List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Absolute quantification of chromosome copy numbers in the polyploid macronucleus of <i>Tetrahymena thermophila</i> at the singleâ€cell level. Journal of Eukaryotic Microbiology, 2022, 69, e12907.	0.8	17
2	Zfp1, a Cys2His2 zinc finger protein is required for meiosis initiation in <i>Tetrahymena thermophila</i> . Cell Cycle, 2022, , 1-12.	1.3	1
3	Identification and Characterization of Base-Substitution Mutations in the Macronuclear Genome of the Ciliate <i>Tetrahymena thermophila</i> . Genome Biology and Evolution, 2021, 13, .	1.1	5
4	A strategy for complete telomere-to-telomere assembly of ciliate macronuclear genome using ultra-high coverage Nanopore data. Computational and Structural Biotechnology Journal, 2021, 19, 1928-1932.	1.9	10
5	Evolution of the mating type gene pair and multiple sexes in Tetrahymena. IScience, 2021, 24, 101950.	1.9	7
6	Proteogenomic Analysis Provides Novel Insight into Genome Annotation and Nitrogen Metabolism in <i>Nostoc</i> sp. PCC 7120. Microbiology Spectrum, 2021, 9, e0049021.	1.2	5
7	RNA Interference by Cyanobacterial Feeding Demonstrates the SCSG1 Gene Is Essential for Ciliogenesis during Oral Apparatus Regeneration in Stentor. Microorganisms, 2021, 9, 176.	1.6	4
8	Single-cell transcriptome sequencing of rumen ciliates provides insight into their molecular adaptations to the anaerobic and carbohydrate-rich rumen microenvironment. Molecular Phylogenetics and Evolution, 2020, 143, 106687.	1.2	14
9	Protist 10,000 Genomes Project. Innovation(China), 2020, 1, 100058.	5.2	14
10	Bacteria-Derived Hemolysis-Related Genes Widely Exist in Scuticociliates. Microorganisms, 2020, 8, 1838.	1.6	4
11	The sexual cell cycle initiation is regulated by CDK19/CYC9 in <i>Tetrahymena thermophila</i> . Journal of Cell Science, 2020, 133, .	1.2	12
12	Proteomic identification and expression of oral apparatus constituents in cell regeneration of giant ciliate Stentor coeruleus (strain WHEL). Gene, 2020, 743, 144624.	1.0	7
13	Sequencing and characterization of the macronuclear rDNA minichromosome of the protozoan Tetrahymena pyriformis. International Journal of Biological Macromolecules, 2020, 147, 576-581.	3.6	1
14	Drivers of Mating Type Composition in <i>Tetrahymena thermophila</i> . Genome Biology and Evolution, 2020, 12, 2328-2343.	1.1	8
15	Transcriptome Analysis Reveals the Molecular Mechanism of Resting Cyst Formation in <i>Colpoda aspera</i> . Journal of Eukaryotic Microbiology, 2019, 66, 212-220.	0.8	11
16	Exploration of Genetic Variations through Singleâ€cell Wholeâ€genome Sequencing in the Model CiliateTetrahymena thermophila. Journal of Eukaryotic Microbiology, 2019, 66, 954-965.	0.8	8
17	Hidden genomic evolution in a morphospecies—The landscape of rapidly evolving genes in Tetrahymena. PLoS Biology, 2019, 17, e3000294.	2.6	31
18	<i>Tetrahymena</i> Comparative Genomics Database (TCGD): a community resource for <i>Tetrahymena</i> . Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	7

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19	RNAi-dependent <i>Polycomb</i> repression controls transposable elements in <i>Tetrahymena</i> . Genes and Development, 2019, 33, 348-364.	2.7	42
20	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.	1.2	50
21	A DP-like transcription factor protein interacts with E2fl1 to regulate meiosis in <i>Tetrahymena thermophila</i> . Cell Cycle, 2018, 17, 634-642.	1.3	31
22	Pseudocohnilembus persalinus genome database - the first genome database of facultative scuticociliatosis pathogens. BMC Genomics, 2018, 19, 676.	1.2	3
23	EOGD: the Euplotes octocarinatus genome database. BMC Genomics, 2018, 19, 63.	1.2	12
24	E2fl1 is a meiosis-specific transcription factor in the protist Tetrahymena thermophila. Cell Cycle, 2017, 16, 123-135.	1.3	9
25	Nonsense-mediated mRNA decay in Tetrahymena is EJC independent and requires a protozoa-specific nuclease. Nucleic Acids Research, 2017, 45, 6848-6863.	6.5	22
26	A germline-limited piggyBac transposase gene is required for precise excision in Tetrahymena genome rearrangement. Nucleic Acids Research, 2017, 45, 9481-9502.	6.5	43
