

Richard K Wilson

List of Publications by Year in descending order

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538
papers

287,283
citations

44

188
h-index

6

495
g-index

573
all docs

573
docs citations

573
times ranked

219454
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	28.3	21,074
2	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	28.3	13,998
3	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	28.3	10,282
4	Structure, function and diversity of the healthy human microbiome. <i>Nature</i> , 2012, 486, 207-214.	28.3	9,614
5	Analysis of the genome sequence of the flowering plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 796-815.	28.3	8,336
6	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010, 467, 1061-1073.	28.3	7,209
7	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	28.3	7,199
8	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	28.3	6,879
9	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	28.3	6,541
10	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	28.3	6,319
11	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010, 17, 98-110.	17.0	6,138
12	The International HapMap Project. <i>Nature</i> , 2003, 426, 789-796.	28.3	5,735
13	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	28.3	4,709
14	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	28.3	4,572
15	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	27.4	4,139
16	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007, 449, 851-861.	28.3	4,137
17	EGF receptor gene mutations are common in lung cancers from "never smokers" and are associated with sensitivity of tumors to gefitinib and erlotinib. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13306-13311.	7.3	4,106
18	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. <i>Genome Research</i> , 2012, 22, 568-576.	5.6	4,086

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19	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	28.3	4,075
20	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	29.4	3,979
21	Mutational landscape and significance across 12 major cancer types. <i>Nature</i> , 2013, 502, 333-339.	28.3	3,695
22	The B73 Maize Genome: Complexity, Diversity, and Dynamics. <i>Science</i> , 2009, 326, 1112-1115.	12.9	3,612
23	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. <i>Genome Research</i> , 2005, 15, 1034-1050.	5.6	3,517
24	The map-based sequence of the rice genome. <i>Nature</i> , 2005, 436, 793-800.	28.3	3,365
25	Somatic mutations affect key pathways in lung adenocarcinoma. <i>Nature</i> , 2008, 455, 1069-1075.	28.3	2,694
26	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. <i>Nature</i> , 2004, 432, 695-716.	28.3	2,421
27	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	29.4	2,277
28	A framework for human microbiome research. <i>Nature</i> , 2012, 486, 215-221.	28.3	2,249
29	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	28.3	2,222
30	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	28.3	2,114
31	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	17.0	2,078
32	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. <i>New England Journal of Medicine</i> , 2009, 361, 1058-1066.	27.4	2,009
33	The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. <i>Nature</i> , 2003, 423, 825-837.	28.3	1,887
34	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	28.3	1,886
35	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. <i>Nature</i> , 2012, 481, 506-510.	28.3	1,795
36	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007, 449, 913-918.	28.3	1,788

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37	<i>DNMT3A</i> Mutations in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2010, 363, 2424-2433.	27.4	1,777
38	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.	29.4	1,718
39	Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium LT2. <i>Nature</i> , 2001, 413, 852-856.	28.3	1,712
40	2.2 Mb of contiguous nucleotide sequence from chromosome III of <i>C. elegans</i> . <i>Nature</i> , 1994, 368, 32-38.	28.3	1,578
41	Age-related mutations associated with clonal hematopoietic expansion and malignancies. <i>Nature Medicine</i> , 2014, 20, 1472-1478.	31.0	1,533
42	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	29.4	1,485
43	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. <i>Nature</i> , 2012, 481, 157-163.	28.3	1,430
44	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	29.4	1,417
45	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. <i>Nature Genetics</i> , 2012, 44, 251-253.	21.7	1,402
46	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. <i>Cell</i> , 2012, 150, 264-278.	29.4	1,365
47	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. <i>Nature Methods</i> , 2009, 6, 677-681.	19.3	1,322
48	De Novo Gene Disruptions in Children on the Autistic Spectrum. <i>Neuron</i> , 2012, 74, 285-299.	8.3	1,311
49	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.9	1,283
50	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. <i>Nature</i> , 2008, 456, 66-72.	28.3	1,275
51	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. <i>Bioinformatics</i> , 2009, 25, 2283-2285.	4.2	1,193
52	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. <i>New England Journal of Medicine</i> , 2014, 371, 1005-1015.	27.4	1,161
53	The DNA sequence of human chromosome 22. <i>Nature</i> , 1999, 402, 489-495.	28.3	1,086
54	Genome remodelling in a basal-like breast cancer metastasis and xenograft. <i>Nature</i> , 2010, 464, 999-1005.	28.3	1,077

