

Wei Miao

List of Publications by Year in descending order

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72
papers

1,960
citations

257450

24
h-index

289244

40
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77
all docs

77
docs citations

77
times ranked

1591
citing authors

#	ARTICLE	IF	CITATIONS
1	Microarray Analyses of Gene Expression during the <i>Tetrahymena thermophila</i> Life Cycle. PLoS ONE, 2009, 4, e4429.	2.5	163
2	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .	6.0	130
3	Transcriptome Analysis of the Model Protozoan, <i>Tetrahymena thermophila</i> , Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	2.5	111
4	Selecting One of Several Mating Types through Gene Segment Joining and Deletion in <i>Tetrahymena thermophila</i> . PLoS Biology, 2013, 11, e1001518.	5.6	81
5	Impaired replication elongation in <i>Tetrahymena</i> mutants deficient in histone H3 Lys 27 monomethylation. Genes and Development, 2013, 27, 1662-1679.	5.9	64
6	Tracing the structural evolution of eukaryotic ATP binding cassette transporter superfamily. Scientific Reports, 2015, 5, 16724.	3.3	55
7	Phylogenetic Relationships of the Subclass Peritrichia (Oligohymenophorea, Ciliophora) with Emphasis on the Genus <i>Epistylis</i> , Inferred from Small Subunit rRNA Gene Sequences. Journal of Eukaryotic Microbiology, 2001, 48, 583-587.	1.7	53
8	<i>Tetrahymena</i> Functional Genomics Database (TetraFGD): an integrated resource for <i>Tetrahymena</i> functional genomics. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat008.	3.0	51
9	Insights into the origin and evolution of Peritrichia (Oligohymenophorea, Ciliophora) based on analyses of morphology and phylogenomics. Molecular Phylogenetics and Evolution, 2019, 132, 25-35.	2.7	50
10	Phylogenetic Relationships of the Subclass Peritrichia (Oligohymenophorea, Ciliophora) Inferred from Small Subunit rRNA Gene Sequences1. Journal of Eukaryotic Microbiology, 2004, 51, 180-186.	1.7	49
11	The Genome of the Myxosporean <i>Thelohanelles kitauei</i> Shows Adaptations to Nutrient Acquisition within Its Fish Host. Genome Biology and Evolution, 2014, 6, 3182-3198.	2.5	48
12	High frequency of +1 programmed ribosomal frameshifting in <i>Euplotes octocarinatus</i> . Scientific Reports, 2016, 6, 21139.	3.3	48
13	Genome of the facultative scuticociliatosis pathogen <i>Pseudocohnilembus persalinus</i> provides insight into its virulence through horizontal gene transfer. Scientific Reports, 2015, 5, 15470.	3.3	46
14	A germline-limited piggyBac transposase gene is required for precise excision in <i>Tetrahymena</i> genome rearrangement. Nucleic Acids Research, 2017, 45, 9481-9502.	14.5	43
15	<i>Vorticella</i> Linnaeus, 1767 (Ciliophora, Oligohymenophora, Peritrichia) is a Grade not a Clade: Redefinition of <i>Vorticella</i> and the Families Vorticellidae and Astylozoidae using Molecular Characters Derived from the Gene Coding for Small Subunit Ribosomal RNA. Protist, 2012, 163, 129-142.	1.5	42
16	RNAi-dependent Polycomb repression controls transposable elements in <i>Tetrahymena</i> . Genes and Development, 2019, 33, 348-364.	5.9	42
17	Reevaluation of the Phylogenetic Relationship between Mobilid and Sessilid Peritrichs (Ciliophora). Tj ETQq1 1 0.784314 rgBT /Overlook Microbiology, 2006, 53, 397-403.	1.7	41
18	<i>Tetrahymena</i> Gene Expression Database (TGED): A resource of microarray data and co-expression analyses for <i>Tetrahymena</i> . Science China Life Sciences, 2011, 54, 65-67.	4.9	37

