

Zemin Ning

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68

papers

40,354

citations

41

h-index

79

g-index

79

ext. papers

48,851

ext. citations

18.5

avg. IF

6.44

L-index

#	Paper	IF	Citations
68	Efficient iterative Hi-C scaffold based on N-best neighbors. <i>BMC Bioinformatics</i> , 2021 , 22, 569	3.6	0
67	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	46.4	161
66	A chromosome-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. <i>Plant Journal</i> , 2021 , 107, 613-628	6.9	3
65	Signatures in SARS-CoV-2 spike protein conferring escape to neutralizing antibodies. <i>PLoS Pathogens</i> , 2021 , 17, e1009772	7.6	24
64	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021 , 12, 5508	17.4	4
63	The genome sequence of the channel bull blenny, (<i>Göther</i> , 1861). <i>Wellcome Open Research</i> , 2020 , 5, 148	4.8	3
62	scanPAV: a pipeline for extracting presence-absence variations in genome pairs. <i>Bioinformatics</i> , 2018 , 34, 3022-3024	7.2	4
61	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018 , 33, 607-619.e15	24.3	65
60	Split-Read Indel and Structural Variant Calling Using PINDEL. <i>Methods in Molecular Biology</i> , 2018 , 1833, 95-105	1.4	8
59	The opium poppy genome and morphinan production. <i>Science</i> , 2018 , 362, 343-347	33.3	118
58	Comparative genomics reveals convergent evolution between the bamboo-eating giant and red pandas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 1081-1086	11.5	113
57	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , 2017 , 7, 3935	4.9	101
56	Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>Molecular Plant</i> , 2016 , 9, 949-52	14.4	173
55	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , 2016 , 128, e1-9	2.2	36
54	Oxford Nanopore MinION Sequencing and Genome Assembly. <i>Genomics, Proteomics and Bioinformatics</i> , 2016 , 14, 265-279	6.5	399
53	The draft genome of the grass carp (<i>Ctenopharyngodon idellus</i>) provides insights into its evolution and vegetarian adaptation. <i>Nature Genetics</i> , 2015 , 47, 625-31	36.3	263
52	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599

51	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , 2015 , 47, 47-56	36.3	59
50	Transmissible [corrected] dog cancer genome reveals the origin and history of an ancient cell lineage. <i>Science</i> , 2014 , 343, 437-440	33.3	116
49	R.I.S.C.L: A Holistic Molecular Diagnostic Tool for Myeloid Malignancies. <i>Blood</i> , 2014 , 124, 2342-2342	2.2	
48	Aging as accelerated accumulation of somatic variants: whole-genome sequencing of centenarian and middle-aged monozygotic twin pairs. <i>Twin Research and Human Genetics</i> , 2013 , 16, 1026-32	2.2	30
47	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013 , 2, 10	7.6	461
46	Genetic basis of Y-linked hearing impairment. <i>American Journal of Human Genetics</i> , 2013 , 92, 301-6	11	21
45	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013 , 496, 498-503	50.4	2550
44	The draft genome of the fast-growing non-timber forest species moso bamboo (<i>Phyllostachys heterocycla</i>). <i>Nature Genetics</i> , 2013 , 45, 456-61, 461e1-2	36.3	340
43	The piggyBac transposon displays local and distant reintegration preferences and can cause mutations at noncanonical integration sites. <i>Molecular and Cellular Biology</i> , 2013 , 33, 1317-30	4.8	59
42	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. <i>Cell</i> , 2012 , 148, 780-91	56.2	251
41	Expansion of CORE-SINEs in the genome of the Tasmanian devil. <i>BMC Genomics</i> , 2012 , 13, 172	4.5	8
40	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
39	Next-generation sequencing and large genome assemblies. <i>Pharmacogenomics</i> , 2012 , 13, 901-15	2.6	92
38	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
37	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. <i>Human Genetics</i> , 2012 , 131, 665-74	6.3	8
36	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. <i>Bioinformatics</i> , 2012 , 28, 479-86	7.2	20
35	PoolHap: inferring haplotype frequencies from pooled samples by next generation sequencing. <i>PLoS ONE</i> , 2011 , 6, e15292	3.7	28
34	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364

