

David A Wheeler

List of Publications by Year in descending order

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Version: 2024-02-01

243
papers

129,066
citations

1046

113
h-index

1072

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. <i>Nature</i> , 2010, 467, 1061-1073.	27.8	7,209
2	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	27.8	7,168
3	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	27.8	6,879
4	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	27.8	6,541
5	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
6	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	27.8	4,572
7	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	27.8	4,137
8	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	27.8	4,075
9	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
10	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	27.8	3,483
11	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	27.8	2,839
12	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
13	Somatic mutations affect key pathways in lung adenocarcinoma. <i>Nature</i> , 2008, 455, 1069-1075.	27.8	2,694
14	Integrating common and rare genetic variation in diverse human populations. <i>Nature</i> , 2010, 467, 52-58.	27.8	2,625
15	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	28.9	2,318
16	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	28.9	2,277
17	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
18	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111

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19	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	27.8	2,104
20	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
21	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
22	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	27.8	1,788
23	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
24	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	28.9	1,718
25	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
26	Insights into social insects from the genome of the honeybee <i>Apis mellifera</i> . <i>Nature</i> , 2006, 443, 931-949.	27.8	1,648
27	The complete genome of an individual by massively parallel DNA sequencing. <i>Nature</i> , 2008, 452, 872-876.	27.8	1,635
28	Exome Sequencing of Head and Neck Squamous Cell Carcinoma Reveals Inactivating Mutations in <i>NOTCH1</i> . <i>Science</i> , 2011, 333, 1154-1157.	12.6	1,568
29	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
30	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
31	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
32	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	27.0	1,040
33	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
34	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	27.8	1,020
35	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	27.8	985
36	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801

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37	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	16.8	750
38	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	12.6	746
39	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
40	Whole-Genome Sequencing in a Patient with Charcotâ€“Marieâ€“Tooth Neuropathy. <i>New England Journal of Medicine</i> , 2010, 362, 1181-1191.	27.0	698
41	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.4	683
42	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	16.8	665
43	Trans-ancestry mutational landscape of hepatocellular carcinoma genomes. <i>Nature Genetics</i> , 2014, 46, 1267-1273.	21.4	655
44	Landscape of Somatic Retrotransposition in Human Cancers. <i>Science</i> , 2012, 337, 967-971.	12.6	631
45	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
46	Direct selection of human genomic loci by microarray hybridization. <i>Nature Methods</i> , 2007, 4, 903-905.	19.0	617
47	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.2	605
48	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	523
49	Mutational Landscape of Aggressive Cutaneous Squamous Cell Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 6582-6592.	7.0	493
50	Integrative Genomic Characterization of Oral Squamous Cell Carcinoma Identifies Frequent Somatic Drivers. <i>Cancer Discovery</i> , 2013, 3, 770-781.	9.4	484
51	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	16.8	482
52	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
53	Mutations in Smooth Muscle Alpha-Actin (ACTA2) Cause Coronary Artery Disease, Stroke, and Moyamoya Disease, Along with Thoracic Aortic Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 617-627.	6.2	466
54	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	5.5	453

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55	Dynamic analyses of alternative polyadenylation from RNA-seq reveal a 3' UTR landscape across seven tumour types. <i>Nature Communications</i> , 2014, 5, 5274.	12.8	430
56	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
57	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
58	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
59	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
60	Molecular analysis of the period locus in <i>Drosophila melanogaster</i> and identification of a transcript involved in biological rhythms. <i>Cell</i> , 1984, 38, 701-710.	28.9	382
61	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019, 28, 1370-1384.e5.	6.4	382
62	Diagnostic Yield of Clinical Tumor and Germline Whole-Exome Sequencing for Children With Solid Tumors. <i>JAMA Oncology</i> , 2016, 2, 616.	7.1	378
63	Effect of Oral Methylprednisolone on Clinical Outcomes in Patients With IgA Nephropathy. <i>JAMA - Journal of the American Medical Association</i> , 2017, 318, 432.	7.4	376
64	Genetic Mechanisms of Immune Evasion in Colorectal Cancer. <i>Cancer Discovery</i> , 2018, 8, 730-749.	9.4	367
65	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , 2016, 164, 538-549.	28.9	363
66	Mutually exclusive recurrent somatic mutations in MAP2K1 and BRAF support a central role for ERK activation in LCH pathogenesis. <i>Blood</i> , 2014, 124, 3007-3015.	1.4	352
67	P-element transformation with period locus DNA restores rhythmicity to mutant, arrhythmic <i>drosophila melanogaster</i> . <i>Cell</i> , 1984, 39, 369-376.	28.9	347
68	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	333
69	TTC21B contributes both causal and modifying alleles across the ciliopathy spectrum. <i>Nature Genetics</i> , 2011, 43, 189-196.	21.4	326
70	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	324
71	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15544-15549.	7.1	317
72	Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence. <i>Genome Biology</i> , 2002, 3, research0079.1.	9.6	313