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19	Phylogenomic analyses reveal subclass Scuticociliatia as the sister group of subclass Hymenostomatia within class Oligohymenophorea. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 104-111.	2.7	37
20	New phylogenomic and comparative analyses provide corroborating evidence that Myxozoa is Cnidaria. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 10-18.	2.7	34
21	Cloning and Characterization of a New Multi-Stress Inducible Metallothionein Gene in <i>Tetrahymena pyriformis</i> . <i>Protist</i> , 2006, 157, 193-203.	1.5	31
22	A DP-like transcription factor protein interacts with E2f1 to regulate meiosis in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2018, 17, 634-642.	2.6	31
23	Hidden genomic evolution in a morphospecies—The landscape of rapidly evolving genes in <i>Tetrahymena</i> . <i>PLoS Biology</i> , 2019, 17, e3000294.	5.6	31
24	Whole Genome Studies of <i>Tetrahymena</i> . <i>Methods in Cell Biology</i> , 2012, 109, 53-81.	1.1	30
25	Genome-wide identification and characterization of cytochrome P450 monooxygenase genes in the ciliate <i>Tetrahymena thermophila</i> . <i>BMC Genomics</i> , 2009, 10, 208.	2.8	29
26	Genome-wide identification and evolution of ATP-binding cassette transporters in the ciliate <i>Tetrahymena thermophila</i> : A case of functional divergence in a multigene family. <i>BMC Evolutionary Biology</i> , 2010, 10, 330.	3.2	29
27	Gene Network Landscape of the Ciliate <i>Tetrahymena thermophila</i> . <i>PLoS ONE</i> , 2011, 6, e20124.	2.5	28
28	Missing Genes, Multiple ORFs, and C-to-U Type RNA Editing in <i>Acrasis kona</i> (Heterolobosea, Excavata) Mitochondrial DNA. <i>Genome Biology and Evolution</i> , 2014, 6, 2240-2257.	2.5	26
29	Dissecting relative contributions of <i>cis</i> - and <i>trans</i> -determinants to nucleosome distribution by comparing <i>Tetrahymena</i> macronuclear and micronuclear chromatin. <i>Nucleic Acids Research</i> , 2016, 44, gkw684.	14.5	25
30	Identification and characterization of the arsenite methyltransferase from a protozoan, <i>Tetrahymena pyriformis</i> . <i>Aquatic Toxicology</i> , 2014, 149, 50-57.	4.0	24
31	The Giant Zooxanthellae-Bearing Ciliate <i>Maristentor dinoferus</i> (Heterotrichea) is Closely Related to Folliculinidae. <i>Journal of Eukaryotic Microbiology</i> , 2005, 52, 11-16.	1.7	23
32	Nonsense-mediated mRNA decay in <i>Tetrahymena</i> is EJC independent and requires a protozoa-specific nuclease. <i>Nucleic Acids Research</i> , 2017, 45, 6848-6863.	14.5	22
33	Intraspecific phylogeography of <i>Carchesium polypinum</i> (Peritrichia, Ciliophora) from China, inferred from 18S-ITS1-5.8S ribosomal DNA. <i>Science in China Series C: Life Sciences</i> , 2004, 47, 11.	1.3	21
34	Differentially expressed genes of <i>Tetrahymena thermophila</i> in response to tributyltin (TBT) identified by suppression subtractive hybridization and real time quantitative PCR. <i>Aquatic Toxicology</i> , 2007, 81, 99-105.	4.0	21
35	Phosphoproteomic Analysis of Protein Phosphorylation Networks in <i>Tetrahymena thermophila</i> , a Model Single-celled Organism. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 503-519.	3.8	21
36	Cloning, characterization, and gene expression analysis of a novel cadmium metallothionein gene in <i>Tetrahymena pigmentosa</i> . <i>Gene</i> , 2008, 423, 29-35.	2.2	19

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37	Independent Transport and Sorting of Functionally Distinct Protein Families in <i>Tetrahymena thermophila</i> Dense Core Secretory Granules. <i>Eukaryotic Cell</i> , 2009, 8, 1575-1583.	3.4	18
38	Cyc17, a meiosis-specific cyclin, is essential for anaphase initiation and chromosome segregation in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2016, 15, 1855-1864.	2.6	17
39	Cdk3, a conjugation-specific cyclin-dependent kinase, is essential for the initiation of meiosis in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2016, 15, 2506-2514.	2.6	17
40	Absolute quantification of chromosome copy numbers in the polyploid macronucleus of <i>Tetrahymena thermophila</i> at the single-cell level. <i>Journal of Eukaryotic Microbiology</i> , 2022, 69, e12907.	1.7	17
41	A P450 gene associated with robust resistance to DDT in ciliated protozoan, <i>Tetrahymena thermophila</i> by efficient degradation. <i>Aquatic Toxicology</i> , 2014, 149, 126-132.	4.0	15
42	Identification of differentially expressed genes in <i>Tetrahymena thermophila</i> in response to dichlorodiphenyltrichloroethane (DDT) by suppression subtractive hybridization. <i>Environmental Microbiology</i> , 2006, 8, 1122-1129.	3.8	14
43	ATP-binding cassette transporter enhances tolerance to DDT in <i>Tetrahymena</i> . <i>Science China Life Sciences</i> , 2015, 58, 297-304.	4.9	14
44	Single-cell transcriptome sequencing of rumen ciliates provides insight into their molecular adaptations to the anaerobic and carbohydrate-rich rumen microenvironment. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106687.	2.7	14
45	Protist 10,000 Genomes Project. <i>Innovation(China)</i> , 2020, 1, 100058.	9.1	14
46	EOGD: the <i>Euplotes octocarinatus</i> genome database. <i>BMC Genomics</i> , 2018, 19, 63.	2.8	12
47	The sexual cell cycle initiation is regulated by CDK19/CYC9 in <i>Tetrahymena thermophila</i> . <i>Journal of Cell Science</i> , 2020, 133, .	2.0	12
48	The key role of CYC2 during meiosis in <i>Tetrahymena thermophila</i> . <i>Protein and Cell</i> , 2016, 7, 236-249.	11.0	11
49	Transcriptome Analysis Reveals the Molecular Mechanism of Resting Cyst Formation in <i>Colpoda aspera</i> . <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 212-220.	1.7	11
50	A Chitinase from <i>Aeromonas veronii</i> CD3 with the Potential to Control Myxozoan Disease. <i>PLoS ONE</i> , 2011, 6, e29091.	2.5	10
51	A strategy for complete telomere-to-telomere assembly of ciliate macronuclear genome using ultra-high coverage Nanopore data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 1928-1932.	4.1	10
52	Toxicogenomic investigation of <i>Tetrahymena thermophila</i> exposed to dichlorodiphenyltrichloroethane (DDT), tributyltin (TBT), and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). <i>Science China Life Sciences</i> , 2011, 54, 617-625.	4.9	9
53	E2f11 is a meiosis-specific transcription factor in the protist <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2017, 16, 123-135.	2.6	9
54	Phylogenomic analysis of <i>Balantidium ctenopharyngodoni</i> (Ciliophora, Litostomatea) based on single-cell transcriptome sequencing. <i>Parasite</i> , 2017, 24, 43.	2.0	9

