List of Publications by Year in descending order

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ZEMIN NINC

#	Article	IF	CITATIONS
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199
3	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
4	The zebrafish reference genome sequence and its relationship to the human genome. Nature, 2013, 496, 498-503.	27.8	3,708
5	Accurate whole human genome sequencing using reversible terminator chemistry. Nature, 2008, 456, 53-59.	27.8	3,118
6	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. Nature, 2001, 409, 928-933.	27.8	2,794
7	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
8	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. Bioinformatics, 2009, 25, 2865-2871.	4.1	1,811
9	A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196.	27.8	1,519
10	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
11	The genome of the blood fluke Schistosoma mansoni. Nature, 2009, 460, 352-358.	27.8	945
12	SSAHA: A Fast Search Method for Large DNA Databases. Genome Research, 2001, 11, 1725-1729.	5.5	843
13	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
14	Oxford Nanopore MinION Sequencing and Genome Assembly. Genomics, Proteomics and Bioinformatics, 2016, 14, 265-279.	6.9	638
15	The Schistosoma japonicum genome reveals features of host–parasite interplay. Nature, 2009, 460, 345-351.	27.8	635
16	A theoretical model for the stick/bounce behaviour of adhesive, elastic-plastic spheres. Powder Technology, 1998, 99, 154-162.	4.2	606
17	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
18	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. Nature Methods, 2009, 6, 291-295.	19.0	520

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19	The draft genome of the fast-growing non-timber forest species moso bamboo (Phyllostachys) Tj ETQq1 1 0.784	314 rgBT / 21.4	Overlock 10
20	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443
21	Assessing the gene space in draft genomes. Nucleic Acids Research, 2009, 37, 289-297.	14.5	395
22	The draft genome of the grass carp (Ctenopharyngodon idellus) provides insights into its evolution and vegetarian adaptation. Nature Genetics, 2015, 47, 625-631.	21.4	352
23	Chromosomal transposition of <i>PiggyBac</i> in mouse embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9290-9295.	7.1	344
24	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. Cell, 2012, 148, 780-791.	28.9	300
25	Analysis of the Genome Sequence of the Medicinal Plant Salvia miltiorrhiza. Molecular Plant, 2016, 9, 949-952.	8.3	255
26	The opium poppy genome and morphinan production. Science, 2018, 362, 343-347.	12.6	225
27	Comparative genomics reveals convergent evolution between the bamboo-eating giant and red pandas. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1081-1086.	7.1	196
28	The Phusion Assembler. Genome Research, 2003, 13, 81-90.	5.5	181
29	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. Scientific Reports, 2017, 7, 3935.	3.3	146
30	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	12.6	144
31	Mobilization of giant piggyBac transposons in the mouse genome. Nucleic Acids Research, 2011, 39, e148-e148.	14.5	141
32	Next-generation sequencing and large genome assemblies. Pharmacogenomics, 2012, 13, 901-915.	1.3	120
33	Distinct element simulation of impact breakage of lactose agglomerates. Advanced Powder Technology, 1997, 8, 15-37.	4.1	108
34	Effect of interface energy on the impact strength of agglomerates. Powder Technology, 1999, 105, 66-73.	4.2	103
35	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. Cancer Cell, 2018, 33, 607-619.e15.	16.8	88
36	The <i>piggyBac</i> Transposon Displays Local and Distant Reintegration Preferences and Can Cause Mutations at Noncanonical Integration Sites. Molecular and Cellular Biology, 2013, 33, 1317-1330.	2.3	77

