Andrew Mungall

List of Publications by Citations

269 papers	106,104 citations	99 h-index	309 g-index
309 ext. papers	133,721 ext. citations	16.5 avg, IF	9.26 L-index

#	Paper	IF	Citations
269	Initial sequencing and analysis of the human genome. *Nature*, **2001**, 409, 860-921	50.4	17366
268	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
267	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
266	The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, **2013**, 45, 1113-20	36.3	3933
265	Integrative analysis of 111 reference human epigenomes. *Nature*, **2015**, 518, 317-30	50.4	3849
264	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
263	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
262	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
261	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
260	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
259	Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*, **2015**, 517, 576-82	50.4	2332
258	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184
257	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
256	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
255	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
254	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
253	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713

252	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
251	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. *Nature Genetics*, **2010**, 42, 181-5	36.3	1273
250	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. *Nature*, **2011**, 476, 298-303	50.4	1180
249	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. *Cell*, **2016**, 164, 550-63	56.2	1140
248	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
247	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
246	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
245	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
244	Integrated genomic characterization of oesophageal carcinoma. *Nature*, **2017**, 541, 169-175	50.4	965
243	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
242	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
241	Mutational analysis reveals the origin and therapy-driven evolution of recurrent glioma. *Science*, **2014**, 343, 189-193	33.3	912
240	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.5	896
239	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
238	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
237	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
236	Integrated genomic and molecular characterization of cervical cancer. *Nature*, **2017**, 543, 378-384	50.4	755
235	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753

234	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. *Nature*, **2012**, 488, 49-56	50.4	596
233	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
232	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
231	The whole-genome landscape of medulloblastoma subtypes. *Nature*, **2017**, 547, 311-317	50.4	472
230	Somatic mutations at EZH2 Y641 act dominantly through a mechanism of selectively altered PRC2 catalytic activity, to increase H3K27 trimethylation. *Blood*, **2011**, 117, 2451-9	2.2	458
229	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. *Nature*, **2015**, 518, 422-6	50.4	451
228	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
227	Mutations in a gene encoding a novel protein tyrosine phosphatase cause progressive myoclonus epilepsy. *Nature Genetics*, **1998**, 20, 171-4	36.3	440
226	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
225	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. *Cancer Cell*, **2017**, 32, 204-220.e15	24.3	391
224	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
223	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
222	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. *Cancer Cell*, **2017**, 31, 181-193	24.3	350
221	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
220	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
219	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
218	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
217	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295

216	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. *Blood*, **2013**, 122, 1256-65	2.2	289
215	Assembling the 20 Gb white spruce (Picea glauca) genome from whole-genome shotgun sequencing data. *Bioinformatics*, **2013**, 29, 1492-7	7.2	278
214	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
213	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	24.3	275
212	The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. *Nature Medicine*, **2018**, 24, 103-112	50.5	272
211	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
210	Comparison of human genetic and sequence-based physical maps. *Nature*, **2001**, 409, 951-3	50.4	237
209	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
208	Complete MHC haplotype sequencing for common disease gene mapping. *Genome Research*, **2004**, 14, 1176-87	9.7	235
207	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
206	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, 15544-9	11.5	229
205	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
204	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. *Journal of Pathology*, **2012**, 226, 7-16	9.4	226
203	Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **2017**, 31, 411-423	24.3	210
202	Divergent modes of clonal spread and intraperitoneal mixing in high-grade serous ovarian cancer. *Nature Genetics*, **2016**, 48, 758-67	36.3	209
201	Divergent clonal selection dominates medulloblastoma at recurrence. *Nature*, **2016**, 529, 351-7	50.4	206
200	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
199	Fate mapping of human glioblastoma reveals an invariant stem cell hierarchy. *Nature*, **2017**, 549, 227-232	50.4	197