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55	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. <i>Cell</i> , 2012, 150, 1121-1134.	29.4	1,038
56	Characterizing the cancer genome in lung adenocarcinoma. <i>Nature</i> , 2007, 450, 893-898.	28.3	1,020
57	A high-resolution map of human evolutionary constraint using 29 mammals. <i>Nature</i> , 2011, 478, 476-482.	28.3	1,016
58	Nibrin, a Novel DNA Double-Strand Break Repair Protein, Is Mutated in Nijmegen Breakage Syndrome. <i>Cell</i> , 1998, 93, 467-476.	29.4	989
59	The DNA sequence of the human X chromosome. <i>Nature</i> , 2005, 434, 325-337.	28.3	985
60	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008, 453, 56-64.	28.3	983
61	Germline Mutations in Predisposition Genes in Pediatric Cancer. <i>New England Journal of Medicine</i> , 2015, 373, 2336-2346.	27.4	949
62	Whole-genome analysis informs breast cancer response to aromatase inhibition. <i>Nature</i> , 2012, 486, 353-360.	28.3	922
63	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.9	895
64	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. <i>Nature Genetics</i> , 2014, 46, 444-450.	21.7	871
65	A physical map of the human genome. <i>Nature</i> , 2001, 409, 934-941.	28.3	865
66	The Next-Generation Sequencing Revolution and Its Impact on Genomics. <i>Cell</i> , 2013, 155, 27-38.	29.4	856
67	The Genome Sequence of <i>Caenorhabditis briggsae</i> : A Platform for Comparative Genomics. <i>PLoS Biology</i> , 2003, 1, e45.	5.8	812
68	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.5	801
69	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	28.3	770
70	Great ape genetic diversity and population history. <i>Nature</i> , 2013, 499, 471-475.	28.3	768
71	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	17.0	750
72	Novel mutations target distinct subgroups of medulloblastoma. <i>Nature</i> , 2012, 488, 43-48.	28.3	742

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73	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	29.4	738
74	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. <i>Genome Research</i> , 2017, 27, 849-864.	5.6	728
75	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.9	708
76	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. <i>Nature Genetics</i> , 2013, 45, 602-612.	21.7	704
77	Elephant shark genome provides unique insights into gnathostome evolution. <i>Nature</i> , 2014, 505, 174-179.	28.3	689
78	Clonal Architecture of Secondary Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2012, 366, 1090-1098.	27.4	688
79	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. <i>Nature</i> , 2015, 518, 552-555.	28.3	685
80	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.5	683
81	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	28.3	663
82	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. <i>New England Journal of Medicine</i> , 2016, 375, 2023-2036.	27.4	663
83	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	28.3	657
84	Landscape of Somatic Retrotransposition in Human Cancers. <i>Science</i> , 2012, 337, 967-971.	12.9	631
85	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	17.0	623
86	A Catalog of Reference Genomes from the Human Microbiome. <i>Science</i> , 2010, 328, 994-999.	12.9	621
87	The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. <i>Nature Genetics</i> , 2001, 29, 279-286.	21.7	617
88	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5859-5864.	7.3	612
89	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.3	605
90	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	7.3	589

