David A Wheeler

List of Publications by Citations

240 papers	94,994 citations	105 h-index	254 g-index
254 ext. papers	115,532 ext. citations	18.4 avg, IF	8.89 L-index

#	Paper	IF	Citations
240	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
239	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, **2008**, 455, 1061-8	50.4	5669
238	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
237	Integrated genomic analyses of ovarian carcinoma. *Nature*, **2011**, 474, 609-15	50.4	5210
236	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
235	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
234	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
233	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
232	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
231	Somatic mutations affect key pathways in lung adenocarcinoma. *Nature*, **2008**, 455, 1069-75	50.4	2280
230	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184
229	Integrating common and rare genetic variation in diverse human populations. *Nature*, **2010**, 467, 52-8	50.4	2135
228	Genomic analyses identify molecular subtypes of pancreatic cancer. *Nature*, **2016**, 531, 47-52	50.4	1785
227	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754
226	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004**, 428, 493-521	50.4	1689
225	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
224	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613

223	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. *Nature*, **2012**, 491, 399-405	50.4	1427
222	The complete genome of an individual by massively parallel DNA sequencing. *Nature*, **2008**, 452, 872-6	50.4	1424
221	Insights into social insects from the genome of the honeybee Apis mellifera. *Nature*, **2006**, 443, 931-49	50.4	1414
220	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
219	Exome sequencing of head and neck squamous cell carcinoma reveals inactivating mutations in NOTCH1. *Science*, **2011**, 333, 1154-7	33.3	1331
218	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
217	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
216	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
215	Evolutionary and biomedical insights from the rhesus macaque genome. *Science*, **2007**, 316, 222-34	33.3	1072
214	Characterizing the cancer genome in lung adenocarcinoma. *Nature*, **2007**, 450, 893-8	50.4	900
213	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.9	896
212	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
211	The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science*, **2009**, 324, 522-8	33.3	863
210	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
209	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
208	The DNA sequence of the human X chromosome. *Nature*, **2005**, 434, 325-37	50.4	822
207	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
206	Whole-genome sequencing in a patient with Charcot-Marie-Tooth neuropathy. *New England Journal of Medicine*, **2010**, 362, 1181-91	59.2	613

205	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. *Science*, **2009**, 324, 528-32	33.3	612
204	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
203	Direct selection of human genomic loci by microarray hybridization. *Nature Methods*, **2007**, 4, 903-5	21.6	543
202	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
201	Landscape of somatic retrotransposition in human cancers. *Science*, **2012**, 337, 967-71	33.3	507
200	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. *Nature Genetics*, **2014**, 46, 1267-73	36.3	491
199	Whole-genome landscape of pancreatic neuroendocrine tumours. *Nature*, **2017**, 543, 65-71	50.4	482
198	Comparative genome sequencing of Drosophila pseudoobscura: chromosomal, gene, and cis-element evolution. *Genome Research*, **2005**, 15, 1-18	9.7	410
197	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
196	Integrative genomic characterization of oral squamous cell carcinoma identifies frequent somatic drivers. *Cancer Discovery*, **2013**, 3, 770-81	24.4	391
195	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
194	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
193	Mutations in smooth muscle alpha-actin (ACTA2) cause coronary artery disease, stroke, and Moyamoya disease, along with thoracic aortic disease. *American Journal of Human Genetics*, **2009**, 84, 617-27	11	364
192	Mutational landscape of aggressive cutaneous squamous cell carcinoma. *Clinical Cancer Research*, **2014**, 20, 6582-92	12.9	362
191	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
190	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
189	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
188	Molecular analysis of the period locus in Drosophila melanogaster and identification of a transcript involved in biological rhythms. *Cell*, **1984**, 38, 701-10	56.2	310