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55	Exploration of Genetic Variations through Single-cell Whole-genome Sequencing in the Model Ciliate <i>Tetrahymena thermophila</i> . <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 954-965.	1.7	8
56	Drivers of Mating Type Composition in <i>Tetrahymena thermophila</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2328-2343.	2.5	8
57	Application of polyurethane foam units and calorimetry to microbial monitoring in Lake Donghu. <i>Thermochimica Acta</i> , 2005, 438, 63-69.	2.7	7
58	The nonhistone, N-terminal tail of an essential, chimeric H2A variant regulates mitotic H3-S10 dephosphorylation. <i>Genes and Development</i> , 2012, 26, 615-629.	5.9	7
59	<i>Tetrahymena</i> Comparative Genomics Database (TCGD): a community resource for <i>Tetrahymena</i> . <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	7
60	Proteomic identification and expression of oral apparatus constituents in cell regeneration of giant ciliate <i>Stentor coeruleus</i> (strain WHEL). <i>Gene</i> , 2020, 743, 144624.	2.2	7
61	Evolution of the mating type gene pair and multiple sexes in <i>Tetrahymena</i> . <i>iScience</i> , 2021, 24, 101950.	4.1	7
62	Identification and Characterization of Base-Substitution Mutations in the Macronuclear Genome of the Ciliate <i>Tetrahymena thermophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	5
63	Proteogenomic Analysis Provides Novel Insight into Genome Annotation and Nitrogen Metabolism in <i>Nostoc</i> sp. PCC 7120. <i>Microbiology Spectrum</i> , 2021, 9, e0049021.	3.0	5
64	Bacteria-Derived Hemolysis-Related Genes Widely Exist in Scuticociliates. <i>Microorganisms</i> , 2020, 8, 1838.	3.6	4
65	RNA Interference by Cyanobacterial Feeding Demonstrates the SCSG1 Gene Is Essential for Ciliogenesis during Oral Apparatus Regeneration in <i>Stentor</i> . <i>Microorganisms</i> , 2021, 9, 176.	3.6	4
66	Phylogenetic relationships among six species of <i>Epistylis</i> inferred from 18S-ITS1 sequences. <i>Science in China Series C: Life Sciences</i> , 2002, 45, 280.	1.3	3
67	Cd-Metallothioneins in Three Additional <i>Tetrahymena</i> Species: Intragenic Repeat Patterns and Induction by Metal Ions. <i>Journal of Eukaryotic Microbiology</i> , 2014, 61, 333-342.	1.7	3
68	<i>Pseudocohnilembus persalinus</i> genome database - the first genome database of facultative scuticociliatosis pathogens. <i>BMC Genomics</i> , 2018, 19, 676.	2.8	3
69	Epidermal growth factor-induced stimulation of proliferation and gene expression changes in the hypotrichous ciliate, <i>Stylonychia lemnae</i> . <i>Gene</i> , 2016, 592, 186-192.	2.2	2
70	Cloning and Expression Analysis of <i>Tetrahymena</i> ; 2-Oxoglutarate/Malate Carrier Gene (<i>OMC</i>) Exposed to Dichlorodiphenyltrichloroethane (DDT)*. <i>Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology</i> , 2010, 16, 216-221.	0.1	2
71	Sequencing and characterization of the macronuclear rDNA minichromosome of the protozoan <i>Tetrahymena pyriformis</i> . <i>International Journal of Biological Macromolecules</i> , 2020, 147, 576-581.	7.5	1
72	Zfp1, a Cys2His2 zinc finger protein is required for meiosis initiation in <i>Tetrahymena thermophila</i> . <i>Cell Cycle</i> , 2022, , 1-12.	2.6	1