Richard K Wilson

List of Publications by Year
in descending order

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538	287,283	43 188	6 494
papers	citations	h-index	g-index

573	573	573	219454
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
3	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
4	Structure, function and diversity of the healthy human microbiome. Nature, 2012, 486, 207-214.	27.8	9,614
5	Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. Nature, 2000, 408, 796-815.	27.8	8,336
6	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	27.8	7,209
7	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
8	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	27.8	6,879
9	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
10	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
11	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	16.8	6,138
12	The International HapMap Project. Nature, 2003, 426, 789-796.	27.8	5,735
13	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
14	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
15	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
16	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
17	EGF receptor gene mutations are common in lung cancers from â€œnever smokersâ€• and are associated with sensitivity of tumors to gefitinib and erlotinib. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13306-13311.	7.1	4,106
18	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	5.5	4,086

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19	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
20	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
21	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	27.8	3,695
22	The B73 Maize Genome: Complexity, Diversity, and Dynamics. Science, 2009, 326, 1112-1115.	12.6	3,612
23	Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research, 2005, 15, 1034-1050.	5.5	3,517
24	The map-based sequence of the rice genome. Nature, 2005, 436, 793-800.	27.8	3,365
25	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	27.8	2,694
26	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
27	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
28	A framework for human microbiome research. Nature, 2012, 486, 215-221.	27.8	2,249
29	Initial sequence of the chimpanzee genome and comparison with the human genome. Nature, 2005, 437, 69-87.	27.8	2,222
30	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
31	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	16.8	2,078
32	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
33	The male-specific region of the human Y chromosome is a mosaic of discrete sequence classes. Nature, 2003, 423, 825-837.	27.8	1,887
34	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
35	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
36	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788

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37	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	27.0	1,777
38	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
39	Complete genome sequence of Salmonella enterica serovar Typhimurium LT2. Nature, 2001, 413, 852-856.	27.8	1,712
40	2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. Nature, 1994, 368, 32-38.	27.8	1,578
41	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	30.7	1,533
42	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
43	The genetic basis of early T-cell precursor acute lymphoblastic leukaemia. Nature, 2012, 481, 157-163.	27.8	1,430
44	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
45	Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. Nature Genetics, 2012, 44, 251-253.	21.4	1,402
46	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
47	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	19.0	1,322
48	De Novo Gene Disruptions in Children on the Autistic Spectrum. Neuron, 2012, 74, 285-299.	8.1	1,311
49	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
50	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
51	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	4.1	1,193
52	Targetable Kinase-Activating Lesions in Ph-like Acute Lymphoblastic Leukemia. New England Journal of Medicine, 2014, 371, 1005-1015.	27.0	1,161
53	The DNA sequence of human chromosome 22. Nature, 1999, 402, 489-495.	27.8	1,086
54	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077

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55	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
56	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	27.8	1,020
57	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	27.8	1,016
58	Nibrin, a Novel DNA Double-Strand Break Repair Protein, Is Mutated in Nijmegen Breakage Syndrome. Cell, 1998, 93, 467-476.	28.9	989
59	The DNA sequence of the human X chromosome. Nature, 2005, 434, 325-337.	27.8	985
60	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	27.8	983
61	Germline Mutations in Predisposition Genes in Pediatric Cancer. New England Journal of Medicine, 2015, 373, 2336-2346.	27.0	949
62	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
63	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	12.6	895
64	The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. Nature Genetics, 2014, 46, 444-450.	21.4	871
65	A physical map of the human genome. Nature, 2001, 409, 934-941.	27.8	865
66	The Next-Generation Sequencing Revolution and Its Impact on Genomics. Cell, 2013, 155, 27-38.	28.9	856
67	The Genome Sequence of Caenorhabditis briggsae: A Platform for Comparative Genomics. PLoS Biology, 2003, 1, e45.	5.6	812
68	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
69	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
70	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	27.8	768
71	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
72	Novel mutations target distinct subgroups of medulloblastoma. Nature, 2012, 488, 43-48.	27.8	742