187	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
186	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
185	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. *JAMA Oncology*, **2016**, 2, 616-624	13.4	276
184	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. *Blood*, **2014**, 124, 3007-15	2.2	272
183	P-element transformation with period locus DNA restores rhythmicity to mutant, arrhythmic Drosophila melanogaster. *Cell*, **1984**, 39, 369-76	56.2	272
182	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. *Nature Genetics*, **2011**, 43, 189-96	36.3	271
181	Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence. *Genome Biology*, **2002**, 3, RESEARCH0079	18.3	265
180	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3′UTR landscape across seven tumour types. *Nature Communications*, **2014**, 5, 5274	17.4	260
179	Behavior in light-dark cycles of Drosophila mutants that are arrhythmic, blind, or both. *Journal of Biological Rhythms*, **1993**, 8, 67-94	3.2	249
178	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
177	Exome sequencing of ion channel genes reveals complex profiles confounding personal risk assessment in epilepsy. *Cell*, **2011**, 145, 1036-48	56.2	240
176	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. *Cell*, **2016**, 164, 538-49	56.2	239
175	Orphan nuclear receptor LRH-1 is required to maintain Oct4 expression at the epiblast stage of embryonic development. *Molecular and Cellular Biology*, **2005**, 25, 3492-505	4.8	239
174	A common allele in RPGRIP1L is a modifier of retinal degeneration in ciliopathies. *Nature Genetics*, **2009**, 41, 739-45	36.3	236
173	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. *Cancer Discovery*, **2018**, 8, 730-749	24.4	235
172	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
171	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
170	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. *Cell Reports*, **2016**, 14, 2476-89	10.6	228

169	Analyses of non-coding somatic drivers in 2,658´cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
168	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. *Nature Communications*, **2015**, 6, 6604	17.4	215
167	Effect of Oral Methylprednisolone on Clinical Outcomes in Patients With IgA Nephropathy: The TESTING Randomized Clinical Trial. *JAMA - Journal of the American Medical Association*, **2017**, 318, 432-442	27.4	214
166	Activation of multiple proto-oncogenic tyrosine kinases in breast cancer via loss of the PTPN12 phosphatase. *Cell*, **2011**, 144, 703-18	56.2	214
165	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. *Nature Genetics*, **2013**, 45, 1226-1231	36.3	205
164	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
163	Genomic profiling of S□ary syndrome identifies alterations of key T cell signaling and differentiation genes. *Nature Genetics*, **2015**, 47, 1426-34	36.3	199
162	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. *Nature Communications*, **2015**, 6, 10001	17.4	199
161	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
160	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. *Genome Research*, **2014**, 24, 1740-50	9.7	187
159	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. *Nature Communications*, **2010**, 1, 131	17.4	183
158	Recurrent DGCR8, DROSHA, and SIX homeodomain mutations in favorable histology Wilms tumors. *Cancer Cell*, **2015**, 27, 286-97	24.3	175
157	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. *Cell*, **2019**, 179, 964-983.e31	56.2	173
156	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
155	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. *Blood*, **2015**, 125, 629-38	2.2	163
154	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, E1128-36	11.5	163
153	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Research*, **2007**, 17, 760-74	9.7	163
152	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. *Cell Reports*, **2019**, 28, 1370-1384.e5	10.6	161

