David A Wheeler

List of Publications by Year
in descending order

243 papers	129,066 citations	1040 113 h-index	1066 233 g-index
254 all docs	254 docs citations	254 times ranked	129572 citing authors

#	Article	IF	Citations
1	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
2	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
3	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	13.7	6,879
4	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
5	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
6	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
7	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
8	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
9	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
10	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	13.7	3,483
11	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	13.7	2,839
12	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
13	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
14	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	13.7	2,625
15	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
16	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
17	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
18	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111

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19	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
20	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
21	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
22	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
23	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
24	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
25	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
26	Insights into social insects from the genome of the honeybee Apis mellifera. Nature, 2006, 443, 931-949.	13.7	1,648
27	The complete genome of an individual by massively parallel DNA sequencing. Nature, 2008, 452, 872-876.	13.7	1,635
28	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in NOTCH1. Science, 2011, 333, 1154-1157.	6.0	1,568
29	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
30	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
31	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	6.0	1,283
32	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	13.9	1,040
33	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
34	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	13.7	1,020
35	The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337.	13.7	985
36	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801

#	Article	IF	Citations
37	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
38	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. Science, 2009, 324, 528-532.	6.0	746
39	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
40	Whole-Genome Sequencing in a Patient with Charcotâ€“Marieâ€“Tooth Neuropathy. New England Journal of Medicine, 2010, 362, 1181-1191.	13.9	698
41	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
42	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	7.7	665
43	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. Nature Genetics, 2014, 46, 1267-1273.	9.4	655
44	Landscape of Somatic Retrotransposition in Human Cancers. Science, 2012, 337, 967-971.	6.0	631
45	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
46	Direct selection of human genomic loci by microarray hybridization. Nature Methods, 2007, 4, 903-905.	9.0	617
47	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
48	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
49	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. Clinical Cancer Research, 2014, 20, 6582-6592.	3.2	493
50	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. Cancer Discovery, 2013, 3, 770-781.	7.7	484
51	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	7.7	482
52	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
53	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, 617-627.	2.6	466
54	Comparative genome sequencing of Drosophila pseudoobscura: Chromosomal, gene, and cis-element evolution. Genome Research, 2005, 15, 1-18.	2.4	453

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55	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3â€²-UTR landscape across seven tumour types. Nature Communications, 2014, 5, 5274.	5.8	430
56	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. Cell, 2019, 179, 964-983.e31.	13.5	430
57	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
58	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
59	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
60	Molecular analysis of the period locus in Drosophila melanogaster and identification of a transcript involved in biological rhythms. Cell, 1984, 38, 701-710.	13.5	382
61	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5.	2.9	382
62	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. JAMA Oncology, 2016, 2, 616.	3.4	378
63	Effect of Oral Methylprednisolone on Clinical Outcomes in Patients With IgA Nephropathy. JAMA - Journal of the American Medical Association, 2017, 318, 432.	3.8	376
64	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. Cancer Discovery, 2018, 8, 730-749.	7.7	367
65	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. Cell, 2016, 164, 538-549.	13.5	363
66	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. Blood, 2014, 124, 3007-3015.	0.6	352
67	P-element transformation with period locus DNA restores rhythmicity to mutant, arrhythmic drosophila melanogaster. Cell, 1984, 39, 369-376.	13.5	347
68	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
69	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. Nature Genetics, 2011, 43, 189-196.	9.4	326
70	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	2.9	324
71	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.	3.3	317
72	Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence. Genome Biology, 2002, 3, research0079.1.	13.9	313