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73	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
74	Evaluation of GRCh38 and de novo haploid genome assemblies demonstrates the enduring quality of the reference assembly. Genome Research, 2017, 27, 849-864.	5.5	728
75	The Genome of the Western Clawed Frog Xenopus tropicalis. Science, 2010, 328, 633-636.	12.6	708
76	Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. Nature Genetics, 2013, 45, 602-612.	21.4	704
77	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	27.8	689
78	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
79	Role of TP53 mutations in the origin and evolution of therapy-related acute myeloid leukaemia. Nature, 2015, 518, 552-555.	27.8	685
80	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
81	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
82	TP53 and Decitabine in Acute Myeloid Leukemia and Myelodysplastic Syndromes. New England Journal of Medicine, 2016, 375, 2023-2036.	27.0	663
83	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
84	Landscape of Somatic Retrotransposition in Human Cancers. Science, 2012, 337, 967-971.	12.6	631
85	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
86	A Catalog of Reference Genomes from the Human Microbiome. Science, 2010, 328, 994-999.	12.6	621
87	The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. Nature Genetics, 2001, 29, 279-286.	21.4	617
88	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5859-5864.	7.1	612
89	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
90	Demographic history and rare allele sharing among human populations. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11983-11988.	7.1	589

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91	Sequencing of the sea lamprey (Petromyzon marinus) genome provides insights into vertebrate evolution. Nature Genetics, 2013, 45, 415-421.	21.4	588
92	The genomic landscape of hypodiploid acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 242-252.	21.4	588
93	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	5.5	586
94	Recurrent Somatic Structural Variations Contribute to Tumorigenesis in Pediatric Osteosarcoma. Cell Reports, 2014, 7, 104-112.	6.4	583
95	The complete nucleotide sequence of the Xenopus laevis mitochondrial genome. Journal of Biological Chemistry, 1985, 260, 9759-74.	3.4	573
96	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
97	C11orf95â€“RELA fusions drive oncogenic NF-ÎºB signalling in ependymoma. Nature, 2014, 506, 451-455.	27.8	559
98	Mammalian Y chromosomes retain widely expressed dosage-sensitive regulators. Nature, 2014, 508, 494-499.	27.8	546
99	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
100	Abundant gene conversion between arms of palindromes in human and ape Y chromosomes. Nature, 2003, 423, 873-876.	27.8	540
101	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
102	The C. elegans genome sequencing project: a beginning. Nature, 1992, 356, 37-41.	27.8	518
103	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. Nature Genetics, 2012, 44, 53-57.	21.4	513
104	Evolution of Symbiotic Bacteria in the Distal Human Intestine. PLoS Biology, 2007, 5, e156.	5.6	490
105	Recurrent DNMT3A mutations in patients with myelodysplastic syndromes. Leukemia, 2011, 25, 1153-1158.	7.2	483
106	Implementing genomic medicine in the clinic: the future is here. Genetics in Medicine, 2013, 15, 258-267.	2.4	472
107	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. Nature, 2013, 500, 335-339.	27.8	468
108	CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants in cancer. Nature Genetics, 2017, 49, 170-174.	21.4	460

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109	Modernizing Reference Genome Assemblies. PLoS Biology, 2011, 9, e1001091.	5.6	458
110	Structure, Organization and Polymorphism of Murine and Human T-Cell Receptor a and beta Chain Gene Families. Immunological Reviews, 1988, 101, 149-172.	6.0	456
111	Genomic and metabolic adaptations of Methanobrevibacter smithii to the human gut. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10643-10648.	7.1	451
112	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
113	DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.	19.0	443
114	A novel retinoblastoma therapy from genomic and epigenetic analyses. Nature, 2012, 481, 329-334.	27.8	442
115	Genomic Landscape of Ewing Sarcoma Defines an Aggressive Subtype with Co-Association of STAG2 and TP53 Mutations. Cancer Discovery, 2014, 4, 1342-1353.	9.4	418
116	Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. Nature, 1999, 402, 769-777.	27.8	413
117	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
118	High Throughput Fingerprint Analysis of Large-Insertâ€‰Clones. Genome Research, 1997, 7, 1072-1084.	5.5	405
119	The landscape of somatic mutations in infant MLL-rearranged acute lymphoblastic leukemias. Nature Genetics, 2015, 47, 330-337.	21.4	405
120	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	3.2	400
121	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
122	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
123	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	27.8	391
124	Viral Discovery and Sequence Recovery Using DNA Microarrays. PLoS Biology, 2003, 1, e2.	5.6	386
125	A survey of expressed genes in Caenorhabditis elegans. Nature Genetics, 1992, 1, 114-123.	21.4	385
126	Chimpanzee and human Y chromosomes are remarkably divergent in structure and gene content. Nature, 2010, 463, 536-539.	27.8	381