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91	Sequencing of the sea lamprey (<i>Petromyzon marinus</i>) genome provides insights into vertebrate evolution. <i>Nature Genetics</i> , 2013, 45, 415-421.	21.7	588
92	The genomic landscape of hypodiploid acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2013, 45, 242-252.	21.7	588
93	MuSIC: Identifying mutational significance in cancer genomes. <i>Genome Research</i> , 2012, 22, 1589-1598.	5.6	586
94	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. <i>Cell Reports</i> , 2014, 7, 104-112.	6.5	583
95	The complete nucleotide sequence of the <i>Xenopus laevis</i> mitochondrial genome. <i>Journal of Biological Chemistry</i> , 1985, 260, 9759-74.	3.5	573
96	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. <i>Bioinformatics</i> , 2012, 28, 311-317.	4.2	566
97	C11orf95-RELA fusions drive oncogenic NF- κ B signalling in ependymoma. <i>Nature</i> , 2014, 506, 451-455.	28.3	559
98	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. <i>Nature</i> , 2014, 508, 494-499.	28.3	546
99	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	28.3	541
100	Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. <i>Nature</i> , 2003, 423, 873-876.	28.3	540
101	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. <i>Cell Reports</i> , 2013, 4, 1116-1130.	6.5	539
102	The <i>C. elegans</i> genome sequencing project: a beginning. <i>Nature</i> , 1992, 356, 37-41.	28.3	518
103	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. <i>Nature Genetics</i> , 2012, 44, 53-57.	21.7	513
104	Evolution of Symbiotic Bacteria in the Distal Human Intestine. <i>PLoS Biology</i> , 2007, 5, e156.	5.8	490
105	Recurrent DNMT3A mutations in patients with myelodysplastic syndromes. <i>Leukemia</i> , 2011, 25, 1153-1158.	7.4	483
106	Implementing genomic medicine in the clinic: the future is here. <i>Genetics in Medicine</i> , 2013, 15, 258-267.	2.5	472
107	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013, 500, 335-339.	28.3	468
108	CIVIC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. <i>Nature Genetics</i> , 2017, 49, 170-174.	21.7	460

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109	Modernizing Reference Genome Assemblies. <i>PLoS Biology</i> , 2011, 9, e1001091.	5.8	458
110	Structure, Organization and Polymorphism of Murine and Human T-Cell Receptor α and β Chain Gene Families. <i>Immunological Reviews</i> , 1988, 101, 149-172.	6.1	456
111	Genomic and metabolic adaptations of <i>Methanobrevibacter smithii</i> to the human gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10643-10648.	7.3	451
112	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <i>Nature Methods</i> , 2011, 8, 652-654.	19.3	451
113	DGIdb: mining the druggable genome. <i>Nature Methods</i> , 2013, 10, 1209-1210.	19.3	443
114	A novel retinoblastoma therapy from genomic and epigenetic analyses. <i>Nature</i> , 2012, 481, 329-334.	28.3	442
115	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of <i>STAG2</i> and <i>TP53</i> Mutations. <i>Cancer Discovery</i> , 2014, 4, 1342-1353.	9.6	418
116	Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 769-777.	28.3	413
117	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.5	407
118	High Throughput Fingerprint Analysis of Large-Insert Clones. <i>Genome Research</i> , 1997, 7, 1072-1084.	5.6	405
119	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. <i>Nature Genetics</i> , 2015, 47, 330-337.	21.7	405
120	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. <i>PLoS Computational Biology</i> , 2014, 10, e1003665.	3.3	400
121	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	17.0	400
122	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	17.0	396
123	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004, 432, 717-722.	28.3	391
124	Viral Discovery and Sequence Recovery Using DNA Microarrays. <i>PLoS Biology</i> , 2003, 1, e2.	5.8	386
125	A survey of expressed genes in <i>Caenorhabditis elegans</i> . <i>Nature Genetics</i> , 1992, 1, 114-123.	21.7	385
126	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. <i>Nature</i> , 2010, 463, 536-539.	28.3	381