198	Mutations in EZH2 cause Weaver syndrome. *American Journal of Human Genetics*, **2012**, 90, 110-8	11	190
197	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
196	Quiescent sox2(+) cells drive hierarchical growth and relapse in sonic hedgehog subgroup medulloblastoma. *Cancer Cell*, **2014**, 26, 33-47	24.3	181
195	Recurrent DGCR8, DROSHA, and SIX homeodomain mutations in favorable histology Wilms tumors. *Cancer Cell*, **2015**, 27, 286-97	24.3	175
194	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
193	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. *Nature Genetics*, **2017**, 49, 1487-1494	36.3	160
192	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
191	DNA hypomethylation within specific transposable element families associates with tissue-specific enhancer landscape. *Nature Genetics*, **2013**, 45, 836-41	36.3	154
190	The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, **2018**, 33, 244-258.e10	24.3	150
189	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
188	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. *Cell Reports*, **2018**, 23, 194-212.e6	10.6	146
187	Genomic consequences of aberrant DNA repair mechanisms stratify ovarian cancer histotypes. *Nature Genetics*, **2017**, 49, 856-865	36.3	141
186	Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians. *Nature Genetics*, **2008**, 40, 971-6	36.3	141
185	The genetic basis and cell of origin of mixed phenotype acute leukaemia. *Nature*, **2018**, 562, 373-379	50.4	140
184	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	2.2	137
183	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
182	The evolution of the DLK1-DIO3 imprinted domain in mammals. *PLoS Biology*, **2008**, 6, e135	9.7	130
181	Genomic analyses identify recurrent MEF2D fusions in acute lymphoblastic leukaemia. *Nature Communications*, **2016**, 7, 13331	17.4	128

180	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
179	Cyclin D3 is a target gene of t(6;14)(p21.1;q32.3) of mature B-cell malignancies. *Blood*, **2001**, 98, 2837-44	2.2	114
178	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
177	Histological Transformation and Progression in Follicular Lymphoma: A Clonal Evolution Study. *PLoS Medicine*, **2016**, 13, e1002197	11.6	110
176	Recurrent targets of aberrant somatic hypermutation in lymphoma. *Oncotarget*, **2012**, 3, 1308-19	3.3	101
175	Analysis of FOXO1 mutations in diffuse large B-cell lymphoma. *Blood*, **2013**, 121, 3666-74	2.2	100
174	The E3 ubiquitin ligase UBR5 is recurrently mutated in mantle cell lymphoma. *Blood*, **2013**, 121, 3161-4	2.2	98
173	Large-scale profiling of microRNAs for The Cancer Genome Atlas. *Nucleic Acids Research*, **2016**, 44, e3	20.1	85
172	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
171	Homologous Recombination Deficiency and Platinum-Based Therapy Outcomes in Advanced Breast Cancer. *Clinical Cancer Research*, **2017**, 23, 7521-7530	12.9	82
170	Genome-Wide Profiles of Extra-cranial Malignant Rhabdoid Tumors Reveal Heterogeneity and Dysregulated Developmental Pathways. *Cancer Cell*, **2016**, 29, 394-406	24.3	81
169	Spatial heterogeneity in medulloblastoma. *Nature Genetics*, **2017**, 49, 780-788	36.3	80
168	Immunogenicity of recurrent mutations in MYD88 and EZH2 in non-Hodgkin lymphomas **2015**, 3,		78
167	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	18.3	77
166	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	2.8	75
165	Cloning and characterization of the common fragile site FRA6F harboring a replicative senescence gene and frequently deleted in human tumors. *Oncogene*, **2002**, 21, 7266-76	9.2	75
164	Genome-wide discovery of somatic coding and noncoding mutations in pediatric endemic and sporadic Burkitt lymphoma. *Blood*, **2019**, 133, 1313-1324	2.2	75
163	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. *Cell*, **2019**, 179, 1207-1221.e22	56.2	73