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73	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016, 14, 2476-2489.	6.4	298
74	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
75	Rise and fall of subclones from diagnosis to relapse in pediatric B-acute lymphoblastic leukaemia. <i>Nature Communications</i> , 2015, 6, 6604.	12.8	281
76	Behavior in Light-Dark Cycles of <i>Drosophila</i> Mutants That Are Arrhythmic, Blind, or Both. <i>Journal of Biological Rhythms</i> , 1993, 8, 67-94.	2.6	280
77	Genomic profiling of SÅ©zary syndrome identifies alterations of key T cell signaling and differentiation genes. <i>Nature Genetics</i> , 2015, 47, 1426-1434.	21.4	276
78	Exome Sequencing of Ion Channel Genes Reveals Complex Profiles Confounding Personal Risk Assessment in Epilepsy. <i>Cell</i> , 2011, 145, 1036-1048.	28.9	274
79	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
80	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 1226-1231.	21.4	270
81	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. <i>Nature Communications</i> , 2015, 6, 10001.	12.8	266
82	Orphan Nuclear Receptor LRH-1 Is Required To Maintain Oct4 Expression at the Epiblast Stage of Embryonic Development. <i>Molecular and Cellular Biology</i> , 2005, 25, 3492-3505.	2.3	265
83	A common allele in RPGRI1L is a modifier of retinal degeneration in ciliopathies. <i>Nature Genetics</i> , 2009, 41, 739-745.	21.4	255
84	A Children's Oncology Group and TARGET initiative exploring the genetic landscape of Wilms tumor. <i>Nature Genetics</i> , 2017, 49, 1487-1494.	21.4	255
85	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. <i>Cell</i> , 2011, 144, 703-718.	28.9	246
86	Exonuclease mutations in DNA polymerase epsilon reveal replication strand specific mutation patterns and human origins of replication. <i>Genome Research</i> , 2014, 24, 1740-1750.	5.5	244
87	Recurrent DGCR8, DROSHA, and SIX Homeodomain Mutations in Favorable Histology Wilms Tumors. <i>Cancer Cell</i> , 2015, 27, 286-297.	16.8	244
88	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. <i>Genome Biology</i> , 2016, 17, 178.	8.8	231
89	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. <i>Nature Communications</i> , 2010, 1, 131.	12.8	213
90	Dnmt3a loss predisposes murine hematopoietic stem cells to malignant transformation. <i>Blood</i> , 2015, 125, 629-638.	1.4	206

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91	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E1128-36.	7.1	200
92	Prediction of missense mutation functionality depends on both the algorithm and sequence alignment employed. <i>Human Mutation</i> , 2011, 32, 661-668.	2.5	195
93	Functional genomics of genes with small open reading frames (sORFs) in <i>S. cerevisiae</i> . <i>Genome Research</i> , 2006, 16, 365-373.	5.5	193
94	Genomic analysis of hepatoblastoma identifies distinct molecular and prognostic subgroups. <i>Hepatology</i> , 2017, 65, 104-121.	7.3	192
95	Genomic Analysis of the Nuclear Receptor Family: New Insights Into Structure, Regulation, and Evolution From the Rat Genome. <i>Genome Research</i> , 2004, 14, 580-590.	5.5	187
96	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	5.5	184
97	Novel somatic and germline mutations in intracranial germ cell tumours. <i>Nature</i> , 2014, 511, 241-245.	27.8	181
98	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
99	Germ-Line Transformation Involving DNA from the <i>period</i> Locus in <i>Drosophila melanogaster</i> : Overlapping Genomic Fragments that Restore Circadian and Ultradian Rhythmicity to <i>per⁰</i> and <i>per^Δ</i> Mutants. <i>Journal of Neurogenetics</i> , 1986, 3, 249-291.	1.4	176
100	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013, 45, 767-775.	21.4	176
101	Comprehensive Genomic Characterization of Upper Tract Urothelial Carcinoma. <i>European Urology</i> , 2017, 72, 641-649.	1.9	170
102	A SNP discovery method to assess variant allele probability from next-generation resequencing data. <i>Genome Research</i> , 2010, 20, 273-280.	5.5	168
103	Orphan Nuclear Receptor GCNF Is Required for the Repression of Pluripotency Genes during Retinoic Acid-Induced Embryonic Stem Cell Differentiation. <i>Molecular and Cellular Biology</i> , 2005, 25, 8507-8519.	2.3	167
104	Behavior of period-altered circadian rhythm mutants of <i>Drosophila</i> in light: Dark cycles (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 2	0.7	166
105	Demographic Histories and Patterns of Linkage Disequilibrium in Chinese and Indian Rhesus Macaques. <i>Science</i> , 2007, 316, 240-243.	12.6	161
106	Assessing structural variation in a personal genome towards a human reference diploid genome. <i>BMC Genomics</i> , 2015, 16, 286.	2.8	153
107	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.2	134
108	Genomic Profiling of Pediatric Acute Myeloid Leukemia Reveals a Changing Mutational Landscape from Disease Diagnosis to Relapse. <i>Cancer Research</i> , 2016, 76, 2197-2205.	0.9	133

