

Gertraud Burger

List of Publications by Year in descending order

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76326

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98
docs citations

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times ranked

9714
citing authors

#	ARTICLE	IF	CITATIONS
1	Trophic flexibility of marine diplomonads - switching from osmotrophy to bacterivory. ISME Journal, 2022, 16, 1409-1419.	9.8	10
2	Diplomonads – A Review on "New" Flagellates on the Oceanic Block. Protist, 2022, 173, 125868.	1.5	15
3	Gene Transfer Agents in Bacterial Endosymbionts of Microbial Eukaryotes. Genome Biology and Evolution, 2022, 14, .	2.5	8
4	Reductionist Pathways for Parasitism in Euglenozoans? Expanded Datasets Provide New Insights. Trends in Parasitology, 2021, 37, 100-116.	3.3	28
5	RNA Editing in Mitochondria and Plastids: Weird and Widespread. Trends in Genetics, 2021, 37, 99-102.	6.7	31
6	An Unexpectedly Complex Mitochondrion in <i>Andalucia godoyi</i> , a Protist with the Most Bacteria-like Mitochondrial Genome. Molecular Biology and Evolution, 2021, 38, 788-804.	8.9	8
7	Complete minicircle genome of <i>Leptomonas pyrrocoris</i> reveals sources of its non-canonical mitochondrial RNA editing events. Nucleic Acids Research, 2021, 49, 3354-3370.	14.5	9
8	Euglenozoa: taxonomy, diversity and ecology, symbioses and viruses. Open Biology, 2021, 11, 200407.	3.6	102
9	Vestiges of the Bacterial Signal Recognition Particle-Based Protein Targeting in Mitochondria. Molecular Biology and Evolution, 2021, 38, 3170-3187.	8.9	8
10	Distribution of Merlin in eukaryotes and first report of DNA transposons in kinetoplastid protists. PLoS ONE, 2021, 16, e0251133.	2.5	1
11	Single-cell genomics unveils a canonical origin of the diverse mitochondrial genomes of euglenozoans. BMC Biology, 2021, 19, 103.	3.8	10
12	Characterization of a new cosmopolitan genus of trypanosomatid parasites, <i>Obscuromonas</i> gen. nov. (Blastocrithidiinae subfam. nov.). European Journal of Protistology, 2021, 79, 125778.	1.5	12
13	A New Model Trypanosomatid, <i>Novymonas esmeraldas</i> : Genomic Perception of Its <i>Candidatus</i> Pandoraea novymonadis Endosymbiont. MBio, 2021, 12, e0160621.	4.1	8
14	Highly flexible metabolism of the marine euglenozoan protist <i>Diplonema papillatum</i> . BMC Biology, 2021, 19, 251.	3.8	19
15	Gene fragmentation and RNA editing without borders: eccentric mitochondrial genomes of diplomonads. Nucleic Acids Research, 2020, 48, 2694-2708.	14.5	31
16	<i>Vickermania</i> gen. nov., trypanosomatids that use two joined flagella to resist midgut peristaltic flow within the fly host. BMC Biology, 2020, 18, 187.	3.8	17
17	Highly Reduced Genomes of Protist Endosymbionts Show Evolutionary Convergence. Current Biology, 2020, 30, 925-933.e3.	3.9	41
18	Catalase and Ascorbate Peroxidase in Euglenozoan Protists. Pathogens, 2020, 9, 317.	2.8	12

