## Dapeng Zhang

List of Publications by Year in descending order

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57	3,943	29 h-index	57
papers	citations		g-index
61	61	61	6537 citing authors
all docs	docs citations	times ranked	

#	Article	IF	CITATIONS
1	N6-Methyladenine DNA Modification in Drosophila. Cell, 2015, 161, 893-906.	13.5	570
2	Polymorphic toxin systems: Comprehensive characterization of trafficking modes, processing, mechanisms of action, immunity and ecology using comparative genomics. Biology Direct, 2012, 7, 18.	1.9	440
3	Discovery of Novel DENN Proteins: Implications for the Evolution of Eukaryotic Intracellular Membrane Structures and Human Disease. Frontiers in Genetics, 2012, 3, 283.	1.1	220
4	Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. Nucleic Acids Research, 2015, 43, 10633-10654.	6.5	200
5	A novel immunity system for bacterial nucleic acid degrading toxins and its recruitment in various eukaryotic and DNA viral systems. Nucleic Acids Research, 2011, 39, 4532-4552.	6.5	184
6	Evolution of the deaminase fold and multiple origins of eukaryotic editing and mutagenic nucleic acid deaminases from bacterial toxin systems. Nucleic Acids Research, 2011, 39, 9473-9497.	6.5	154
7	The goldfish (Carassius auratus) as a model for neuroendocrine signaling. Molecular and Cellular Endocrinology, 2008, 293, 43-56.	1.6	147
8	A conserved NAD <sup>+</sup> binding pocket that regulates protein-protein interactions during aging. Science, 2017, 355, 1312-1317.	6.0	140
9	Adenine methylation in eukaryotes: Apprehending the complex evolutionary history and functional potential of an epigenetic modification. BioEssays, 2016, 38, 27-40.	1.2	132
10	Identification of novel families and classification of the C2 domain superfamily elucidate the origin and evolution of membrane targeting activities in eukaryotes. Gene, 2010, 469, 18-30.	1.0	124
11	Computational identification of novel biochemical systems involved in oxidation, glycosylation and other complex modifications of bases in DNA. Nucleic Acids Research, 2013, 41, 7635-7655.	6.5	115
12	<i>O-</i> GlcNAcylation destabilizes the active tetrameric PKM2 to promote the Warburg effect. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13732-13737.	3.3	105
13	The Natural History of ADP-Ribosyltransferases and the ADP-Ribosylation System. Current Topics in Microbiology and Immunology, 2014, 384, 3-32.	0.7	99
14	Bacterial GRAS domain proteins throw new light on gibberellic acid response mechanisms. Bioinformatics, 2012, 28, 2407-2411.	1.8	93
15	Integration of membrane and nuclear estrogen receptor signaling. Comparative Biochemistry and Physiology Part A, Molecular & Samp; Integrative Physiology, 2006, 144, 306-315.	0.8	81
16	Novel Immunoglobulin Domain Proteins Provide Insights into Evolution and Pathogenesis of SARS-CoV-2-Related Viruses. MBio, 2020, $11$ , .	1.8	81
17	EFCAB7 and IQCE Regulate Hedgehog Signaling by Tethering the EVC-EVC2 Complex to the Base of Primary Cilia. Developmental Cell, 2014, 28, 483-496.	3.1	76
18	OST-HTH: a novel predicted RNA-binding domain. Biology Direct, 2010, 5, 13.	1.9	67

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19	Gene flow and biological conflict systems in the origin and evolution of eukaryotes. Frontiers in Cellular and Infection Microbiology, 2012, 2, 89.	1.8	67
20	New insights into granin-derived peptides: evolution and endocrine roles. General and Comparative Endocrinology, 2009, 164, 161-174.	0.8	58
21	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. Nucleic Acids Research, 2016, 44, 3513-3533.	6.5	54
22	Lineage-specific expansions of TET/JBP genes and a new class of DNA transposons shape fungal genomic and epigenetic landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1676-1683.	3.3	51
23	Functional insight into Maelstrom in the germline piRNA pathway: a unique domain homologous to the DnaQ-H 3'–5' exonuclease, its lineage-specific expansion/loss and evolutionarily active site switch. Biology Direct, 2008, 3, 48.	1.9	49
24	Novel transglutaminase-like peptidase and C2 domains elucidate the structure, biogenesis and evolution of the ciliary compartment. Cell Cycle, 2012, 11, 3861-3875.	1.3	46
25	Antimicrobial Peptides, Polymorphic Toxins, and Self-Nonself Recognition Systems in Archaea: an Untapped Armory for Intermicrobial Conflicts. MBio, 2019, 10, .	1.8	41
26	Resilience of biochemical activity in protein domains in the face of structural divergence. Current Opinion in Structural Biology, 2014, 26, 92-103.	2.6	39
27	Defining Global Neuroendocrine Gene Expression Patterns Associated with Reproductive Seasonality in Fish. PLoS ONE, 2009, 4, e5816.	1.1	39
28	Using Generalized Procrustes Analysis (GPA) for normalization of cDNA microarray data. BMC Bioinformatics, 2008, 9, 25.	1.2	38
29	Profiling neuroendocrine gene expression changes following fadrozole-induced estrogen decline in the female goldfish. Physiological Genomics, 2009, 38, 351-361.	1.0	29
30	Whole exome sequencing identifies the TNNI3K gene as a cause of familial conduction system disease and congenital junctional ectopic tachycardia. International Journal of Cardiology, 2015, 185, 114-116.	0.8	29
31	Protein and DNA Modifications: Evolutionary Imprints of Bacterial Biochemical Diversification and Geochemistry on the Provenance of Eukaryotic Epigenetics. Cold Spring Harbor Perspectives in Biology, 2014, 6, a016063-a016063.	2.3	26
32	Profiling the rainbow trout hepatic miRNAome under diet-induced hyperglycemia. Physiological Genomics, 2019, 51, 411-431.	1.0	26
33	The XS domain of a plant specific SGS3 protein adopts a unique RNA recognition motif (RRM) fold. Cell Cycle, 2008, 7, 2268-2270.	1.3	25
34	SANTA domain: a novel conserved protein module in Eukaryota with potential involvement in chromatin regulation. Bioinformatics, 2006, 22, 2459-2462.	1.8	23
35	Loss of the Spinocerebellar Ataxia type 3 disease protein ATXN3 alters transcription of multiple signal transduction pathways. PLoS ONE, 2018, 13, e0204438.	1.1	23
36	The catalytic core of DEMETER guides active DNA demethylation in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17563-17571.	3.3	23