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73	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	2.9	298
74	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	13.5	296
75	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. Nature Communications, 2015, 6, 6604.	5.8	281
76	Behavior in Light-Dark Cycles of Drosophila Mutants That Are Arrhythmic, Blind, or Both. Journal of Biological Rhythms, 1993, 8, 67-94.	1.4	280
77	Genomic profiling of SÃ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. Nature Genetics, 2015, 47, 1426-1434.	9.4	276
78	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. Cell, 2011, 145, 1036-1048.	13.5	274
79	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
80	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	9.4	270
81	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
82	Orphan Nuclear Receptor LRH-1 Is Required To Maintain Oct4 Expression at the Epiblast Stage of Embryonic Development. Molecular and Cellular Biology, 2005, 25, 3492-3505.	1.1	265
83	A common allele in RPGRIP1L is a modifier of retinal degeneration in ciliopathies. Nature Genetics, 2009, 41, 739-745.	9.4	255
84	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. Nature Genetics, 2017, 49, 1487-1494.	9.4	255
85	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. Cell, 2011, 144, 703-718.	13.5	246
86	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. Genome Research, 2014, 24, 1740-1750.	2.4	244
87	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. Cancer Cell, 2015, 27, 286-297.	7.7	244
88	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.	3.8	231
89	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. Nature Communications, 2010, 1, 131.	5.8	213
90	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. Blood, 2015, 125, 629-638.	0.6	206

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91	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.	3.3	200
92	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. Human Mutation, 2011, 32, 661-668.	1.1	195
93	Functional genomics of genes with small open reading frames (sORFs) in S. cerevisiae. Genome Research, 2006, 16, 365-373.	2.4	193
94	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. Hepatology, 2017, 65, 104-121.	3.6	192
95	Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. Genome Research, 2004, 14, 580-590.	2.4	187
96	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. Genome Research, 2007, 17, 760-774.	2.4	184
97	Novel somatic and germline mutations in intracranial germ cell tumours. Nature, 2014, 511, 241-245.	13.7	181
98	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
99	Germ-Line Transformation Involving DNA from theperiodLocus inDrosophila melanogaster: Overlapping Genomic Fragments that Restore Circadian and Ultradian Rhythmicity toper⁰andper^{â”}Mutants. Journal of Neurogenetics, 1986, 3, 249-291.	0.6	176
100	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	9.4	176
101	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. European Urology, 2017, 72, 641-649.	0.9	170
102	A SNP discovery method to assess variant allele probability from next-generation resequencing data. Genome Research, 2010, 20, 273-280.	2.4	168
103	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, 8507-8519.	1.1	167
104	Behavior of period-altered circadian rhythm mutants ofDrosophila in light: Dark cycles (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.4	166
105	Demographic Histories and Patterns of Linkage Disequilibrium in Chinese and Indian Rhesus Macaques. Science, 2007, 316, 240-243.	6.0	161
106	Assessing structural variation in a personal genomeâ€”towards a human reference diploid genome. BMC Genomics, 2015, 16, 286.	1.2	153
107	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.	2.9	134
108	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. Cancer Research, 2016, 76, 2197-2205.	0.4	133

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109	From human genome to cancer genome: The first decade. Genome Research, 2013, 23, 1054-1062.	2.4	132
110	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. Nature Communications, 2015, 6, 8891.	5.8	126
111	Squamous Cell Carcinoma of the Oral Tongue in Young Non-Smokers Is Genomically Similar to Tumors in Older Smokers. Clinical Cancer Research, 2014, 20, 3842-3848.	3.2	124
112	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. Nature Communications, 2016, 7, 12601.	5.8	123
113	BCORâ€“CCNB3 fusions are frequent in undifferentiated sarcomas of male children. Modern Pathology, 2015, 28, 575-586.	2.9	122
114	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. Blood, 2016, 128, 2533-2537.	0.6	122
115	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.	3.3	122
116	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
117	Onceâ€Daily versus Twiceâ€Daily Lopinavir/Ritonavir in Antiretroviralâ€Naive HIVâ€Positive Patients: A 48â€Week Randomized Clinical Trial. Journal of Infectious Diseases, 2004, 189, 265-272.	1.9	114
118	SNPdetector: A Software Tool for Sensitive and Accurate SNP Detection. PLoS Computational Biology, 2005, 1, e53.	1.5	109
119	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. Cell Reports, 2016, 14, 907-919.	2.9	107
120	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor-Î² Pathway. Gastroenterology, 2018, 154, 195-210.	0.6	105
121	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. PLoS ONE, 2012, 7, e34546.	1.1	104
122	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. Nature Communications, 2013, 4, 2730.	5.8	104
123	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. Cell Reports, 2019, 29, 1675-1689.e9.	2.9	103
124	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. Cell, 2018, 173, 864-878.e29.	13.5	102
125	Disruptive TP53 Mutation Is Associated with Aggressive Disease Characteristics in an Orthotopic Murine Model of Oral Tongue Cancer. Clinical Cancer Research, 2011, 17, 6658-6670.	3.2	94
126	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. Cancer Discovery, 2021, 11, 3008-3027.	7.7	88