27	Phylogenomic analysis of <i>Balantidium ctenopharyngodoni</i> (Ciliophora, Litostomatea) based on single-cell transcriptome sequencing. Parasite, 2017, 24, 43.	0.8	9
28	Dissecting relative contributions of <i>cis</i> - and <i>trans</i> -determinants to nucleosome distribution by comparing <i>Tetrahymena</i> macronuclear and micronuclear chromatin. Nucleic Acids Research, 2016, 44, gkw684.	6.5	25
29	The key role of CYC2 during meiosis in Tetrahymena thermophila. Protein and Cell, 2016, 7, 236-249.	4.8	11
30	Cyc17, a meiosis-specific cyclin, is essential for anaphase initiation and chromosome segregation in <i>Tetrahymena thermophila</i> . Cell Cycle, 2016, 15, 1855-1864.	1.3	17
31	Epidermal growth factor-induced stimulation of proliferation and gene expression changes in the hypotrichous ciliate, Stylonychia lemnae. Gene, 2016, 592, 186-192.	1.0	2
32	Cdk3, a conjugation-specific cyclin-dependent kinase, is essential for the initiation of meiosis in Tetrahymena thermophila. Cell Cycle, 2016, 15, 2506-2514.	1.3	17
33	High frequency of +1 programmed ribosomal frameshifting in Euplotes octocarinatus. Scientific Reports, 2016, 6, 21139.	1.6	48
34	Structure of the germline genome of Tetrahymena thermophila and relationship to the massively rearranged somatic genome. ELife, 2016, 5, .	2.8	130
35	Tracing the structural evolution of eukaryotic ATP binding cassette transporter superfamily. Scientific Reports, 2015, 5, 16724.	1.6	55
36	Genome of the facultative scuticociliatosis pathogen Pseudocohnilembus persalinus provides insight into its virulence through horizontal gene transfer. Scientific Reports, 2015, 5, 15470.	1.6	46

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37	ATP-binding cassette transporter enhances tolerance to DDT in Tetrahymena. Science China Life Sciences, 2015, 58, 297-304.	2.3	14
38	Phylogenomic analyses reveal subclass Scuticociliatia as the sister group of subclass Hymenostomatia within class Oligohymenophorea. Molecular Phylogenetics and Evolution, 2015, 90, 104-111.	1.2	37
39	The Genome of the Myxosporean Thelohanellus kitauei Shows Adaptations to Nutrient Acquisition within Its Fish Host. Genome Biology and Evolution, 2014, 6, 3182-3198.	1.1	48
40	Missing Genes, Multiple ORFs, and C-to-U Type RNA Editing in Acrasis kona (Heterolobosea, Excavata) Mitochondrial DNA. Genome Biology and Evolution, 2014, 6, 2240-2257.	1.1	26
41	Cdâ€Metallothioneins in Three Additional <i>Tetrahymena</i> Species: Intragenic Repeat Patterns and Induction by Metal Ions. Journal of Eukaryotic Microbiology, 2014, 61, 333-342.	0.8	3
42	Phosphoproteomic Analysis of Protein Phosphorylation Networks in Tetrahymena thermophila, a Model Single-celled Organism. Molecular and Cellular Proteomics, 2014, 13, 503-519.	2.5	21
43	New phylogenomic and comparative analyses provide corroborating evidence that Myxozoa is Cnidaria. Molecular Phylogenetics and Evolution, 2014, 81, 10-18.	1.2	34
44	Identification and characterization of the arsenite methyltransferase from a protozoan, Tetrahymena pyriformis. Aquatic Toxicology, 2014, 149, 50-57.	1.9	24
45	A P450 gene associated with robust resistance to DDT in ciliated protozoan, Tetrahymena thermophila by efficient degradation. Aquatic Toxicology, 2014, 149, 126-132.	1.9	15
46	Tetrahymena Functional Genomics Database (TetraFGD): an integrated resource for Tetrahymena functional genomics. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat008.	1.4	51
47	Impaired replication elongation in <i>Tetrahymena</i> mutants deficient in histone H3 Lys 27 monomethylation. Genes and Development, 2013, 27, 1662-1679.	2.7	64
48	Selecting One of Several Mating Types through Gene Segment Joining and Deletion in Tetrahymena thermophila. PLoS Biology, 2013, 11, e1001518.	2.6	81
49	The nonhistone, N-terminal tail of an essential, chimeric H2A variant regulates mitotic H3-S10 dephosphorylation. Genes and Development, 2012, 26, 615-629.	2.7	7
50	Whole Genome Studies of Tetrahymena. Methods in Cell Biology, 2012, 109, 53-81.	0.5	30