151	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. *Human Mutation*, **2011**, 32, 661-8	4.7	161
150	Germ-line transformation involving DNA from the period locus in Drosophila melanogaster: overlapping genomic fragments that restore circadian and ultradian rhythmicity to per0 and per- mutants. *Journal of Neurogenetics*, **1986**, 3, 249-91	1.6	161
149	A Children Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. *Nature Genetics*, **2017**, 49, 1487-1494	36.3	160
148	Genomic analysis of the nuclear receptor family: new insights into structure, regulation, and evolution from the rat genome. *Genome Research*, **2004**, 14, 580-90	9.7	158
147	Behavior of period-altered circadian rhythm mutants ofDrosophila in light: Dark cycles (Diptera: Drosophilidae). *Journal of Insect Behavior*, **1992**, 5, 417-446	1.1	151
146	Functional genomics of genes with small open reading frames (sORFs) in S. cerevisiae. *Genome Research*, **2006**, 16, 365-73	9.7	150
145	Orphan nuclear receptor GCNF is required for the repression of pluripotency genes during retinoic acid-induced embryonic stem cell differentiation. *Molecular and Cellular Biology*, **2005**, 25, 8507-19	4.8	150
144	Demographic histories and patterns of linkage disequilibrium in Chinese and Indian rhesus macaques. *Science*, **2007**, 316, 240-3	33.3	146
143	Novel somatic and germline mutations in intracranial germ cell tumours. *Nature*, **2014**, 511, 241-5	50.4	131
142	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. *Nature Genetics*, **2013**, 45, 767-75	36.3	131
141	A SNP discovery method to assess variant allele probability from next-generation resequencing data. *Genome Research*, **2010**, 20, 273-80	9.7	130
140	Proteogenomic Characterization of Endometrial Carcinoma. *Cell*, **2020**, 180, 729-748.e26	56.2	122
139	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
138	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. *Genome Biology*, **2016**, 17, 178	18.3	120
137	Assessing structural variation in a personal genome-towards a human reference diploid genome. *BMC Genomics*, **2015**, 16, 286	4.5	117
136	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. *European Urology*, **2017**, 72, 641-649	10.2	111
135	Once-daily versus twice-daily lopinavir/ritonavir in antiretroviral-naive HIV-positive patients: a 48-week randomized clinical trial. *Journal of Infectious Diseases*, **2004**, 189, 265-72	7	105
134	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. *Hepatology*, **2017**, 65, 104-121	11.2	104

133	From human genome to cancer genome: the first decade. *Genome Research*, **2013**, 23, 1054-62	9.7	103
132	Squamous cell carcinoma of the oral tongue in young non-smokers is genomically similar to tumors in older smokers. *Clinical Cancer Research*, **2014**, 20, 3842-8	12.9	96
131	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. *Cancer Research*, **2016**, 76, 2197-205	10.1	95
130	SNPdetector: a software tool for sensitive and accurate SNP detection. *PLoS Computational Biology*, **2005**, 1, e53	5	95
129	Integrated analyses of microRNAs demonstrate their widespread influence on gene expression in high-grade serous ovarian carcinoma. *PLoS ONE*, **2012**, 7, e34546	3.7	94
128	BCOR-CCNB3 fusions are frequent in undifferentiated sarcomas of male children. *Modern Pathology*, **2015**, 28, 575-86	9.8	93
127	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. *Blood*, **2016**, 128, 2533-2537	2.2	93
126	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. *Nature Communications*, **2015**, 6, 8891	17.4	92
125	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. *Nature Communications*, **2013**, 4, 2730	17.4	91
124	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. *Nature Communications*, **2016**, 7, 12601	17.4	88
123	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
122	Disruptive TP53 mutation is associated with aggressive disease characteristics in an orthotopic murine model of oral tongue cancer. *Clinical Cancer Research*, **2011**, 17, 6658-70	12.9	79
121	TBIO-20. CLINICAL TUMOR WHOLE EXOME SEQUENCING FOR PEDIATRIC NEURO-ONCOLOGY PATIENTS RESULTS FROM THE BAYLOR ADVANCING SEQUENCING IN CHILDHOOD CANCER CARE (BASIC3) CLINICAL SEQUENCING STUDY. *Neuro-Oncology*, **2018**, 20, i184-i184	1	78
120	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. *Cell Reports*, **2016**, 14, 907-919	10.6	75
119	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- Pathway. *Gastroenterology*, **2018**, 154, 195-210	13.3	68
118	The Repertoire of Mutational Signatures in Human Cancer		67
117	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
116	Phylogenetic and structural analyses of MMTV LTR ORF sequences of exogenous and endogenous origins. *Virology*, **1993**, 193, 171-85	3.6	66