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127	Whole-genome sequencing and variant discovery in <i>C. elegans</i> . <i>Nature Methods</i> , 2008, 5, 183-188.	19.3	380
128	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. <i>JAMA - Journal of the American Medical Association</i> , 2012, 307, 1062.	7.6	379
129	The R882H DNMT3A Mutation Associated with AML Dominantly Inhibits Wild-Type DNMT3A by Blocking Its Ability to Form Active Tetramers. <i>Cancer Cell</i> , 2014, 25, 442-454.	17.0	374
130	Long-read sequence assembly of the gorilla genome. <i>Science</i> , 2016, 352, aae0344.	12.9	368
131	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of <i>Salmonella enterica</i> that cause typhoid. <i>Nature Genetics</i> , 2004, 36, 1268-1274.	21.7	367
132	Characterizing the Major Structural Variant Alleles of the Human Genome. <i>Cell</i> , 2019, 176, 663-675.e19.	29.4	364
133	DGIdb 2.0: mining clinically relevant drug-gene interactions. <i>Nucleic Acids Research</i> , 2016, 44, D1036-D1044.	14.9	359
134	A genome-wide comparison of recent chimpanzee and human segmental duplications. <i>Nature</i> , 2005, 437, 88-93.	28.3	353
135	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. <i>Nature Communications</i> , 2014, 5, 3630.	13.1	342
136	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. <i>Cell</i> , 2012, 149, 912-922.	29.4	341
137	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.5	333
138	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2014, 25, 379-392.	17.0	330
139	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	7.3	329
140	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	6.5	329
141	Discovery and genotyping of structural variation from long-read haploid genome sequence data. <i>Genome Research</i> , 2017, 27, 677-685.	5.6	323
142	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. <i>New England Journal of Medicine</i> , 2018, 379, 2330-2341.	27.4	322
143	Gibbon genome and the fast karyotype evolution of small apes. <i>Nature</i> , 2014, 513, 195-201.	28.3	320
144	The Pediatric Cancer Genome Project. <i>Nature Genetics</i> , 2012, 44, 619-622.	21.7	315

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145	The <i>Pristionchus pacificus</i> genome provides a unique perspective on nematode lifestyle and parasitism. <i>Nature Genetics</i> , 2008, 40, 1193-1198.	21.7	310
146	Genetic variation and the de novo assembly of human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 627-640.	16.6	310
147	High-resolution comparative analysis of great ape genomes. <i>Science</i> , 2018, 360, .	12.9	304
148	Complete nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome VIII. <i>Science</i> , 1994, 265, 2077-2082.	12.9	303
149	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 314, 811.	7.6	302
150	Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells. <i>Nature</i> , 1984, 309, 806-810.	28.3	294
151	Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes. <i>Cell</i> , 2014, 159, 800-813.	29.4	291
152	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. <i>Acta Neuropathologica</i> , 2016, 131, 833-845.	7.9	288
153	The draft genome of the parasitic nematode <i>Trichinella spiralis</i> . <i>Nature Genetics</i> , 2011, 43, 228-235.	21.7	285
154	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	6.3	284
155	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17230-17235.	7.3	281
156	Sequence and Comparative Analysis of the Maize NB Mitochondrial Genome. <i>Plant Physiology</i> , 2004, 136, 3486-3503.	4.9	279
157	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	9.6	276
158	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	29.4	272
159	Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. <i>Leukemia</i> , 2013, 27, 1275-1282.	7.4	260
160	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.9	254
161	Integrated analysis of germline and somatic variants in ovarian cancer. <i>Nature Communications</i> , 2014, 5, 3156.	13.1	253
162	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. <i>Cancer Cell</i> , 2013, 24, 710-724.	17.0	252

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163	Genome of the house fly, <i>Musca domestica</i> L., a global vector of diseases with adaptations to a septic environment. <i>Genome Biology</i> , 2014, 15, 466.	9.0	252
164	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. <i>Nature Genetics</i> , 2013, 45, 567-572.	21.7	251
165	A Human Genome Structural Variation Sequencing Resource Reveals Insights into Mutational Mechanisms. <i>Cell</i> , 2010, 143, 837-847.	29.4	249
166	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. <i>Nature</i> , 2012, 483, 82-86.	28.3	245
167	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015, 6, 10086.	13.1	243
168	Human Genome Ultraconserved Elements Are Ultraselected. <i>Science</i> , 2007, 317, 915-915.	12.9	240
169	Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research. <i>PLoS ONE</i> , 2012, 7, e39315.	2.5	240
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