51	Vorticella Linnaeus, 1767 (Ciliophora, Oligohymenophora, Peritrichia) is a Grade not a Clade: Redefinition of Vorticella and the Families Vorticellidae and Astylozoidae using Molecular Characters Derived from the Gene Coding for Small Subunit Ribosomal RNA. Protist, 2012, 163, 129-142.	0.6	42
52	Transcriptome Analysis of the Model Protozoan, Tetrahymena thermophila, Using Deep RNA Sequencing. PLoS ONE, 2012, 7, e30630.	1.1	111
53	Gene Network Landscape of the Ciliate Tetrahymena thermophila. PLoS ONE, 2011, 6, e20124.	1.1	28
54	A Chitinase from Aeromonas veronii CD3 with the Potential to Control Myxozoan Disease. PLoS ONE, 2011, 6, e29091.	1.1	10

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55	Tetrahymena Gene Expression Database (TGED): A resource of microarray data and co-expression analyses for Tetrahymena. Science China Life Sciences, 2011, 54, 65-67.	2.3	37
56	Toxicogenomic investigation of Tetrahymena thermophila exposed to dichlorodiphenyltrichloroethane (DDT), tributyltin (TBT), and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD). Science China Life Sciences, 2011, 54, 617-625.	2.3	9
57	Genome-wide identification and evolution of ATP-binding cassette transporters in the ciliate Tetrahymena thermophila: A case of functional divergence in a multigene family. BMC Evolutionary Biology, 2010, 10, 330.	3.2	29
58	Cloning and Expression Analysis of <i>Tetrahymena</i> 2-Oxoglutarate/Malate Carrier Gene (<i>OMC</i>) Exposed to Dichlorodiphenyltrichloroethane (DDT)*. Ying Yong Yu Huan Jing Sheng Wu Xue Bao = Chinese Journal of Applied and Environmental Biology, 2010, 16, 216-221.	0.1	2
59	Independent Transport and Sorting of Functionally Distinct Protein Families in <i>Tetrahymena thermophila</i> Dense Core Secretory Granules. Eukaryotic Cell, 2009, 8, 1575-1583.	3.4	18
60	Genome-wide identification and characterization of cytochrome P450 monooxygenase genes in the ciliate Tetrahymena thermophila. BMC Genomics, 2009, 10, 208.	1.2	29
61	Microarray Analyses of Gene Expression during the Tetrahymena thermophila Life Cycle. PLoS ONE, 2009, 4, e4429.	1.1	163
62	Cloning, characterization, and gene expression analysis of a novel cadmium metallothionein gene in Tetrahymena pigmentosa. Gene, 2008, 423, 29-35.	1.0	19
63	Differentially expressed genes of Tetrahymena thermophila in response to tributyltin (TBT) identified by suppression subtractive hybridization and real time quantitative PCR. Aquatic Toxicology, 2007, 81, 99-105.	1.9	21
64	Identification of differentially expressed genes in Tetrahymena thermophila in response to dichlorodiphenyltrichloroethane (DDT) by suppression subtractive hybridization. Environmental Microbiology, 2006, 8, 1122-1129.	1.8	14
65	Reevaluation of the Phylogenetic Relationship between Mobilid and Sessilid Peritrichs (Ciliophora,) Tj ETQq1 Microbiology, 2006, 53, 397-403.	1 0.784314 0.8	rgBT /Overloc 41
66	Cloning and Characterization of a New Multi-Stress Inducible Metallothionein Gene in Tetrahymena pyriformis. Protist, 2006, 157, 193-203.	0.6	31
67	Application of polyurethane foam units and calorimetry to microbial monitoring in Lake Donghu. Thermochimica Acta, 2005, 438, 63-69.	1.2	7
68	The Giant Zooxanthellae-Bearing Ciliate Maristentor dinoferus (Heterotrichea) is Closely Related to Folliculinidae. Journal of Eukaryotic Microbiology, 2005, 52, 11-16.	0.8	23
69	Phylogenetic Relationships of the Subclass Peritrichia (Oligohymenophorea, Ciliophora) Inferred from Small Subunit rRNA Gene Sequences1. Journal of Eukaryotic Microbiology, 2004, 51, 180-186.	0.8	49
70	Intraspecific phylogeography of Carchesium polypinum (Peritrichia, Ciliophora) from China, inferred from 18S-ITS1-5.8S ribosomal DNA. Science in China Series C: Life Sciences, 2004, 47, 11.	1.3	21
71	Phylogenetic relationships among six species of Epistylis inferred from 18S-ITS1 sequences. Science in China Series C: Life Sciences, 2002, 45, 280.	1.3	3
72	Phylogenetic Relationships of the Subclass Peritrichia (Oligohymenophorea, Ciliophora) with Emphasis on the Genus Epistylis, Inferred from Small Subunit rRNA Gene Sequences. Journal of Eukaryotic Microbiology, 2001, 48, 583-587.	0.8	53