

# Zemin Ning

## List of Publications by Citations

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**Version:** 2024-04-28

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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	A global reference for human genetic variation. <i>Nature</i> , <b>2015</b> , 526, 68-74	50.4	8599
67	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , <b>2012</b> , 491, 56-65	50.4	6049
66	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , <b>2002</b> , 420, 520-62	50.4	5376
65	Accurate whole human genome sequencing using reversible terminator chemistry. <i>Nature</i> , <b>2008</b> , 456, 53-9	50.4	2615
64	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , <b>2013</b> , 496, 498-503	50.4	2550
63	A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. <i>Nature</i> , <b>2001</b> , 409, 928-33	50.4	2398
62	International network of cancer genome projects. <i>Nature</i> , <b>2010</b> , 464, 993-8	50.4	1613
61	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , <b>2009</b> , 25, 2865-71	7.2	1423
60	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , <b>2010</b> , 463, 191-50.4	50.4	1303
59	The genome of the blood fluke <i>Schistosoma mansoni</i> . <i>Nature</i> , <b>2009</b> , 460, 352-8	50.4	822
58	SSAHA: a fast search method for large DNA databases. <i>Genome Research</i> , <b>2001</b> , 11, 1725-9	9.7	720
57	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , <b>2009</b> , 460, 345-51.4	50.4	562
56	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , <b>2012</b> , 483, 169-75	50.4	517
55	A theoretical model for the stick/bounce behaviour of adhesive, elastic-plastic spheres. <i>Powder Technology</i> , <b>1998</b> , 99, 154-162	5.2	485
54	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , <b>2013</b> , 2, 10	7.6	461
53	Amplification-free Illumina sequencing-library preparation facilitates improved mapping and assembly of (G+C)-biased genomes. <i>Nature Methods</i> , <b>2009</b> , 6, 291-5	21.6	431
52	Oxford Nanopore MinION Sequencing and Genome Assembly. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2016</b> , 14, 265-279	6.5	399

51	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , <b>2011</b> , 21, 2224-41	9.7	364
50	Assessing the gene space in draft genomes. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 289-97	20.1	353
49	The draft genome of the fast-growing non-timber forest species moso bamboo ( <i>Phyllostachys heterocycla</i> ). <i>Nature Genetics</i> , <b>2013</b> , 45, 456-61, 461e1-2	36.3	340
48	Chromosomal transposition of PiggyBac in mouse embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 9290-5	11.5	292
47	The draft genome of the grass carp ( <i>Ctenopharyngodon idellus</i> ) provides insights into its evolution and vegetarian adaptation. <i>Nature Genetics</i> , <b>2015</b> , 47, 625-31	36.3	263
46	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. <i>Cell</i> , <b>2012</b> , 148, 780-91	56.2	251
45	Analysis of the Genome Sequence of the Medicinal Plant <i>Salvia miltiorrhiza</i> . <i>Molecular Plant</i> , <b>2016</b> , 9, 949-52	14.4	173
44	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , <b>2021</b> , 592, 737-746	46.4	161
43	The phusion assembler. <i>Genome Research</i> , <b>2003</b> , 13, 81-90	9.7	144
42	Mobilization of giant piggyBac transposons in the mouse genome. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e14820.1	20.1	118
41	The opium poppy genome and morphinan production. <i>Science</i> , <b>2018</b> , 362, 343-347	33.3	118
40	Transmissible [corrected] dog cancer genome reveals the origin and history of an ancient cell lineage. <i>Science</i> , <b>2014</b> , 343, 437-440	33.3	116
39	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> , <b>2017</b> , 114, 10811-10866	11.5	113
38	De novo yeast genome assemblies from MinION, PacBio and MiSeq platforms. <i>Scientific Reports</i> , <b>2017</b> , 7, 3935	4.9	101
37	Distinct element simulation of impact breakage of lactose agglomerates. <i>Advanced Powder Technology</i> , <b>1997</b> , 8, 15-37	4.6	94
36	Effect of interface energy on the impact strength of agglomerates. <i>Powder Technology</i> , <b>1999</b> , 105, 66-73	5.2	94
35	Next-generation sequencing and large genome assemblies. <i>Pharmacogenomics</i> , <b>2012</b> , 13, 901-15	2.6	92
34	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , <b>2018</b> , 33, 607-619.e15	24.3	65