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109	From human genome to cancer genome: The first decade. <i>Genome Research</i> , 2013, 23, 1054-1062.	5.5	132
110	Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. <i>Nature Communications</i> , 2015, 6, 8891.	12.8	126
111	Squamous Cell Carcinoma of the Oral Tongue in Young Non-Smokers Is Genomically Similar to Tumors in Older Smokers. <i>Clinical Cancer Research</i> , 2014, 20, 3842-3848.	7.0	124
112	Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. <i>Nature Communications</i> , 2016, 7, 12601.	12.8	123
113	BCOR-CCNB3 fusions are frequent in undifferentiated sarcomas of male children. <i>Modern Pathology</i> , 2015, 28, 575-586.	5.5	122
114	Alternative genetic mechanisms of BRAF activation in Langerhans cell histiocytosis. <i>Blood</i> , 2016, 128, 2533-2537.	1.4	122
115	Molecular profiling predicts meningioma recurrence and reveals loss of DREAM complex repression in aggressive tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21715-21726.	7.1	122
116	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	119
117	Once-Daily versus Twice-Daily Lopinavir/Ritonavir in Antiretroviral-Naive HIV-Positive Patients: A 48-Week Randomized Clinical Trial. <i>Journal of Infectious Diseases</i> , 2004, 189, 265-272.	4.0	114
118	SNPdetector: A Software Tool for Sensitive and Accurate SNP Detection. <i>PLoS Computational Biology</i> , 2005, 1, e53.	3.2	109
119	Ampullary Cancers Harbor ELF3 Tumor Suppressor Gene Mutations and Exhibit Frequent WNT Dysregulation. <i>Cell Reports</i> , 2016, 14, 907-919.	6.4	107
120	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- β Pathway. <i>Gastroenterology</i> , 2018, 154, 195-210.	1.3	105
121	Integrated Analyses of microRNAs Demonstrate Their Widespread Influence on Gene Expression in High-Grade Serous Ovarian Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34546.	2.5	104
122	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. <i>Nature Communications</i> , 2013, 4, 2730.	12.8	104
123	Genomic Profiling of Childhood Tumor Patient-Derived Xenograft Models to Enable Rational Clinical Trial Design. <i>Cell Reports</i> , 2019, 29, 1675-1689.e9.	6.4	103
124	Chemistry-First Approach for Nomination of Personalized Treatment in Lung Cancer. <i>Cell</i> , 2018, 173, 864-878.e29.	28.9	102
125	Disruptive TP53 Mutation Is Associated with Aggressive Disease Characteristics in an Orthotopic Murine Model of Oral Tongue Cancer. <i>Clinical Cancer Research</i> , 2011, 17, 6658-6670.	7.0	94
126	Genomes for Kids: The Scope of Pathogenic Mutations in Pediatric Cancer Revealed by Comprehensive DNA and RNA Sequencing. <i>Cancer Discovery</i> , 2021, 11, 3008-3027.	9.4	88