162	Analysis of Normal Human Mammary Epigenomes Reveals Cell-Specific Active Enhancer States and Associated Transcription Factor Networks. *Cell Reports*, **2016**, 17, 2060-2074	10.6	72
161	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. *Genome Biology*, **2015**, 16, 18	18.3	71
160	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
159	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons' Data. *Cell Systems*, **2019**, 9, 24-34.e10	10.6	64
158	Successful targeting of the NRG1 pathway indicates novel treatment strategy for metastatic cancer. *Annals of Oncology*, **2017**, 28, 3092-3097	10.3	64
157	Genome-wide discovery of somatic regulatory variants in diffuse large B-cell lymphoma. *Nature Communications*, **2018**, 9, 4001	17.4	64
156	Gene Fusions Are Recurrent, Clinically Actionable Gene Rearrangements in Wild-Type Pancreatic Ductal Adenocarcinoma. *Clinical Cancer Research*, **2019**, 25, 4674-4681	12.9	63
155	A transgenic mouse model demonstrating the oncogenic role of mutations in the polycomb-group gene EZH2 in lymphomagenesis. *Blood*, **2014**, 123, 3914-24	2.2	63
154	Altered Gene Expression along the Glycolysis-Cholesterol Synthesis Axis Is Associated with Outcome in Pancreatic Cancer. *Clinical Cancer Research*, **2020**, 26, 135-146	12.9	61
153	Vanin genes are clustered (human 6q22-24 and mouse 10A2B1) and encode isoforms of pantetheinase ectoenzymes. *Immunogenetics*, **2001**, 53, 296-306	3.2	60
152	Ocular developmental abnormalities and glaucoma associated with interstitial 6p25 duplications and deletions. *Investigative Ophthalmology and Visual Science*, **2002**, 43, 1843-9		59
151	Replication timing of human chromosome 6. *Cell Cycle*, **2005**, 4, 172-6	4.7	58
150	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	26.6	56
149	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. *Nature Communications*, **2017**, 8, 1433	17.4	56
148	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. *Bioinformatics*, **2012**, 28, 1923-4	7.2	52
147	TBL1XR1/TP63: a novel recurrent gene fusion in B-cell non-Hodgkin lymphoma. *Blood*, **2012**, 119, 4949-52	2.2	50
146	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	12.9	49
145	Epigenetic and transcriptional determinants of the human breast. *Nature Communications*, **2015**, 6, 6351	17.4	44

144	The genomic and transcriptomic landscape of anaplastic thyroid cancer: implications for therapy. *BMC Cancer*, **2015**, 15, 984	4.8	44
143	The organization of the gamma-glutamyl transferase genes and other low copy repeats in human chromosome 22q11. *Genome Research*, **1997**, 7, 522-31	9.7	44
142	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. *Journal of Pathology*, **2013**, 230, 249-60	9.4	43
141	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	5.1	42
140	Integrative genomic analysis identifies key pathogenic mechanisms in primary mediastinal large B-cell lymphoma. *Blood*, **2019**, 134, 802-813	2.2	41
139	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. *Nature Communications*, **2015**, 6, 10013	17.4	41
138	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	10.6	40
137	High resolution analysis of follicular lymphoma genomes reveals somatic recurrent sites of copy-neutral loss of heterozygosity and copy number alterations that target single genes. *Genes Chromosomes and Cancer*, **2010**, 49, 669-81	5	40
136	Comprehensive characterization of programmed death ligand structural rearrangements in B-cell non-Hodgkin lymphomas. *Blood*, **2016**, 128, 1206-13	2.2	40
135	A somatic reference standard for cancer genome sequencing. *Scientific Reports*, **2016**, 6, 24607	4.9	39
134	miR-509-3p is clinically significant and strongly attenuates cellular migration and multi-cellular spheroids in ovarian cancer. *Oncotarget*, **2016**, 7, 25930-48	3.3	39
133	CSF3R mutations have a high degree of overlap with CEBPA mutations in pediatric AML. *Blood*, **2016**, 127, 3094-8	2.2	38
132	High-resolution architecture and partner genes of rearrangements in lymphoma with DLBCL morphology. *Blood Advances*, **2018**, 2, 2755-2765	7.8	38
131	The evolution of imprinting: chromosomal mapping of orthologues of mammalian imprinted domains in monotreme and marsupial mammals. *BMC Evolutionary Biology*, **2007**, 7, 157	3	37
130	Recurrent genomic rearrangements in primary testicular lymphoma. *Journal of Pathology*, **2015**, 236, 136-41	9.4	36
129	The genomic structure and promoter region of the human parkin gene. *Biochemical and Biophysical Research Communications*, **2001**, 286, 863-8	3.4	36
128	Pan-cancer analysis of advanced patient tumors reveals interactions between therapy and genomic landscapes.. *Nature Cancer*, **2020**, 1, 452-468	15.4	34
127	A novel mechanistic spectrum underlies glaucoma-associated chromosome 6p25 copy number variation. *Human Molecular Genetics*, **2008**, 17, 3446-58	5.6	33