115	Transcription of mouse mammary tumor virus: identification of a candidate mRNA for the long terminal repeat gene product. *Journal of Virology*, **1983**, 46, 42-9	6.6	66
114	Spectral analysis of Drosophila courtship songs: D. melanogaster, D. simulans, and their interspecific hybrid. *Behavior Genetics*, **1988**, 18, 675-703	3.2	61
113	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. *Cell*, **2018**, 173, 864-878.e29	56.2	58
112	MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. *Journal of Pathology*, **2013**, 229, 99-110	9.4	58
111	Initial testing (stage 1) of the PARP inhibitor BMN 673 by the pediatric preclinical testing program: PALB2 mutation predicts exceptional in vivo response to BMN 673. *Pediatric Blood and Cancer*, **2015**, 62, 91-8	3	55
110	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. *Nature Communications*, **2017**, 8, 14098	17.4	54
109	Effects of TP53 mutational status on gene expression patterns across 10 human cancer types. *Journal of Pathology*, **2014**, 232, 522-33	9.4	52
108	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. *Journal of Clinical Investigation*, **2016**, 126, 2881-92	15.9	52
107	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. *Cell Reports*, **2019**, 29, 1675-1689.e9	10.6	51
106	Novel estrogen response elements identified by genetic selection in yeast are differentially responsive to estrogens and antiestrogens in mammalian cells. *Molecular Endocrinology*, **1994**, 8, 1193-1207		51
105	Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 21715-21726	11.5	49
104	Mammalian hexokinase 1: evolutionary conservation and structure to function analysis. *Genomics*, **1991**, 11, 1014-24	4.3	49
103	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children Oncology Group. *Clinical Cancer Research*, **2016**, 22, 5582-5591	12.9	49
102	Kallmann syndrome gene on the X and Y chromosomes: implications for evolutionary divergence of human sex chromosomes. *Nature Genetics*, **1992**, 2, 311-4	36.3	48
101	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. *Genome Biology*, **2014**, 15, 443	18.3	47
100	Spectral analysis of courtship songs in behavioral mutants of Drosophila melanogaster. *Behavior Genetics*, **1989**, 19, 503-28	3.2	47
99	The finished DNA sequence of human chromosome 12. *Nature*, **2006**, 440, 346-51	50.4	43
98	The DNA sequence, annotation and analysis of human chromosome 3. *Nature*, **2006**, 440, 1194-8	50.4	43

97	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. *Journal of Neuropathology and Experimental Neurology*, **2017**, 76, 126-134	3.1	41
96	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. *Nature Communications*, **2015**, 6, 10013	17.4	41
95	Novel microRNA candidates and miRNA-mRNA pairs in embryonic stem (ES) cells. *PLoS ONE*, **2008**, 3, e2548	3.7	41
94	The breast cancer gene database: a collaborative information resource. *Oncogene*, **1999**, 18, 7958-65	9.2	41
93	Identification of TP53 as an acute lymphocytic leukemia susceptibility gene through exome sequencing. *Pediatric Blood and Cancer*, **2013**, 60, E1-3	3	40
92	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
91	Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene. *Nature Genetics*, **1993**, 4, 367-72	36.3	38
90	Genome-wide analysis of binding sites and direct target genes of the orphan nuclear receptor NR2F1/COUP-TFI. *PLoS ONE*, **2010**, 5, e8910	3.7	33
89	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. *Experimental Hematology*, **2016**, 44, 740-4	3.1	33
88	Genomic sequencing for cancer diagnosis and therapy. *Annual Review of Medicine*, **2014**, 65, 33-48	17.4	30
87	Zebrafish dax1 is required for development of the interrenal organ, the adrenal cortex equivalent. *Molecular Endocrinology*, **2006**, 20, 2630-40		29
86	Defects in courtship and vision caused by amino acid substitutions in a putative RNA-binding protein encoded by the no-on-transient A (nonA) gene of Drosophila. *Journal of Neuroscience*, **1996**, 16, 1511-22	6.6	29
85	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). *BMC Genomics*, **2011**, 12, 311	4.5	27
84	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. *Cancer Research*, **2020**, 80, 2663-2675	10.1	25
83	An enhanced genetic model of colorectal cancer progression history. *Genome Biology*, **2019**, 20, 168	18.3	21
82	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. *Cancer Discovery*, **2021**,	24.4	21
81	Iron homeostasis regulates facultative heterochromatin assembly in adaptive genome control. *Nature Structural and Molecular Biology*, **2018**, 25, 372-383	17.6	20
80	Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. *Leukemia*, **2014**, 28, 935-8	10.7	19