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19	Targeted integration by homologous recombination enables in situ tagging and replacement of genes in the marine microeukaryote <i>Diplonema papillatum</i> . <i>Environmental Microbiology</i> , 2020, 22, 3660-3670.	3.8	9
20	A Uniquely Complex Mitochondrial Proteome from <i>Euglena gracilis</i> . <i>Molecular Biology and Evolution</i> , 2020, 37, 2173-2191.	8.9	22
21	The draft nuclear genome sequence and predicted mitochondrial proteome of <i>Andalucia godoyi</i> , a protist with the most gene-rich and bacteria-like mitochondrial genome. <i>BMC Biology</i> , 2020, 18, 22.	3.8	43
22	Evolution of metabolic capabilities and molecular features of diplomonads, kinetoplastids, and euglenids. <i>BMC Biology</i> , 2020, 18, 23.	3.8	48
23	Unique Dynamics of Paramylon Storage in the Marine Euglenozoan <i>Diplonema papillatum</i> . <i>Protist</i> , 2020, 171, 125717.	1.5	8
24	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. <i>Nature Methods</i> , 2020, 17, 481-494.	19.0	97
25	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	8
26	A Revised Taxonomy of Diplomonads Including the Eupelagonemidae n. fam. and a Type Species, <i>Eupelagonema oceanica</i> n. gen. & sp.. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 519-524.	1.7	17
27	Causes and Effects of Loss of Classical Nonhomologous End Joining Pathway in Parasitic Eukaryotes. <i>MBio</i> , 2019, 10, .	4.1	31
28	Parasite microbiome project: Grand challenges. <i>PLoS Pathogens</i> , 2019, 15, e1008028.	4.7	50
29	Morphological, Ultrastructural, Motility and Evolutionary Characterization of Two New Hemistasiidae Species. <i>Protist</i> , 2019, 170, 259-282.	1.5	32
30	Revisions to the Classification, Nomenclature, and Diversity of Eukaryotes. <i>Journal of Eukaryotic Microbiology</i> , 2019, 66, 4-119.	1.7	904
31	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. <i>ELife</i> , 2019, 8, .	6.0	91
32	Phylogeny and Morphology of New Diplomonads from Japan. <i>Protist</i> , 2018, 169, 158-179.	1.5	44
33	Extensive molecular tinkering in the evolution of the membrane attachment mode of the Rheb GTPase. <i>Scientific Reports</i> , 2018, 8, 5239.	3.3	9
34	Neobodonids are dominant kinetoplastids in the global ocean. <i>Environmental Microbiology</i> , 2018, 20, 878-889.	3.8	27
35	Trypanosomatid mitochondrial RNA editing: dramatically complex transcript repertoires revealed with a dedicated mapping tool. <i>Nucleic Acids Research</i> , 2018, 46, 765-781.	14.5	30
36	Transformation of <i>Diplonema papillatum</i> , the type species of the highly diverse and abundant marine microeukaryotes Diplomonada (Euglenozoa). <i>Environmental Microbiology</i> , 2018, 20, 1030-1040.	3.8	20

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37	Massive mitochondrial DNA content in diplomemid and kinetoplastid protists. IUBMB Life, 2018, 70, 1267-1274.	3.4	39
38	TbUTP10, a protein involved in early stages of pre-18S rRNA processing in Trypanosoma brucei. Molecular and Biochemical Parasitology, 2018, 225, 84-93.	1.1	7
39	Respiratory chain Complex I of unparalleled divergence in diplomemids. Journal of Biological Chemistry, 2018, 293, 16043-16056.	3.4	18
40	Perfection of eccentricity: Mitochondrial genomes of diplomemids. IUBMB Life, 2018, 70, 1197-1206.	3.4	24
41	Trypanosomal mitochondrial intermediate peptidase does not behave as a classical mitochondrial processing peptidase. PLoS ONE, 2018, 13, e0196474.	2.5	9
42	Life Cycle, Ultrastructure, and Phylogeny of New Diplonemids and Their Endosymbiotic Bacteria. MBio, 2018, 9, .	4.1	50
43	Keeping it complicated: Mitochondrial genome plasticity across diplomemids. Scientific Reports, 2017, 7, 14166.	3.3	18
44	Comparative Metabolism of Free-living <i>Bodo saltans</i> and Parasitic Trypanosomatids. Journal of Eukaryotic Microbiology, 2016, 63, 657-678.	1.7	86
45	Non-functional genes repaired at the RNA level. Comptes Rendus - Biologies, 2016, 339, 289-295.	0.2	2
46	Post-transcriptional mending of gene sequences: Looking under the hood of mitochondrial gene expression in diplomemids. RNA Biology, 2016, 13, 1204-1211.	3.1	14
47	Trypanosome <i>scp</i> RNA editing: the complexity of getting U in and taking U out. Wiley Interdisciplinary Reviews RNA, 2016, 7, 33-51.	6.4	124
48	Morphological Identification and Single-Cell Genomics of Marine Diplonemids. Current Biology, 2016, 26, 3053-3059.	3.9	83
49	Extreme Diversity of Diplonemid Eukaryotes in the Ocean. Current Biology, 2016, 26, 3060-3065.	3.9	105
50	Genes in Hiding. Trends in Genetics, 2016, 32, 553-565.	6.7	16
51	Novel modes of RNA editing in mitochondria. Nucleic Acids Research, 2016, 44, 4907-4919.	14.5	49
52	Aerobic mitochondria of parasitic protists: Diverse genomes and complex functions. Molecular and Biochemical Parasitology, 2016, 209, 46-57.	1.1	24
53	From simple to supercomplex: mitochondrial genomes of euglenozoan protists. F1000Research, 2016, 5, 392.	1.6	12
54	Three-dimensional structure model and predicted ATP interaction rewiring of a deviant RNA ligase 2. BMC Structural Biology, 2015, 15, 20.	2.3	4