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127	Whole-genome sequencing and variant discovery in C. elegans. Nature Methods, 2008, 5, 183-188.	19.0	380
128	Association of Age at Diagnosis and Genetic Mutations in Patients With Neuroblastoma. JAMA - Journal of the American Medical Association, 2012, 307, 1062.	7.4	379
129	The R882H DNMT3A Mutation Associated with AML Dominantly Inhibits Wild-Type DNMT3A by Blocking Its Ability to Form Active Tetramers. Cancer Cell, 2014, 25, 442-454.	16.8	374
130	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	12.6	368
131	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. Nature Genetics, 2004, 36, 1268-1274.	21.4	367
132	Characterizing the Major Structural Variant Alleles of the Human Genome. Cell, 2019, 176, 663-675.e19.	28.9	364
133	DGIdb 2.0: mining clinically relevant drugâ€“gene interactions. Nucleic Acids Research, 2016, 44, D1036-D1044.	14.5	359
134	A genome-wide comparison of recent chimpanzee and human segmental duplications. Nature, 2005, 437, 88-93.	27.8	353
135	The landscape of somatic mutations in epigenetic regulators across 1,000 paediatric cancer genomes. Nature Communications, 2014, 5, 3630.	12.8	342
136	Evolution of Human-Specific Neural SRGAP2 Genes by Incomplete Segmental Duplication. Cell, 2012, 149, 912-922.	28.9	341
137	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
138	Functional Heterogeneity of Genetically Defined Subclones in Acute Myeloid Leukemia. Cancer Cell, 2014, 25, 379-392.	16.8	330
139	Genome of Rhodnius prolixus , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	7.1	329
140	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
141	Discovery and genotyping of structural variation from long-read haploid genome sequence data. Genome Research, 2017, 27, 677-685.	5.5	323
142	Immune Escape of Relapsed AML Cells after Allogeneic Transplantation. New England Journal of Medicine, 2018, 379, 2330-2341.	27.0	322
143	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	27.8	320
144	The Pediatric Cancer Genome Project. Nature Genetics, 2012, 44, 619-622.	21.4	315

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145	The Pristionchus pacificus genome provides a unique perspective on nematode lifestyle and parasitism. Nature Genetics, 2008, 40, 1193-1198.	21.4	310
146	Genetic variation and the de novo assembly of human genomes. Nature Reviews Genetics, 2015, 16, 627-640.	16.3	310
147	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	12.6	304
148	Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII. Science, 1994, 265, 2077-2082.	12.6	303
149	Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811.	7.4	302
150	Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs overproduced in A431 carcinoma cells. Nature, 1984, 309, 806-810.	27.8	294
151	Sequencing the Mouse Y Chromosome Reveals Convergent Gene Acquisition and Amplification on Both Sex Chromosomes. Cell, 2014, 159, 800-813.	28.9	291
152	Genetic alterations in uncommon low-grade neuroepithelial tumors: BRAF, FGFR1, and MYB mutations occur at high frequency and align with morphology. Acta Neuropathologica, 2016, 131, 833-845.	7.7	288
153	The draft genome of the parasitic nematode Trichinella spiralis. Nature Genetics, 2011, 43, 228-235.	21.4	285
154	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
155	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17230-17235.	7.1	281
156	Sequence and Comparative Analysis of the Maize NB Mitochondrial Genome. Plant Physiology, 2004, 136, 3486-3503.	4.8	279
157	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. Genome Biology, 2013, 14, R28.	9.6	276
158	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
159	Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. Leukemia, 2013, 27, 1275-1282.	7.2	260
160	Genome Sequence of the Tsetse Fly (Glossina morsitans): Vector of African Trypanosomiasis. Science, 2014, 344, 380-386.	12.6	254
161	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	12.8	253
162	Targeting Oxidative Stress in Embryonal Rhabdomyosarcoma. Cancer Cell, 2013, 24, 710-724.	16.8	252