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127	Transcription of mouse mammary tumor virus: identification of a candidate mRNA for the long terminal repeat gene product. Journal of Virology, 1983, 46, 42-49.	1.5	84
128	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.	3.2	82
129	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. Nature Communications, 2017, 8, 14098.	5.8	80
130	Phylogenetic and Structural Analyses of MMTV LTR ORF Sequences of Exogenous and Endogenous Origins. Virology, 1993, 193, 171-185.	1.1	78
131	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
132	MLH1â€silenced and nonâ€silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. Journal of Pathology, 2013, 229, 99-110.	2.1	67
133	Spectral analysis ofDrosophila courtship songs:D. melanogaster, D. simulans, and their interspecific hybrid. Behavior Genetics, 1988, 18, 675-703.	1.4	66
134	Effects of <scp>TP53</scp> mutational status on gene expression patterns across 10 human cancer types. Journal of Pathology, 2014, 232, 522-533.	2.1	65
135	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, 91-98.	0.8	65
136	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. Cancer Cell, 2021, 39, 38-53.e7.	7.7	65
137	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. Journal of Clinical Investigation, 2016, 126, 2881-2892.	3.9	65
138	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. Nature Communications, 2015, 6, 10013.	5.8	64
139	Spectral analysis of courtship songs in behavioral mutants ofDrosophila melanogaster. Behavior Genetics, 1989, 19, 503-528.	1.4	59
140	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. Genome Biology, 2014, 15, 443.	3.8	59
141	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. Nature Communications, 2020, 11, 3644.	5.8	55
142	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. Cancer Research, 2020, 80, 2663-2675.	0.4	55
143	Mammalian hexokinase 1: Evolutionary conservation and structure to function analysis. Genomics, 1991, 11, 1014-1024.	1.3	54
144	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. Journal of Neuropathology and Experimental Neurology, 2017, 76, nlw116.	0.9	54