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55	Eukaryotic plankton diversity in the sunlit ocean. <i>Science</i> , 2015, 348, 1261605.	12.6	1,551
56	Gene Loss and Error-Prone RNA Editing in the Mitochondrion of <i>Perkinsella</i> , an Endosymbiotic Kinetoplastid. <i>MBio</i> , 2015, 6, e01498-15.	4.1	28
57	Unexpectedly Streamlined Mitochondrial Genome of the Euglenozoan <i>Euglena gracilis</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 3358-3367.	2.5	57
58	Programmed translational bypassing elements in mitochondria: structure, mobility, and evolutionary origin. <i>Trends in Genetics</i> , 2015, 31, 187-194.	6.7	19
59	Diplonemids. <i>Current Biology</i> , 2015, 25, R702-R704.	3.9	46
60	Massive programmed translational jumping in mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5926-5931.	7.1	58
61	Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. <i>Nucleic Acids Research</i> , 2014, 42, 13764-13777.	14.5	129
62	Trans-splicing and RNA editing of LSU rRNA in <i>Diplonema</i> mitochondria. <i>Nucleic Acids Research</i> , 2014, 42, 2660-2672.	14.5	30
63	Strikingly Bacteria-Like and Gene-Rich Mitochondrial Genomes throughout Jakobid Protists. <i>Genome Biology and Evolution</i> , 2013, 5, 418-438.	2.5	222
64	Dual core processing: MRB1 is an emerging kinetoplast RNA editing complex. <i>Trends in Parasitology</i> , 2013, 29, 91-99.	3.3	53
65	An Advanced System of the Mitochondrial Processing Peptidase and Core Protein Family in <i>Trypanosoma brucei</i> and Multiple Origins of the Core I Subunit in Eukaryotes. <i>Genome Biology and Evolution</i> , 2013, 5, 860-875.	2.5	16
66	RNA-level unscrambling of fragmented genes in <i>Diplonema</i> mitochondria. <i>RNA Biology</i> , 2013, 10, 301-313.	3.1	33
67	CBOL Protist Working Group: Barcoding Eukaryotic Richness beyond the Animal, Plant, and Fungal Kingdoms. <i>PLoS Biology</i> , 2012, 10, e1001419.	5.6	488
68	The Revised Classification of Eukaryotes. <i>Journal of Eukaryotic Microbiology</i> , 2012, 59, 429-514.	1.7	1,340
69	Unscrambling genetic information at the RNA level. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 213-228.	6.4	25
70	Unusual Mitochondrial Genomes and Genes. , 2012, , 41-77.		9
71	Gene fragmentation: a key to mitochondrial genome evolution in Euglenozoa?. <i>Current Genetics</i> , 2011, 57, 225-232.	1.7	48
72	How a neutral evolutionary ratchet can build cellular complexity. <i>IUBMB Life</i> , 2011, 63, 528-537.	3.4	160