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163	Genome of the house fly, Musca domestica L., a global vector of diseases with adaptations to a septic environment. Genome Biology, 2014, 15, 466.	8.8	252
164	The genome of the platyfish, Xiphophorus maculatus, provides insights into evolutionary adaptation and several complex traits. Nature Genetics, 2013, 45, 567-572.	21.4	251
165	A Human Genome Structural Variation Sequencing Resource Reveals Insights into Mutational Mechanisms. Cell, 2010, 143, 837-847.	28.9	249
166	Strict evolutionary conservation followed rapid gene loss on human and rhesus Y chromosomes. Nature, 2012, 483, 82-86.	27.8	245
167	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
168	Human Genome Ultraconserved Elements Are Ultraselected. Science, 2007, 317, 915-915.	12.6	240
169	Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research. PLoS ONE, 2012, 7, e39315.	2.5	240
170	Molecular Study of Malignant Gliomas Treated with Epidermal Growth Factor Receptor Inhibitors: Tissue Analysis from North American Brain Tumor Consortium Trials 01-03 and 00-01. Clinical Cancer Research, 2005, 11, 7841-7850.	7.0	238
171	The DNA sequence of human chromosome 7. Nature, 2003, 424, 157-164.	27.8	236
172	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233
173	Acquired copy number alterations in adult acute myeloid leukemia genomes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12950-12955.	7.1	231
174	Deregulation of DUX4 and ERG in acute lymphoblastic leukemia. Nature Genetics, 2016, 48, 1481-1489.	21.4	231
175	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
176	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	21.4	225
177	Complete Haplotype Sequence of the Human Immunoglobulin Heavy-Chain Variable, Diversity, and Joining Genes and Characterization of Allelic and Copy-Number Variation. American Journal of Human Genetics, 2013, 92, 530-546.	6.2	223
178	Orthotopic patient-derived xenografts of paediatric solid tumours. Nature, 2017, 549, 96-100.	27.8	223
179	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	27.8	222
180	Reconstructing complex regions of genomes using long-read sequencing technology. Genome Research, 2014, 24, 688-696.	5.5	222

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181	The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. Neuron, 2017, 94, 550-568.e10.	8.1	222
182	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. Nature Communications, 2017, 8, 15451.	12.8	216
183	The genomic landscape of core-binding factor acute myeloid leukemias. Nature Genetics, 2016, 48, 1551-1556.	21.4	215
184	An Inv(16)(p13.3q24.3)-Encoded CBFA2T3-GLIS2 Fusion Protein Defines an Aggressive Subtype of Pediatric Acute Megakaryoblastic Leukemia. Cancer Cell, 2012, 22, 683-697.	16.8	213
185	Convergent evolution of chicken Z and human X chromosomes by expansion and gene acquisition. Nature, 2010, 466, 612-616.	27.8	210
186	Comparative genomics of protoploid Saccharomycetaceae. Genome Research, 2009, 19, 1696-1709.	5.5	207
187	Genomic analysis of germ line and somatic variants in familial myelodysplasia/acute myeloid leukemia. Blood, 2015, 126, 2484-2490.	1.4	207
188	Novel MEK1 Mutation Identified by Mutational Analysis of Epidermal Growth Factor Receptor Signaling Pathway Genes in Lung Adenocarcinoma. Cancer Research, 2008, 68, 5524-5528.	0.9	206
189	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
190	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
191	Use of Cigarette-Smoking History to Estimate the Likelihood of Mutations in Epidermal Growth Factor Receptor Gene Exons 19 and 21 in Lung Adenocarcinomas. Journal of Clinical Oncology, 2006, 24, 1700-1704.	1.6	202
192	A physical map of the chicken genome. Nature, 2004, 432, 761-764.	27.8	200
193	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.1	199
194	Somatic mutations and germline sequence variants in the expressed tyrosine kinase genes of patients with de novo acute myeloid leukemia. Blood, 2008, 111, 4797-4808.	1.4	198
195	The Oxytricha trifallax Macronuclear Genome: A Complex Eukaryotic Genome with 16,000 Tiny Chromosomes. PLoS Biology, 2013, 11, e1001473.	5.6	198
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