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127	Transcription of mouse mammary tumor virus: identification of a candidate mRNA for the long terminal repeat gene product. <i>Journal of Virology</i> , 1983, 46, 42-49.	3.4	84
128	Significance of TP53 Mutation in Wilms Tumors with Diffuse Anaplasia: A Report from the Children's Oncology Group. <i>Clinical Cancer Research</i> , 2016, 22, 5582-5591.	7.0	82
129	SMARCA4-inactivating mutations increase sensitivity to Aurora kinase A inhibitor VX-680 in non-small cell lung cancers. <i>Nature Communications</i> , 2017, 8, 14098.	12.8	80
130	Phylogenetic and Structural Analyses of MMTV LTR ORF Sequences of Exogenous and Endogenous Origins. <i>Virology</i> , 1993, 193, 171-185.	2.4	78
131	Pathway and network analysis of more than 2500 whole cancer genomes. <i>Nature Communications</i> , 2020, 11, 729.	12.8	73
132	MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. <i>Journal of Pathology</i> , 2013, 229, 99-110.	4.5	67
133	Spectral analysis of <i>Drosophila</i> courtship songs: <i>D. melanogaster</i> , <i>D. simulans</i> , and their interspecific hybrid. <i>Behavior Genetics</i> , 1988, 18, 675-703.	2.1	66
134	Effects of TP53 mutational status on gene expression patterns across 10 human cancer types. <i>Journal of Pathology</i> , 2014, 232, 522-533.	4.5	65
135	Initial testing (stage 1) of the PARP inhibitor BMN 673 by the pediatric preclinical testing program: PALB2 mutation predicts exceptional <i>in vivo</i> response to BMN 673. <i>Pediatric Blood and Cancer</i> , 2015, 62, 91-98.	1.5	65
136	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	16.8	65
137	Destabilized SMC5/6 complex leads to chromosome breakage syndrome with severe lung disease. <i>Journal of Clinical Investigation</i> , 2016, 126, 2881-2892.	8.2	65
138	MLLT1 YEATS domain mutations in clinically distinctive Favourable Histology Wilms tumours. <i>Nature Communications</i> , 2015, 6, 10013.	12.8	64
139	Spectral analysis of courtship songs in behavioral mutants of <i>Drosophila melanogaster</i> . <i>Behavior Genetics</i> , 1989, 19, 503-528.	2.1	59
140	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. <i>Genome Biology</i> , 2014, 15, 443.	8.8	59
141	Landscape of somatic single nucleotide variants and indels in colorectal cancer and impact on survival. <i>Nature Communications</i> , 2020, 11, 3644.	12.8	55
142	Telomere Maintenance Mechanisms Define Clinical Outcome in High-Risk Neuroblastoma. <i>Cancer Research</i> , 2020, 80, 2663-2675.	0.9	55
143	Mammalian hexokinase 1: Evolutionary conservation and structure to function analysis. <i>Genomics</i> , 1991, 11, 1014-1024.	2.9	54
144	Genomic Alterations of Adamantinomatous and Papillary Craniopharyngioma. <i>Journal of Neuropathology and Experimental Neurology</i> , 2017, 76, n116.	1.7	54

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145	Kallmann syndrome gene on the X and Y chromosomes: implications for evolutionary divergence of human sex chromosomes. <i>Nature Genetics</i> , 1992, 2, 311-314.	21.4	53
146	The DNA sequence, annotation and analysis of human chromosome 3. <i>Nature</i> , 2006, 440, 1194-1198.	27.8	53
147	Novel estrogen response elements identified by genetic selection in yeast are differentially responsive to estrogens and antiestrogens in mammalian cells. <i>Molecular Endocrinology</i> , 1994, 8, 1193-1207.	3.7	52
148	The finished DNA sequence of human chromosome 12. <i>Nature</i> , 2006, 440, 346-351.	27.8	51
149	Novel MicroRNA Candidates and miRNA-mRNA Pairs in Embryonic Stem (ES) Cells. <i>PLoS ONE</i> , 2008, 3, e2548.	2.5	48
150	Mixed-phenotype acute leukemia (MPAL) exhibits frequent mutations in DNMT3A and activated signaling genes. <i>Experimental Hematology</i> , 2016, 44, 740-744.	0.4	48
151	Genomic scanning for expressed sequences in Xp21 identifies the glycerol kinase gene. <i>Nature Genetics</i> , 1993, 4, 367-372.	21.4	44
152	The Breast Cancer Gene Database: a collaborative information resource. <i>Oncogene</i> , 1999, 18, 7958-7965.	5.9	44
153	Identification of <i>TP53</i> as an acute lymphocytic leukemia susceptibility gene through exome sequencing. <i>Pediatric Blood and Cancer</i> , 2013, 60, E1-3.	1.5	44
154	Genome-Wide Analysis of Binding Sites and Direct Target Genes of the Orphan Nuclear Receptor NR2F1/COUP-TFI. <i>PLoS ONE</i> , 2010, 5, e8910.	2.5	41
155	Genotype-Environment mismatch of kelp forests under climate change. <i>Molecular Ecology</i> , 2021, 30, 3730-3746.	3.9	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 <i>Drosophila</i> . <i>Journal of Neuroscience</i> , 1996, 16, 1511-1522.	3.6	38
157	Zebrafish <i>dax1</i> Is Required for Development of the Interrenal Organ, the Adrenal Cortex Equivalent. <i>Molecular Endocrinology</i> , 2006, 20, 2630-2640.	3.7	36
158	Genomic Sequencing for Cancer Diagnosis and Therapy. <i>Annual Review of Medicine</i> , 2014, 65, 33-48.	12.2	35
159	An enhanced genetic model of colorectal cancer progression history. <i>Genome Biology</i> , 2019, 20, 168.	8.8	34
160	Differences in Breast and Colorectal Cancer Screening Adherence Among Women Residing in Urban and Rural Communities in the United States. <i>JAMA Network Open</i> , 2021, 4, e2128000.	5.9	34
161	Characterization of single-nucleotide variation in Indian-origin rhesus macaques (<i>Macaca mulatta</i>). <i>BMC Genomics</i> , 2011, 12, 311.	2.8	30
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