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73	Systematically fragmented genes in a multipartite mitochondrial genome. <i>Nucleic Acids Research</i> , 2011, 39, 979-988.	14.5	72
74	Evolutionarily Conserved cox1 Trans-Splicing Without cis-Motifs. <i>Molecular Biology and Evolution</i> , 2011, 28, 2425-2428.	8.9	28
75	Irremediable Complexity?. <i>Science</i> , 2010, 330, 920-921.	12.6	204
76	Group I-intron trans-splicing and mRNA editing in the mitochondria of placozoan animals. <i>Trends in Genetics</i> , 2009, 25, 381-386.	6.7	79
77	Plasticity of a key metabolic pathway in fungi. <i>Functional and Integrative Genomics</i> , 2009, 9, 145-151.	3.5	56
78	EST Databases and Web Tools for EST Projects. <i>Methods in Molecular Biology</i> , 2009, 533, 241-256.	0.9	2
79	Construction of cDNA Libraries: Focus on Protists and Fungi. <i>Methods in Molecular Biology</i> , 2009, 533, 33-47.	0.9	18
80	Unassigned MURF1 of kinetoplastids codes for NADH dehydrogenase subunit 2. <i>BMC Genomics</i> , 2008, 9, 455.	2.8	13
81	Mitochondrial DNA as a Genomic Jigsaw Puzzle. <i>Science</i> , 2007, 318, 415-415.	12.6	110
82	Purification of mitochondrial and plastid DNA. <i>Nature Protocols</i> , 2007, 2, 652-660.	12.0	58
83	Sequencing complete mitochondrial and plastid genomes. <i>Nature Protocols</i> , 2007, 2, 603-614.	12.0	84
84	Description of <i>Rhynchopus euleeides</i> n. sp. (Diplonemea), a Free-Living Marine Euglenozoan. <i>Journal of Eukaryotic Microbiology</i> , 2007, 54, 137-145.	1.7	32
85	Unusual Mitochondrial Genome Structures throughout the Euglenozoa. <i>Protist</i> , 2007, 158, 385-396.	1.5	50
86	Mitochondria of Protists. <i>Annual Review of Genetics</i> , 2004, 38, 477-524.	7.6	295
87	Parallels in Genome Evolution in Mitochondria and Bacterial Symbionts. <i>IUBMB Life</i> , 2003, 55, 205-212.	3.4	45
88	Mitochondrial genomes: anything goes. <i>Trends in Genetics</i> , 2003, 19, 709-716.	6.7	555
89	Unique mitochondrial genome architecture in unicellular relatives of animals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 892-897.	7.1	209
90	The enigmatic mitochondrial ORF ymf39 codes for ATP synthase chain b. <i>Nucleic Acids Research</i> , 2003, 31, 2353-2360.	14.5	38

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91	The Complete Mitochondrial DNA Sequence of <i>Scenedesmus obliquus</i> Reflects an Intermediate Stage in the Evolution of the Green Algal Mitochondrial Genome. <i>Genome Research</i> , 2000, 10, 819-831.	5.5	98
92	Complete Sequence of the Mitochondrial DNA of the Red Alga <i>Porphyra purpurea</i> : Cyanobacterial Introns and Shared Ancestry of Red and Green Algae. <i>Plant Cell</i> , 1999, 11, 1675-1694.	6.6	178
93	The Complete Mitochondrial DNA Sequences of <i>Nephroselmis olivacea</i> and <i>Pedinomonas minor</i> : Two Radically Different Evolutionary Patterns within Green Algae. <i>Plant Cell</i> , 1999, 11, 1717-1729.	6.6	154
94	A Comparative Genomics Approach to the Evolution of Eukaryotes and their Mitochondria. <i>Journal of Eukaryotic Microbiology</i> , 1999, 46, 320-326.	1.7	79
95	Mitochondrial Genome Evolution and the Origin of Eukaryotes. <i>Annual Review of Genetics</i> , 1999, 33, 351-397.	7.6	603
96	An ancestral mitochondrial DNA resembling a eubacterial genome in miniature. <i>Nature</i> , 1997, 387, 493-497.	27.8	658
97	UTILITY OF THE MITOCHONDRIAL <i>nad4L</i> GENE FOR ALGAL AND PROTISTAN PHYLOGENETIC ANALYSIS1. <i>Journal of Phycology</i> , 1996, 32, 452-456.	2.3	19