33	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , <b>2015</b> , 47, 47-56	36.3	59
32	The piggyBac transposon displays local and distant reintegration preferences and can cause mutations at noncanonical integration sites. <i>Molecular and Cellular Biology</i> , <b>2013</b> , 33, 1317-30	4.8	59
31	The leukocyte receptor complex in chicken is characterized by massive expansion and diversification of immunoglobulin-like Loci. <i>PLoS Genetics</i> , <b>2006</b> , 2, e73	6	58
30	Disintegration of weak lactose agglomerates for inhalation applications. <i>International Journal of Pharmaceutics</i> , <b>1998</b> , 172, 199-209	6.5	53
29	Attrition of granular solids in a shear cell. <i>Chemical Engineering Science</i> , <b>2000</b> , 55, 5445-5456	4.4	50
28	Distinct element analysis of bulk crushing: effect of particle properties and loading rate. <i>Powder Technology</i> , <b>2000</b> , 109, 241-254	5.2	49
27	Towards complete and error-free genome assemblies of all vertebrate species		38
26	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. <i>Blood</i> , <b>2016</b> , 128, e1-9	2.2	36
25	Distinct element analysis of attrition of granular solids under shear deformation. <i>Chemical Engineering Science</i> , <b>2006</b> , 61, 5991-6001	4.4	35
24	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> , <b>2009</b> , 10, R112	18.3	32
23	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> , <b>2013</b> , 16, 1026-32	2.2	30
22	PoolHap: inferring haplotype frequencies from pooled samples by next generation sequencing. <i>PLoS ONE</i> , <b>2011</b> , 6, e15292	3.7	28
21	Breakage of macroporous alumina beads under compressive loading: simulation and experimental validation. <i>Powder Technology</i> , <b>1999</b> , 105, 57-65	5.2	26
20	Signatures in SARS-CoV-2 spike protein conferring escape to neutralizing antibodies. <i>PLoS Pathogens</i> , <b>2021</b> , 17, e1009772	7.6	24
19	A numerical model for simulating mechanical behavior of flexible fibers. <i>Journal of Chemical Physics</i> , <b>1999</b> , 111, 10717-10726	3.9	23
18	Genetic basis of Y-linked hearing impairment. <i>American Journal of Human Genetics</i> , <b>2013</b> , 92, 301-6	11	21
17	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. <i>Bioinformatics</i> , <b>2012</b> , 28, 479-86	7.2	20
16	Finishing the finished human chromosome 22 sequence. <i>Genome Biology</i> , <b>2008</b> , 9, R78	18.3	17

15	TranscriptSNPView: a genome-wide catalog of mouse coding variation. <i>Nature Genetics</i> , <b>2006</b> , 38, 853	36.3	14
14	Contact Mechanics and Coefficients of Restitution. <i>Lecture Notes in Physics</i> , <b>2001</b> , 184-194	0.8	13
13	HI: haplotype improver using paired-end short reads. <i>Bioinformatics</i> , <b>2009</b> , 25, 2436-7	7.2	12
12	Split-Read Indel and Structural Variant Calling Using PINDEL. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1833, 95-105	1.4	8
11	Expansion of CORE-SINEs in the genome of the Tasmanian devil. <i>BMC Genomics</i> , <b>2012</b> , 13, 172	4.5	8
10	Exploration of signals of positive selection derived from genotype-based human genome scans using re-sequencing data. <i>Human Genetics</i> , <b>2012</b> , 131, 665-74	6.3	8
9	ssahaSNP - a polymorphism detection tool on a whole genome scale		6
8	scanPAV: a pipeline for extracting presence-absence variations in genome pairs. <i>Bioinformatics</i> , <b>2018</b> , 34, 3022-3024	7.2	4
7	Amino acids 484 and 494 of SARS-CoV-2 spike are hotspots of immune evasion affecting antibody but not ACE2 binding		4
6	Incipient diploidization of the medicinal plant <i>Perilla</i> within 10,000 years. <i>Nature Communications</i> , <b>2021</b> , 12, 5508	17.4	4
5	The genome sequence of the channel bull blenny, (Güther, 1861). <i>Wellcome Open Research</i> , <b>2020</b> , 5, 148	4.8	3
4	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> , <b>2021</b> , 107, 613-628	6.9	3
3	Out of the sequencer and into the wiki as we face new challenges in genome informatics. <i>Genome Biology</i> , <b>2010</b> , 11, 308	18.3	2
2	Efficient iterative Hi-C scaffolder based on N-best neighbors. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 569	3.6	0
1	R.I.S.C.L: A Holistic Molecular Diagnostic Tool for Myeloid Malignancies. <i>Blood</i> , <b>2014</b> , 124, 2342-2342	2.2	