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145	Kallmann syndrome gene on the X and Y chromosomes: implications for evolutionary divergence of human sex chromosomes. Nature Genetics, 1992, 2, 311-314.	9.4	53
146	The DNA sequence, annotation and analysis of human chromosome 3. Nature, 2006, 440, 1194-1198.	13.7	53
147	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.	3.7	52
148	The finished DNA sequence of human chromosome 12. Nature, 2006, 440, 346-351.	13.7	51
149	Novel MicroRNA Candidates and miRNA-mRNA Pairs in Embryonic Stem (ES) Cells. PLoS ONE, 2008, 3, e2548.	1.1	48
150	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. Experimental Hematology, 2016, 44, 740-744.	0.2	48
151	Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene. Nature Genetics, 1993, 4, 367-372.	9.4	44
152	The Breast Cancer Gene Database: a collaborative information resource. Oncogene, 1999, 18, 7958-7965.	2.6	44
153	Identification of TP53 as an acute lymphocytic leukemia susceptibility gene through exome sequencing. Pediatric Blood and Cancer, 2013, 60, E1-3.	0.8	44
154	Genome-Wide Analysis of Binding Sites and Direct Target Genes of the Orphan Nuclear Receptor NR2F1/COUP-TFI. PLoS ONE, 2010, 5, e8910.	1.1	41
155	Genotypeâ€“Environment mismatch of kelp forests under climate change. Molecular Ecology, 2021, 30, 3730-3746.	2.0	39
156	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, 1511-1522.	1.7	38
157	Zebrafish dax1 Is Required for Development of the Interrenal Organ, the Adrenal Cortex Equivalent. Molecular Endocrinology, 2006, 20, 2630-2640.	3.7	36
158	Genomic Sequencing for Cancer Diagnosis and Therapy. Annual Review of Medicine, 2014, 65, 33-48.	5.0	35
159	An enhanced genetic model of colorectal cancer progression history. Genome Biology, 2019, 20, 168.	3.8	34
160	Differences in Breast and Colorectal Cancer Screening Adherence Among Women Residing in Urban and Rural Communities in the United States. JAMA Network Open, 2021, 4, e2128000.	2.8	34
161	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (Macaca mulatta). BMC Genomics, 2011, 12, 311.	1.2	30
162	Iron homeostasis regulates facultative heterochromatin assembly in adaptive genome control. Nature Structural and Molecular Biology, 2018, 25, 372-383.	3.6	28

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163	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. Journal of Thoracic Oncology, 2016, 11, 52-61.	0.5	27
164	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
165	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
166	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.	2.1	24
167	Activating MAPK1 (ERK2) mutation in an aggressive case of disseminated juvenile xanthogranuloma. Oncotarget, 2017, 8, 46065-46070.	0.8	24
168	Whole-exome sequencing of polycythemia vera revealed novel driver genes and somatic mutation shared by T cells and granulocytes. Leukemia, 2014, 28, 935-938.	3.3	22
169	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.	0.8	22
170	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. Journal of Thoracic Oncology, 2018, 13, 1483-1495.	0.5	22
171	Coexistence of gain-of-function JAK2 germ line mutations with JAK2V617F in polycythemia vera. Blood, 2016, 128, 2266-2270.	0.6	21
172	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.	0.5	21
173	TOR targets an RNA processing network to regulate facultative heterochromatin, developmental gene expression and cell proliferation. Nature Cell Biology, 2021, 23, 243-256.	4.6	20
174	Management and Outcome of Pneumothoraces in Patients Infected with Human Immunodeficiency Virus. Clinical Infectious Diseases, 1996, 23, 624-627.	2.9	19
175	An open access pilot freely sharing cancer genomic data from participants in Texas. Scientific Data, 2016, 3, 160010.	2.4	19
176	Overview of the Development of Personalized Genomic Medicine and Surgery. World Journal of Surgery, 2011, 35, 1693-1699.	0.8	18
177	The relationship of JAK2V617F and acquired UPD at chromosome 9p in polycythemia vera. Leukemia, 2014, 28, 938-941.	3.3	18
178	Framework for microRNA variant annotation and prioritization using human population and disease datasets. Human Mutation, 2019, 40, 73-89.	1.1	18
179	Accumulation of Molecular Aberrations Distinctive to Hepatocellular Carcinoma Progression. Cancer Research, 2020, 80, 3810-3819.	0.4	18
180	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. Journal of the National Cancer Institute, 2021, 113, 27-37.	3.0	17

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181	High incidence of IDH mutations in acute myeloid leukaemia with cuplike nuclei. British Journal of Haematology, 2011, 155, 125-128.	1.2	16
182	ITD assembler: an algorithm for internal tandem duplication discovery from short-read sequencing data. BMC Bioinformatics, 2016, 17, 188.	1.2	16
183	RNAseqCNV: analysis of large-scale copy number variations from RNA-seq data. Leukemia, 2022, 36, 1492-1498.	3.3	16
184	Building a Comprehensive Genomic Program for Hepatocellular Carcinoma. World Journal of Surgery, 2011, 35, 1746-1750.	0.8	15
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