33	Mobilization of giant piggyBac transposons in the mouse genome. <i>Nucleic Acids Research</i> , 2011 , 39, e14820.1	118
32	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010 , 463, 191-50.4	1303
31	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4 1613
30	Out of the sequencer and into the wiki as we face new challenges in genome informatics. <i>Genome Biology</i> , 2010 , 11, 308	18.3 2
29	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009 , 25, 2865-71	7.2 1423
28	Assessing the gene space in draft genomes. <i>Nucleic Acids Research</i> , 2009 , 37, 289-97	20.1 353
27	HI: haplotype improver using paired-end short reads. <i>Bioinformatics</i> , 2009 , 25, 2436-7	7.2 12
26	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009 , 460, 345-51.4	562
25	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009 , 460, 352-8	50.4 822
24	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. <i>Nature Methods</i> , 2009 , 6, 291-5	21.6 431
23	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. <i>Genome Biology</i> , 2009 , 10, R112	18.3 32
22	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008 , 456, 53-9	50.4 2615
21	Finishing the finished human chromosome 22 sequence. <i>Genome Biology</i> , 2008 , 9, R78	18.3 17
20	Chromosomal transposition of PiggyBac in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 9290-5	11.5 292
19	The leukocyte receptor complex in chicken is characterized by massive expansion and diversification of immunoglobulin-like Loci. <i>PLoS Genetics</i> , 2006 , 2, e73	6 58
18	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006 , 38, 853	36.3 14
17	Distinct element analysis of attrition of granular solids under shear deformation. <i>Chemical Engineering Science</i> , 2006 , 61, 5991-6001	4.4 35
16	The phusion assembler. <i>Genome Research</i> , 2003 , 13, 81-90	9.7 144

15	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
14	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. <i>Nature</i> , 2001 , 409, 928-33	50.4	2398
13	Contact Mechanics and Coefficients of Restitution. <i>Lecture Notes in Physics</i> , 2001 , 184-194	0.8	13
12	SSAHA: a fast search method for large DNA databases. <i>Genome Research</i> , 2001 , 11, 1725-9	9.7	720
11	Attrition of granular solids in a shear cell. <i>Chemical Engineering Science</i> , 2000 , 55, 5445-5456	4.4	50
10	Distinct element analysis of bulk crushing: effect of particle properties and loading rate. <i>Powder Technology</i> , 2000 , 109, 241-254	5.2	49
9	A numerical model for simulating mechanical behavior of flexible fibers. <i>Journal of Chemical Physics</i> , 1999 , 111, 10717-10726	3.9	23
8	Breakage of macroporous alumina beads under compressive loading: simulation and experimental validation. <i>Powder Technology</i> , 1999 , 105, 57-65	5.2	26
7	Effect of interface energy on the impact strength of agglomerates. <i>Powder Technology</i> , 1999 , 105, 66-73	5.2	94
6	A theoretical model for the stick/bounce behaviour of adhesive, elastic-plastic spheres. <i>Powder Technology</i> , 1998 , 99, 154-162	5.2	485
5	Disintegration of weak lactose agglomerates for inhalation applications. <i>International Journal of Pharmaceutics</i> , 1998 , 172, 199-209	6.5	53
4	Distinct element simulation of impact breakage of lactose agglomerates. <i>Advanced Powder Technology</i> , 1997 , 8, 15-37	4.6	94
3	ssahaSNP - a polymorphism detection tool on a whole genome scale		6
2	Towards complete and error-free genome assemblies of all vertebrate species		38
1	Amino acids 484 and 494 of SARS-CoV-2 spike are hotspots of immune evasion affecting antibody but not ACE2 binding		4