

# Zemin Ning

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

54,359  
citations

66250

44  
h-index

104191

69  
g-index

79  
all docs

79  
docs citations

79  
times ranked

90213  
citing authors

#	ARTICLE	IF	CITATIONS
1	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012, 491, 56-65.	13.7	7,199
3	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002, 420, 520-562.	13.7	6,319
4	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708
5	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , 2008, 456, 53-59.	13.7	3,118
6	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. <i>Nature</i> , 2001, 409, 928-933.	13.7	2,794
7	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
8	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, 2865-2871.	1.8	1,811
9	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010, 463, 191-196.	13.7	1,519
10	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
11	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , 2009, 460, 352-358.	13.7	945
12	SSAHA: A Fast Search Method for Large DNA Databases. <i>Genome Research</i> , 2001, 11, 1725-1729.	2.4	843
13	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012, 483, 169-175.	13.7	663
14	Oxford Nanopore MinION Sequencing and Genome Assembly. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 265-279.	3.0	638
15	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351.	13.7	635
16	A theoretical model for the stick/bounce behaviour of adhesive, elastic-plastic spheres. <i>Powder Technology</i> , 1998, 99, 154-162.	2.1	606
17	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
18	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. <i>Nature Methods</i> , 2009, 6, 291-295.	9.0	520

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19	The draft genome of the fast-growing non-timber forest species moso bamboo ( <i>Phyllostachys</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 107	9.45	483
20	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
21	Assessing the gene space in draft genomes. <i>Nucleic Acids Research</i> , 2009, 37, 289-297.	6.5	395
22	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, 625-631.	9.4	352
23	Chromosomal transposition of <i>PiggyBac</i> in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9290-9295.	3.3	344
24	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 2012, 148, 780-791.	13.5	300
25	Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>Molecular Plant</i> , 2016, 9, 949-952.	3.9	255
26	The opium poppy genome and morphinan production. <i>Science</i> , 2018, 362, 343-347.	6.0	225
27	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.	3.3	196
28	The Phusion Assembler. <i>Genome Research</i> , 2003, 13, 81-90.	2.4	181
29	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , 2017, 7, 3935.	1.6	146
30	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	6.0	144
31	Mobilization of giant piggyBac transposons in the mouse genome. <i>Nucleic Acids Research</i> , 2011, 39, e148-e148.	6.5	141
32	Next-generation sequencing and large genome assemblies. <i>Pharmacogenomics</i> , 2012, 13, 901-915.	0.6	120
33	Distinct element simulation of impact breakage of lactose agglomerates. <i>Advanced Powder Technology</i> , 1997, 8, 15-37.	2.0	108
34	Effect of interface energy on the impact strength of agglomerates. <i>Powder Technology</i> , 1999, 105, 66-73.	2.1	103
35	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018, 33, 607-619.e15.	7.7	88
36	The <i>piggyBac</i> Transposon Displays Local and Distant Reintegration Preferences and Can Cause Mutations at Noncanonical Integration Sites. <i>Molecular and Cellular Biology</i> , 2013, 33, 1317-1330.	1.1	77

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37	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , 2015, 47, 47-56.	9.4	77
38	Signatures in SARS-CoV-2 spike protein conferring escape to neutralizing antibodies. <i>PLoS Pathogens</i> , 2021, 17, e1009772.	2.1	74
39	The Leukocyte Receptor Complex in Chicken Is Characterized by Massive Expansion and Diversification of Immunoglobulin-Like Loci. <i>PLoS Genetics</i> , 2006, 2, e73.	1.5	70
40	Disintegration of weak lactose agglomerates for inhalation applications. <i>International Journal of Pharmaceutics</i> , 1998, 172, 199-209.	2.6	64
41	Distinct element analysis of bulk crushing: effect of particle properties and loading rate. <i>Powder Technology</i> , 2000, 109, 241-254.	2.1	58
42	Attrition of granular solids in a shear cell. <i>Chemical Engineering Science</i> , 2000, 55, 5445-5456.	1.9	56
43	Contact Mechanics and Coefficients of Restitution. <i>Lecture Notes in Physics</i> , 2001, , 184-194.	0.3	51
44	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , 2016, 128, e1-e9.	0.6	49
45	Distinct element analysis of attrition of granular solids under shear deformation. <i>Chemical Engineering Science</i> , 2006, 61, 5991-6001.	1.9	41
46	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, 1026-1032.	0.3	40
47	PoolHap: Inferring Haplotype Frequencies from Pooled Samples by Next Generation Sequencing. <i>PLoS ONE</i> , 2011, 6, e15292.	1.1	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. <i>Genome Biology</i> , 2009, 10, R112.	13.9	36
49	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , 2021, 12, 5508.	5.8	35
50	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.	2.8	30
51	Breakage of macroporous alumina beads under compressive loading: simulation and experimental validation. <i>Powder Technology</i> , 1999, 105, 57-65.	2.1	29
52	A numerical model for simulating mechanical behavior of flexible fibers. <i>Journal of Chemical Physics</i> , 1999, 111, 10717-10726.	1.2	28
53	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. <i>Bioinformatics</i> , 2012, 28, 479-486.	1.8	26
54	Genetic Basis of Y-Linked Hearing Impairment. <i>American Journal of Human Genetics</i> , 2013, 92, 301-306.	2.6	25

#	ARTICLE	IF	CITATIONS
55	Finishing the finished human chromosome 22 sequence. <i>Genome Biology</i> , 2008, 9, R78.	13.9	20
56	Split-Read Indel and Structural Variant Calling Using PINDEL. <i>Methods in Molecular Biology</i> , 2018, 1833, 95-105.	0.4	20
57	The genome sequence of the channel bull blenny, <i>Cottoperca gobio</i> (Günther, 1861). <i>Wellcome Open Research</i> , 2020, 5, 148.	0.9	18
58	ssahaSNP A Polymorphism Detection Tool on a Whole Genome Scale. , 0, , .		14
59	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , 2006, 38, 853-853.	9.4	14
60	HI: haplotype improver using paired-end short reads. <i>Bioinformatics</i> , 2009, 25, 2436-2437.	1.8	12
61	Efficient iterative Hi-C scaffolder based on N-best neighbors. <i>BMC Bioinformatics</i> , 2021, 22, 569.	1.2	12
62	Expansion of CORE-SINEs in the genome of the Tasmanian devil. <i>BMC Genomics</i> , 2012, 13, 172.	1.2	10
63	scanPAV: a pipeline for extracting presence-absence variations in genome pairs. <i>Bioinformatics</i> , 2018, 34, 3022-3024.	1.8	9
64	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. <i>Human Genetics</i> , 2012, 131, 665-674.	1.8	8
65	A functionally conserved STORR gene fusion in <i>Papaver</i> species that diverged 16.8 million years ago. <i>Nature Communications</i> , 2022, 13, .	5.8	7
66	Out of the sequencer and into the wiki as we face new challenges in genome informatics. <i>Genome Biology</i> , 2010, 11, 308.	13.9	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. <i>Blood</i> , 2014, 124, 2342-2342.	0.6	0