

# Zhengdong D Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

1,647  
citations

394421

19  
h-index

345221

36  
g-index

38  
all docs

38  
docs citations

38  
times ranked

3147  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unravelling genetic components of longevity. <i>Nature Aging</i> , 2022, 2, 5-6.	11.6	3
2	Enhancer release and retargeting activates disease-susceptibility genes. <i>Nature</i> , 2021, 595, 735-740.	27.8	76
3	Genetic signature of human longevity in PKC and NF- $\kappa$ B signaling. <i>Aging Cell</i> , 2021, 20, e13362.	6.7	12
4	Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. <i>Nature Immunology</i> , 2021, 22, 1219-1230.	14.5	45
5	Rare genetic coding variants associated with human longevity and protection against age-related diseases. <i>Nature Aging</i> , 2021, 1, 783-794.	11.6	22
6	Ectopic cervical thymic and no thymic involution until midlife in naked mole rats. <i>Aging Cell</i> , 2021, 20, e13477.	6.7	12
7	Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. <i>Molecular Psychiatry</i> , 2021, 26, 4496-4510.	7.9	87
8	Deep post-GWAS analysis identifies potential risk genes and risk variants for Alzheimer's disease, providing new insights into its disease mechanisms. <i>Scientific Reports</i> , 2021, 11, 20511.	3.3	16
9	Genomic expansion of <i>Aldh1a1</i> protects beavers against high metabolic aldehydes from lipid oxidation. <i>Cell Reports</i> , 2021, 37, 109965.	6.4	7
10	Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. <i>Cell Reports</i> , 2020, 32, 107949.	6.4	26
11	Genetics of extreme human longevity to guide drug discovery for healthy ageing. <i>Nature Metabolism</i> , 2020, 2, 663-672.	11.9	32
12	Inducible aging in <i>Hydra oligactis</i> implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. <i>GeroScience</i> , 2020, 42, 1119-1132.	4.6	13
13	The nutritional environment determines which and how intestinal stem cells contribute to homeostasis and tumorigenesis. <i>Carcinogenesis</i> , 2019, 40, 937-946.	2.8	26
14	SIRT6 Is Responsible for More Efficient DNA Double-Strand Break Repair in Long-Lived Species. <i>Cell</i> , 2019, 177, 622-638.e22.	28.9	225
15	Global, integrated analysis of methylomes and transcriptomes from laser capture microdissected bronchial and alveolar cells in human lung. <i>Epigenetics</i> , 2018, 13, 264-274.	2.7	7
16	Epigenetic alterations to Polycomb targets precede malignant transition in a mouse model of breast cancer. <i>Scientific Reports</i> , 2018, 8, 5535.	3.3	9
17	PGA: post-GWAS analysis for disease gene identification. <i>Bioinformatics</i> , 2018, 34, 1786-1788.	4.1	4
18	HEDD: Human Enhancer Disease Database. <i>Nucleic Acids Research</i> , 2018, 46, D113-D120.	14.5	47

#	ARTICLE	IF	CITATIONS
19	Transcriptomic dynamics of breast cancer progression in the MMTV-PyMT mouse model. <i>BMC Genomics</i> , 2017, 18, 185.	2.8	31
20	Translation fidelity coevolves with longevity. <i>Aging Cell</i> , 2017, 16, 988-993.	6.7	53
21	Network analysis of mitonuclear GWAS reveals functional networks and tissue expression profiles of disease-associated genes. <i>Human Genetics</i> , 2017, 136, 55-65.	3.8	14
22	Integrated rare variant-based risk gene prioritization in disease case-control sequencing studies. <i>PLoS Genetics</i> , 2017, 13, e1007142.	3.5	7
23	Integrated Post-GWAS Analysis Sheds New Light on the Disease Mechanisms of Schizophrenia. <i>Genetics</i> , 2016, 204, 1587-1600.	2.9	41
24	Systems-level analysis of human aging genes shed new light on mechanisms of aging. <i>Human Molecular Genetics</i> , 2016, 25, ddw145.	2.9	31
25	MicroRNA expression and gene regulation drive breast cancer progression and metastasis in PyMT mice. <i>Breast Cancer Research</i> , 2016, 18, 75.	5.0	14
26	Sensitivity of primary fibroblasts in culture to atmospheric oxygen does not correlate with species lifespan. <i>Aging</i> , 2016, 8, 841-847.	3.1	10
27	Cell culture-based profiling across mammals reveals DNA repair and metabolism as determinants of species longevity. <i>ELife</i> , 2016, 5, .	6.0	69
28	RNA:DNA hybrids in the human genome have distinctive nucleotide characteristics, chromatin composition, and transcriptional relationships. <i>Epigenetics and Chromatin</i> , 2015, 8, 46.	3.9	134
29	Whole-Genome Sequencing and Integrative Genomic Analysis Approach on Two 22q11.2 Deletion Syndrome Family Trios for Genotype to Phenotype Correlations. <i>Human Mutation</i> , 2015, 36, 797-807.	2.5	16
30	DNA repair in species with extreme lifespan differences. <i>Aging</i> , 2015, 7, 1171-1182.	3.1	132
31	<i>INK4</i> locus of the tumor-resistant rodent, the naked mole rat, expresses a functional p15/p16 hybrid isoform. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1053-1058.	7.1	92
32	Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. <i>PLoS Genetics</i> , 2014, 10, e1004402.	3.5	93
33	Comparative genetics of longevity and cancer: insights from long-lived rodents. <i>Nature Reviews Genetics</i> , 2014, 15, 531-540.	16.3	169
34	SubNet: a Java application for subnetwork extraction. <i>Bioinformatics</i> , 2013, 29, 2958-2958.	4.1	7
35	Identification of genomic indels and structural variations using split reads. <i>BMC Genomics</i> , 2011, 12, 375.	2.8	57
36	Detection of copy number variation from array intensity and sequencing read depth using a stepwise Bayesian model. <i>BMC Bioinformatics</i> , 2010, 11, 539.	2.6	7