126	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, 421-6	5	33
125	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	20.1	33
124	Pyruvate Kinase Inhibits Proliferation during Postnatal Cerebellar Neurogenesis and Suppresses Medulloblastoma Formation. *Cancer Research*, **2017**, 77, 3217-3230	10.1	32
123	MicroRNA Expression-Based Model Indicates Event-Free Survival in Pediatric Acute Myeloid Leukemia. *Journal of Clinical Oncology*, **2017**, 35, 3964-3977	2.2	31
122	High-resolution structural genomics reveals new therapeutic vulnerabilities in glioblastoma. *Genome Research*, **2019**, 29, 1211-1222	9.7	31
121	An exon splice enhancer primes IGF2:IGF2R binding site structure and function evolution. *Science*, **2012**, 338, 1209-13	33.3	30
120	The Genome of the Beluga Whale (Delphinapterus leucas). *Genes*, **2017**, 8,	4.2	28
119	A clinically validated diagnostic second-generation sequencing assay for detection of hereditary BRCA1 and BRCA2 mutations. *Journal of Molecular Diagnostics*, **2013**, 15, 796-809	5.1	27
118	Response to angiotensin blockade with irbesartan in a patient with metastatic colorectal cancer. *Annals of Oncology*, **2016**, 27, 801-6	10.3	27
117	Application of a Neural Network Whole Transcriptome-Based Pan-Cancer Method for Diagnosis of Primary and Metastatic Cancers. *JAMA Network Open*, **2019**, 2, e192597	10.4	25
116	Opposing Effects of CREBBP Mutations Govern the Phenotype of Rubinstein-Taybi Syndrome and Adult SHH Medulloblastoma. *Developmental Cell*, **2018**, 44, 709-724.e6	10.2	25
115	Investigation of PD-L1 Biomarker Testing Methods for PD-1 Axis Inhibition in Non-squamous Non-small Cell Lung Cancer. *Journal of Histochemistry and Cytochemistry*, **2016**, 64, 587-600	3.4	24
114	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	11.5	23
113	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, 387-99	9.2	23
112	Tumor necrosis factor overcomes immune evasion in p53-mutant medulloblastoma. *Nature Neuroscience*, **2020**, 23, 842-853	25.5	22
111	TMEM30A loss-of-function mutations drive lymphomagenesis and confer therapeutically exploitable vulnerability in B-cell lymphoma. *Nature Medicine*, **2020**, 26, 577-588	50.5	22
110	Cloning and characterization of two overlapping genes in a subregion at 6q21 involved in replicative senescence and schizophrenia. *Gene*, **2000**, 252, 217-25	3.8	22
109	Mapping the human T cell repertoire to recurrent driver mutations in MYD88 and EZH2 in lymphoma. *OncoImmunology*, **2017**, 6, e1321184	7.2	20