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37	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. Nature Genetics, 2015, 47, 47-56.	21.4	77
38	Signatures in SARS-CoV-2 spike protein conferring escape to neutralizing antibodies. PLoS Pathogens, 2021, 17, e1009772.	4.7	74
39	The Leukocyte Receptor Complex in Chicken Is Characterized by Massive Expansion and Diversification of Immunoglobulin-Like Loci. PLoS Genetics, 2006, 2, e73.	3.5	70
40	Disintegration of weak lactose agglomerates for inhalation applications. International Journal of Pharmaceutics, 1998, 172, 199-209.	5.2	64
41	Distinct element analysis of bulk crushing: effect of particle properties and loading rate. Powder Technology, 2000, 109, 241-254.	4.2	58
42	Attrition of granular solids in a shear cell. Chemical Engineering Science, 2000, 55, 5445-5456.	3.8	56
43	Contact Mechanics and Coefficients of Restitution. Lecture Notes in Physics, 2001, , 184-194.	0.7	51
44	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. Blood, 2016, 128, e1-e9.	1.4	49
45	Distinct element analysis of attrition of granular solids under shear deformation. Chemical Engineering Science, 2006, 61, 5991-6001.	3.8	41
46	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. Twin Research and Human Genetics, 2013, 16, 1026-1032.	0.6	40
47	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. PLoS ONE, 2011, 6, e15292.	2.5	38
48	Deep short-read sequencing of chromosome 17 from the mouse strains A/J and CAST/Ei identifies significant germline variation and candidate genes that regulate liver triglyceride levels. Genome Biology, 2009, 10, R112.	9.6	36
49	Incipient diploidization of the medicinal plant Perilla within 10,000 years. Nature Communications, 2021, 12, 5508.	12.8	35
50	A chromosomeâ€level <i>Amaranthus cruentus</i> genome assembly highlights gene family evolution and biosynthetic gene clusters that may underpin the nutritional value of this traditional crop. Plant Journal, 2021, 107, 613-628.	5.7	30
51	Breakage of macroporous alumina beads under compressive loading: simulation and experimental validation. Powder Technology, 1999, 105, 57-65.	4.2	29
52	A numerical model for simulating mechanical behavior of flexible fibers. Journal of Chemical Physics, 1999, 111, 10717-10726.	3.0	28
53	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. Bioinformatics, 2012, 28, 479-486.	4.1	26
54	Genetic Basis of Y-Linked Hearing Impairment. American Journal of Human Genetics, 2013, 92, 301-306.	6.2	25

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55	Finishing the finished human chromosome 22 sequence. Genome Biology, 2008, 9, R78.	9.6	20
56	Split-Read Indel and Structural Variant Calling Using PINDEL. Methods in Molecular Biology, 2018, 1833, 95-105.	0.9	20
57	The genome sequence of the channel bull blenny, Cottoperca gobio (Günther, 1861). Wellcome Open Research, 2020, 5, 148.	1.8	18
58	ssahaSNP A Polymorphism Detection Tool on a Whole Genome Scale. , 0, , .		14
59	TranscriptSNPView: a genome-wide catalog of mouse coding variation. Nature Genetics, 2006, 38, 853-853.	21.4	14
60	HI: haplotype improver using paired-end short reads. Bioinformatics, 2009, 25, 2436-2437.	4.1	12
61	Efficient iterative Hi-C scaffolder based on N-best neighbors. BMC Bioinformatics, 2021, 22, 569.	2.6	12
62	Expansion of CORE-SINEs in the genome of the Tasmanian devil. BMC Genomics, 2012, 13, 172.	2.8	10
63	scanPAV: a pipeline for extracting presence–absence variations in genome pairs. Bioinformatics, 2018, 34, 3022-3024.	4.1	9
64	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. Human Genetics, 2012, 131, 665-674.	3.8	8
65	A functionally conserved STORR gene fusion in Papaver species that diverged 16.8 million years ago. Nature Communications, 2022, 13, .	12.8	7
66	Out of the sequencer and into the wiki as we face new challenges in genome informatics. Genome Biology, 2010, 11, 308.	9.6	3
67	The SSAHA trace server. , 0, , .		0
68	SIMULATION OF FLEXIBLE FIBERS. , 2000, , .		0
69	R.I.S.C.L: A Holistic Molecular Diagnostic Tool for Myeloid Malignancies. Blood, 2014, 124, 2342-2342.	1.4	0