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37	Long nonâ€coding <scp>RNA ELDR</scp> enhances oral cancer growth by promoting <scp>ILF</scp> 3â€cyclin E1 signaling. EMBO Reports, 2020, 21, e51042.	2.0	21
38	Secretoneurin is a potential paracrine factor from lactotrophs stimulating gonadotropin release in the goldfish pituitary. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2010, 299, R1290-R1297.	0.9	20
39	MicroTrout: A comprehensive, genome-wide miRNA target prediction framework for rainbow trout, Oncorhynchus mykiss. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 20, 19-26.	0.4	20
40	Unification and extensive diversification of M/Orf3-related ion channel proteins in coronaviruses and other nidoviruses. Virus Evolution, 2021, 7, veab $014$ .	2.2	17
41	Temporal expression and steroidal regulation of piRNA pathway genes (mael, piwi, vasa) during Silurana (Xenopus) tropicalis embryogenesis and early larval development. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2010, 152, 202-206.	1.3	16
42	Functional prediction and physiological characterization of a novel short trans-membrane protein 1 as a subunit of mitochondrial respiratory complexes. Physiological Genomics, 2012, 44, 1133-1140.	1.0	16
43	Rapid modulation of gene expression profiles in the telencephalon of male goldfish following exposure to waterborne sex pheromones. General and Comparative Endocrinology, 2013, 192, 204-213.	0.8	16
44	Novel clades of the HU/IHF superfamily point to unexpected roles in the eukaryotic centrosome, chromosome partitioning, and biologic conflicts. Cell Cycle, 2017, 16, 1093-1103.	1.3	14
45	Social status regulates the hepatic miRNAome in rainbow trout: Implications for posttranscriptional regulation of metabolic pathways. PLoS ONE, 2019, 14, e0217978.	1.1	14
46	Acidic pH irreversibly activates the signaling enzyme SARM1. FEBS Journal, 2021, 288, 6783-6794.	2.2	11
47	The eukaryotic translation initiation regulator CDC123 defines a divergent clade of ATP-grasp enzymes with a predicted role in novel protein modifications. Biology Direct, 2015, 10, 21.	1.9	9
48	Comparative analysis reveals the expansion of mitochondrial DNA control region containing unusually high G-C tandem repeat arrays in Nasonia vitripennis. International Journal of Biological Macromolecules, 2021, 166, 1246-1257.	3.6	9
49	"RETRACTED ARTICLE: Vibrio parahaemolyticus RhsP represents a widespread group of pro-effectors for type VI secretion systems. Nature Communications, 2018, 9, 3899.	5.8	8
50	Homology between DUF784, DUF1278 domains and the plant prolamin superfamily typifies evolutionary changes of disulfide bonding patterns. Cell Cycle, 2009, 8, 3428-3430.	1.3	6
51	Screening for novel hexanucleotide repeat expansions at ALS- and FTD-associated loci. Neurology: Genetics, 2016, 2, e71.	0.9	6
52	Comparative Phylogenomic Analysis Reveals Evolutionary Genomic Changes and Novel Toxin Families in Endophytic <i>Liberibacter</i> Pathogens. Microbiology Spectrum, 2021, 9, e0050921.	1.2	6
53	Photoglobin, a distinct family of non-heme binding globins, defines a potential photosensor in prokaryotic signal transduction systems. Computational and Structural Biotechnology Journal, 2022, 20, 261-273.	1.9	4
54	Characterization of multiple nestin isoforms in the goldfish brain. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 19, 8-17.	0.4	2

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55	Draft Genome Assemblies of Two Staphylococcus pseudintermedius Strains Isolated from Canine Skin Biopsy Specimens. Microbiology Resource Announcements, 2020, 9, .	0.3	2
56	Genomic and <i>in vitro</i> pharmacodynamic analysis of rifampicin resistance in multidrugâ€resistant canine <i>Staphylococcus pseudintermedius</i> isolates. Veterinary Dermatology, 2021, 32, 219.	0.4	2
57	Estrogen Signaling Mechanisms. , 2010, , 273-288.		0