108	Molecular characterization of metastatic pancreatic neuroendocrine tumors (PNETs) using whole-genome and transcriptome sequencing. *Journal of Physical Education and Sports Management*, **2018**, 4,	2.8	20
107	Coding and noncoding drivers of mantle cell lymphoma identified through exome and genome sequencing. *Blood*, **2020**, 136, 572-584	2.2	19
106	Genome and Transcriptome Biomarkers of Response to Immune Checkpoint Inhibitors in Advanced Solid Tumors. *Clinical Cancer Research*, **2021**, 27, 202-212	12.9	19
105	Base excision repair deficiency signatures implicate germline and somatic aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. *Journal of Physical Education and Sports Management*, **2019**, 5,	2.8	17
104	MEN1 mutations in H□thle cell (oncocytic) thyroid carcinoma. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E611-5	5.6	17
103	Analysis of Ugandan cervical carcinomas identifies human papillomavirus clade-specific epigenome and transcriptome landscapes. *Nature Genetics*, **2020**, 52, 800-810	36.3	17
102	Improved structural variant interpretation for hereditary cancer susceptibility using long-read sequencing. *Genetics in Medicine*, **2020**, 22, 1892-1897	8.1	15
101	The Genome of the Northern Sea Otter (Enhydra lutris kenyoni). *Genes*, **2017**, 8,	4.2	15
100	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	2.2	15
99	Intratumoral Genetic and Functional Heterogeneity in Pediatric Glioblastoma. *Cancer Research*, **2019**, 79, 2111-2123	10.1	14
98	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,	2.8	14
97	Whole-Genome Sequencing in Cancer. *Cold Spring Harbor Perspectives in Medicine*, **2019**, 9,	5.4	14
96	Integrative genomic analysis of ghost cell odontogenic carcinoma. *Oral Oncology*, **2015**, 51, e71-5	4.4	14
95	RhoGAP domain-containing fusions and PPAPDC1A fusions are recurrent and prognostic in diffuse gastric cancer. *Nature Communications*, **2018**, 9, 4439	17.4	14
94	Application of genomics to identify therapeutic targets in recurrent pediatric papillary thyroid carcinoma. *Journal of Physical Education and Sports Management*, **2018**, 4,	2.8	13
93	MAVIS: merging, annotation, validation, and illustration of structural variants. *Bioinformatics*, **2019**, 35, 515-517	7.2	13
92	The expression level of small non-coding RNAs derived from the first exon of protein-coding genes is predictive of cancer status. *EMBO Reports*, **2014**, 15, 402-10	6.5	13
91	The human homologue of unc-93 maps to chromosome 6q27 - characterisation and analysis in sporadic epithelial ovarian cancer. *BMC Genetics*, **2002**, 3, 20	2.6	13

90	Automated high throughput nucleic acid purification from formalin-fixed paraffin-embedded tissue samples for next generation sequence analysis. *PLoS ONE*, **2017**, 12, e0178706	3.7	13
89	The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis. *Genes*, **2018**, 9,	4.2	13
88	Whole genome and whole transcriptome genomic profiling of a metastatic eccrine porocarcinoma. *Npj Precision Oncology*, **2018**, 2, 8	9.8	11
87	Putative BRAF activating fusion in a medullary thyroid cancer. *Journal of Physical Education and Sports Management*, **2016**, 2, a000729	2.8	11
86	An integrated map of human 6q22.3-q24 including a 3-Mb high-resolution BAC/PAC contig encompassing a QTL for fetal hemoglobin. *Genomics*, **2000**, 64, 264-76	4.3	11
85	Validation and calibration of next-generation sequencing to identify Epstein-Barr virus-positive gastric cancer in The Cancer Genome Atlas. *Gastric Cancer*, **2016**, 19, 676-681	7.6	10
84	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. *BMC Genomics*, **2013**, 14, 550	4.5	10
83	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. *Nature Communications*, **2021**, 12, 2474	17.4	10
82	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. *Nature*, **2021**, 595, 585-590	50.4	10
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