicine, 2020, 26, 577-588.	30.7	46
149	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. Cancer Research, 2017, 77, 3217-3230.	0.9	45
150	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. Blood, 2020, 136, 572-584.	1.4	44
151	Comprehensive genomic profiling of glioblastoma tumors, BTICs, and xenografts reveals stability and adaptation to growth environments. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19098-19108.	7.1	42
152	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. Genetics in Medicine, 2020, 22, 1892-1897.	2.4	42
153	The Genomic Structure and Promoter Region of the Human Parkin Gene. Biochemical and Biophysical Research Communications, 2001, 286, 863-868.	2.1	41
154	An Exon Splice Enhancer Primes IGF2:IGF2R Binding Site Structure and Function Evolution. Science, 2012, 338, 1209-1213.	12.6	40
155	Analysis of Ugandan cervical carcinomas identifies human papillomavirus cladeâ€“specific epigenome and transcriptome landscapes. Nature Genetics, 2020, 52, 800-810.	21.4	40
156	Identification of candidate tumor-suppressor genes in 6q27 by combined deletion mapping and electronic expression profiling in lymphoid neoplasms. Genes Chromosomes and Cancer, 2003, 37, 421-426.	2.8	39
157	Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. Annals of Oncology, 2016, 27, 801-806.	1.2	39
158	The Genome of the Beluga Whale (Delphinapterus leucas). Genes, 2017, 8, 378.	2.4	39
159	The evolution of imprinting: chromosomal mapping of orthologues of mammalian imprinted domains in monotreme and marsupial mammals. BMC Evolutionary Biology, 2007, 7, 157.	3.2	38
160	A novel mechanistic spectrum underlies glaucoma-associated chromosome 6p25 copy number variation. Human Molecular Genetics, 2008, 17, 3446-3458.	2.9	38
161	Whole-Genome Sequencing in Cancer. Cold Spring Harbor Perspectives in Medicine, 2019, 9, a034579.	6.2	38
162	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. Developmental Cell, 2018, 44, 709-724.e6.	7.0	35

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163	The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis. Genes, 2018, 9, 598.	2.4	34
164	Base excision repair deficiency signatures implicate germline and somatic MUTYH aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681.	1.2	33
165	Investigation of PD-L1 Biomarker Testing Methods for PD-1 Axis Inhibition in Non-squamous Nonâ€“small Cell Lung Cancer. Journal of Histochemistry and Cytochemistry, 2016, 64, 587-600.	2.5	30
166	Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. Journal of Physical Education and Sports Management, 2018, 4, a002329.	1.2	30
167	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	2.8	29
168	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. Cancer Research, 2019, 79, 2111-2123.	0.9	28
169	Physical and transcript map of the region between D6S264 and D6S149 on chromosome 6q27, the minimal region of allele loss in sporadic epithelial ovarian cancer. Oncogene, 2002, 21, 387-399.	5.9	26
170	Cloning and characterization of two overlapping genes in a subregion at 6q21 involved in replicative senescence and schizophrenia. Gene, 2000, 252, 217-225.	2.2	24
171	The Genome of the Northern Sea Otter (Enhydra lutris kenyoni). Genes, 2017, 8, 379.	2.4	24
172	Subtype-Discordant Pancreatic Ductal Adenocarcinoma Tumors Show Intermediate Clinical and Molecular Characteristics. Clinical Cancer Research, 2021, 27, 150-157.	7.0	24
173	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. OncoImmunology, 2017, 6, e1321184.	4.6	23
174	MAVIS: merging, annotation, validation, and illustration of structural variants. Bioinformatics, 2019, 35, 515-517.	4.1	22
175	The human homologue of unc-93 maps to chromosome 6q27 - characterisation and analysis in sporadic epithelial ovarian cancer. BMC Genetics, 2002, 3, 20.	2.7	21
176	RhoGAP domain-containing fusions and PPAPDC1A fusions are recurrent and prognostic in diffuse gastric cancer. Nature Communications, 2018, 9, 4439.	12.8	21
177	Integrative genomic analysis of ghost cell odontogenic carcinoma. Oral Oncology, 2015, 51, e71-e75.	1.5	20
178	MEN1 Mutations in HÃ¼rthle Cell (Oncocytic) Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, E611-E615.	3.6	20
179	Discovery and Functional Validation of Novel Pediatric Specific FLT3 Activating Mutations in Acute Myeloid Leukemia: Results from the COG/NCI Target Initiative. Blood, 2015, 126, 87-87.	1.4	19
180	Personalized oncogenomic analysis of metastatic adenoid cystic carcinoma: using whole-genome sequencing to inform clinical decision-making. Journal of Physical Education and Sports Management, 2018, 4, a002626.	1.2	18

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181	Impact of MYC and BCL2 structural variants in tumors of DLBCL morphology and mechanisms of false-negative MYC IHC. Blood, 2021, 137, 2196-2208.	1.4	18
182	Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. PLoS ONE, 2017, 12, e0178706.	2.5	18
183	Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. Journal of Physical Education and Sports Management, 2019, 5, a003814.	1.2	17
184	Spruce gigaâ€genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. Plant Journal, 2022, 111, 1469-1485.	5.7	17
185	Molecular characterization of ERBB2-amplified colorectal cancer identifies potential mechanisms of resistance to targeted therapies: a report of two instructive cases. Journal of Physical Education and Sports Management, 2018, 4, a002535.	1.2	16
186	Delving into Early-onset Pancreatic Ductal Adenocarcinoma: How Does Age Fit In?. Clinical Cancer Research, 2021, 27, 246-254.	7.0	16
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