79	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. *Journal of Thoracic Oncology*, **2016**, 11, 52-61	8.9	18
78	Activating MAPK1 (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. *Oncotarget*, **2017**, 8, 46065-46070	3.3	18
77	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. *Cancer Cell*, **2021**, 39, 38-53.e7	24.3	18
76	Coexistence of gain-of-function JAK2 germ line mutations with JAK2V617F in polycythemia vera. *Blood*, **2016**, 128, 2266-2270	2.2	17
75	Integrated tumor and germline whole-exome sequencing identifies mutations in MAPK and PI3K pathway genes in an adolescent with rosette-forming glioneuronal tumor of the fourth ventricle. *Journal of Physical Education and Sports Management*, **2016**, 2, a001057	2.8	17
74	Non-malignant respiratory epithelial cells preferentially proliferate from resected non-small cell lung cancer specimens cultured under conditionally reprogrammed conditions. *Oncotarget*, **2017**, 8, 11114-11126	3.3	16
73	Gene expression profiling and immune cell-type deconvolution highlight robust disease progression and survival markers in multiple cohorts of CTCL patients. *OncoImmunology*, **2018**, 7, e1467856	7.2	16
72	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. *Nature Communications*, **2020**, 11, 3644	17.4	16
71	The relationship of JAK2(V617F) and acquired UPD at chromosome 9p in polycythemia vera. *Leukemia*, **2014**, 28, 938-41	10.7	15
70	Management and outcome of pneumothoraces in patients infected with human immunodeficiency virus. *Clinical Infectious Diseases*, **1996**, 23, 624-7	11.6	15
69	Identification of genetic susceptibility to childhood cancer through analysis of genes in parallel. *Cancer Genetics*, **2011**, 204, 19-25	2.3	14
68	Deep resequencing and association analysis of schizophrenia candidate genes. *Molecular Psychiatry*, **2013**, 18, 138-40	15.1	13
67	High incidence of IDH mutations in acute myeloid leukaemia with cuplike nuclei. *British Journal of Haematology*, **2011**, 155, 125-8	4.5	13
66	Building a comprehensive genomic program for hepatocellular carcinoma. *World Journal of Surgery*, **2011**, 35, 1746-50	3.3	13
65	Overview of the development of personalized genomic medicine and surgery. *World Journal of Surgery*, **2011**, 35, 1693-9	3.3	13
64	An open access pilot freely sharing cancer genomic data from participants in Texas. *Scientific Data*, **2016**, 3, 160010	8.2	12
63	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. *Journal of Thoracic Oncology*, **2018**, 13, 1483-1495	8.9	12
62	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12

61	ITD assembler: an algorithm for internal tandem duplication discovery from short-read sequencing data. *BMC Bioinformatics*, **2016**, 17, 188	3.6	11
60	Molecular basis of altered mouse mammary tumor virus expression in the D-2 hyperplastic alveolar nodule line of BALB/c mice. *Virology*, **1985**, 143, 1-15	3.6	11
59	Mutation signatures reveal biological processes in human cancer		11
58	Framework for microRNA variant annotation and prioritization using human population and disease datasets. *Human Mutation*, **2019**, 40, 73-89	4.7	11
57	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. *Communications Biology*, **2021**, 4, 155	6.7	11
56	Common and rare variants of DAOA in bipolar disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 960-6	3.5	10
55	Selecting the right protein-scoring matrix. *Current Protocols in Bioinformatics*, **2002**, Chapter 3, Unit 3.5	24.2	10
54	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
53	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. *Cancer Research*, **2020**, 80, 3810-3819	10.1	9
52	Artificial neural network classification of Drosophila courtship song mutants. *Biological Cybernetics*, **1992**, 66, 485-96	2.8	9
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