# Zhengdong D Zhang

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | SIRT6 Is Responsible for More Efficient DNA Double-Strand Break Repair in Long-Lived Species. Cell, 2019, 177, 622-638.e22. | 28.9 | 225 |
| 2 | Comparative genetics of longevity and cancer: insights from long-lived rodents. Nature Reviews Genetics, 2014, 15, 531-540. | 16.3 | 169 |
| 3 | RNA:DNA hybrids in the human genome have distinctive nucleotide characteristics, chromatin composition, and transcriptional relationships. Epigenetics and Chromatin, 2015, 8, 46. | 3.9 | 134 |
| 4 | DNA repair in species with extreme lifespan differences. Aging, 2015, 7, 1171-1182. | 3.1 | 132 |
| 5 | Mosaic Epigenetic Dysregulation of Ectodermal Cells in Autism Spectrum Disorder. PLoS Genetics, 2014, 10, e1004402. | 3.5 | 93 |
| 6 | INK4 locus of the tumor-resistant rodent, the naked mole rat, expresses a functional p15/p16 hybrid isoform. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1053-1058. | 7.1 | 92 |
| 7 | Genetic contributors to risk of schizophrenia in the presence of a 22q11.2 deletion. Molecular Psychiatry, 2021, 26, 4496-4510. | 7.9 | 87 |
| 8 | Enhancer release and retargeting activates disease-susceptibility genes. Nature, 2021, 595, 735-740. | 27.8 | 76 |
| 9 | Cell culture-based profiling across mammals reveals DNA repair and metabolism as determinants of species longevity. ELife, 2016, 5, . | 6.0 | 69 |
| 10 | Identification of genomic indels and structural variations using split reads. BMC Genomics, 2011, 12, 375. | 2.8 | 57 |
| 11 | Translation fidelity coevolves with longevity. Aging Cell, 2017, 16, 988-993. | 6.7 | 53 |
| 12 | HEDD: Human Enhancer Disease Database. Nucleic Acids Research, 2018, 46, D113-D120. | 14.5 | 47 |
| 13 | Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. Nature Immunology, 2021, 22, 1219-1230. | 14.5 | 45 |
| 14 | Integrated Post-GWAS Analysis Sheds New Light on the Disease Mechanisms of Schizophrenia. Genetics, 2016, 204, 1587-1600. | 2.9 | 41 |
| 15 | Genetics of extreme human longevity to guide drug discovery for healthy ageing. Nature Metabolism, 2020, 2, 663-672. | 11.9 | 32 |
| 16 | Systems-level analysis of human aging genes shed new light on mechanisms of aging. Human Molecular Genetics, 2016, 25, ddw145. | 2.9 | 31 |
| 17 | Transcriptomic dynamics of breast cancer progression in the MMTV-PyMT mouse model. BMC Genomics, 2017, 18, 185. | 2.8 | 31 |
| 18 | The nutritional environment determines which and how intestinal stem cells contribute to homeostasis and tumorigenesis. Carcinogenesis, 2019, 40, 937-946. | 2.8 | 26 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Beaver and Naked Mole Rat Genomes Reveal Common Paths to Longevity. Cell Reports, 2020, 32, 107949. | 6.4 | 26 |
| 20 | Rare genetic coding variants associated with human longevity and protection against age-related diseases. Nature Aging, 2021, 1, 783-794. | 11.6 | 22 |
| 21 | Whole-Genome Sequencing and Integrative Genomic Analysis Approach on Two 22q11.2 Deletion Syndrome Family Trios for Genotype to Phenotype Correlations. Human Mutation, 2015, 36, 797-807. | 2.5 | 16 |
| 22 | Deep post-GWAS analysis identifies potential risk genes and risk variants for Alzheimerâ€™s disease, providing new insights into its disease mechanisms. Scientific Reports, 2021, 11, 20511. | 3.3 | 16 |
| 23 | MicroRNA expression and gene regulation drive breast cancer progression and metastasis in PyMT mice. Breast Cancer Research, 2016, 18, 75. | 5.0 | 14 |
| 24 | Network analysis of mitonuclear GWAS reveals functional networks and tissue expression profiles of disease-associated genes. Human Genetics, 2017, 136, 55-65. | 3.8 | 14 |
| 25 | Inducible aging in Hydra oligactis implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. GeroScience, 2020, 42, 1119-1132. | 4.6 | 13 |
| 26 | Genetic signature of human longevity in PKC and NFâ€ºB signaling. Aging Cell, 2021, 20, e13362. | 6.7 | 12 |
| 27 | Ectopic cervical thymi and no thymic involution until midlife in naked mole rats. Aging Cell, 2021, 20, e13477. | 6.7 | 12 |
| 28 | Sensitivity of primary fibroblasts in culture to atmospheric oxygen does not correlate with species lifespan. Aging, 2016, 8, 841-847. | 3.1 | 10 |
| 29 | Epigenetic alterations to Polycomb targets precede malignant transition in a mouse model of breast cancer. Scientific Reports, 2018, 8, 5535. | 3.3 | 9 |
| 30 | Detection of copy number variation from array intensity and sequencing read depth using a stepwise Bayesian model. BMC Bioinformatics, 2010, 11, 539. | 2.6 | 7 |
| 31 | SubNet: a Java application for subnetwork extraction. Bioinformatics, 2013, 29, 2958-2958. | 4.1 | 7 |
| 32 | Integrated rare variant-based risk gene prioritization in disease case-control sequencing studies. PLoS Genetics, 2017, 13, e1007142. | 3.5 | 7 |
| 33 | Global, integrated analysis of methylomes and transcriptomes from laser capture microdissected bronchial and alveolar cells in human lung. Epigenetics, 2018, 13, 264-274. | 2.7 | 7 |
| 34 | Genomic expansion of Aldh1a1 protects beavers against high metabolic aldehydes from lipid oxidation. Cell Reports, 2021, 37, 109965. | 6.4 | 7 |
| 35 | PGA: post-GWAS analysis for disease gene identification. Bioinformatics, 2018, 34, 1786-1788. | 4.1 | 4 |
| 36 | Unravelling genetic components of longevity. Nature Aging, 2022, 2, 5-6. | 11.6 | 3 |