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List of Publications by Year
in descending order

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78 papers	8,386 citations	57758 44 h-index	79698 73 g-index
82 all docs	82 docs citations	82 times ranked	7865 citing authors

#	Article	IF	Citations
1	Endosymbionts in cranberry: Diversity, effect on plant growth, and pathogen biocontrol. Plants People Planet, 2022, 4, 511-522.	3.3	4
2	An Unexpectedly Complex Mitoribosome in Andalucia godoyi, a Protist with the Most Bacteria-like Mitochondrial Genome. Molecular Biology and Evolution, 2021, 38, 788-804.	8.9	8
3	Mitochondrial genomes of the human pathogensCoccidioides immitisandCoccidioides posadasii. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	8
4	Analysis of diverse eukaryotes suggests the existence of an ancestral mitochondrial apparatus derived from the bacterial type II secretion system. Nature Communications, 2021, 12, 2947.	12.8	19
5	New Insights Into Acidithiobacillus thiooxidans Sulfur Metabolism Through Coupled Gene Expression, Solution Chemistry, Microscopy, and Spectroscopy Analyses. Frontiers in Microbiology, 2020, 11, 411.	3.5	24
6	The draft nuclear genome sequence and predicted mitochondrial proteome of Andalucia godoyi, a protist with the most gene-rich and bacteria-like mitochondrial genome. BMC Biology, 2020, 18, 22.	3.8	43
7	Genome sequence of the opportunistic human pathogen Magnusiomyces capitatus. Current Genetics, 2019, 65, 539-560.	1.7	14
8	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. ELife, 2019, 8, .	6.0	91
9	Mitochondrial Genomes in Unicellular Relatives of Animals. , 2018, , 742-745.		0
10	Mitochondrial Genomes in Fungi. , 2018, , 722-728.		12
11	Genome Sequence of Spizellomyces punctatus. Genome Announcements, 2016, 4, .	0.8	20
12	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
13	Bacterial proteins pinpoint a single eukaryotic root. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E693-9.	7.1	159
14	Updating algal evolutionary relationships through plastid genome sequencing: did alveolate plastids emerge through endosymbiosis of an ochrophyte?. Scientific Reports, 2015, 5, 10134.	3.3	102
15	Evolution of tRNA Repertoires in Bacillus Inferred with OrthoAlign. Molecular Biology and Evolution, 2015, 32, 1643-1656.	8.9	16
16	An ancestral bacterial division system is widespread in eukaryotic mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10239-10246.	7.1	70
17	Programmed translational bypassing elements in mitochondria: structure, mobility, and evolutionary origin. Trends in Genetics, 2015, 31, 187-194.	6.7	19
18	Massive programmed translational jumping in mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5926-5931.	7.1	58

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19	Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. Nucleic Acids Research, 2014, 42, 13764-13777.	14.5	129
20	Natural reassignment of CUU and CUA sense codons to alanine in Ashbya mitochondria. Nucleic Acids Research, 2014, 42, 499-508.	14.5	23
21	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. Nature Communications, 2014, 5, 4471.	12.8	133
22	Mitochondrial Genomes in Fungi. , 2014, , 1-7.		4
23	Mitochondrial Genomes in Unicellular Relatives of Animals. , 2014, , 1-4.		2
24	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate Salpingoeca rosetta. Genome Biology, 2013, 14, R15.	9.6	219
25	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	12.8	244
26	Phylogenomics demonstrates that breviate flagellates are related to opisthokonts and apusomonads. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131755.	2.6	119
27	Strikingly Bacteria-Like and Gene-Rich Mitochondrial Genomes throughout Jakobid Protists. Genome Biology and Evolution, 2013, 5, 418-438.	2.5	222
28	Mitochondrial DNA of Clathrina clathrus (Calcarea, Calcinea): Six Linear Chromosomes, Fragmented rRNAs, tRNA Editing, and a Novel Genetic Code. Molecular Biology and Evolution, 2013, 30, 865-880.	8.9	78
29	A Broad Phylogenetic Survey Unveils the Diversity and Evolution of Telomeres in Eukaryotes. Genome Biology and Evolution, 2013, 5, 468-483.	2.5	89
30	A second eukaryotic group with mitochondrion-encoded tmRNA. RNA Biology, 2013, 10, 1117-1124.	3.1	18
31	Insights into the Origin of Metazoan Filopodia and Microvilli. Molecular Biology and Evolution, 2013, 30, 2013-2023.	8.9	78
32	Yeast mitochondrial RNase P, RNase Z and the RNA degradosome are part of a stable supercomplex. Nucleic Acids Research, 2012, 40, 1728-1736.	14.5	31
33	Group I Intronâ€“Mediated Trans-splicing in Mitochondria of Gigaspora rosea and a Robust Phylogenetic Affiliation of Arbuscular Mycorrhizal Fungi with Mortierellales. Molecular Biology and Evolution, 2012, 29, 2199-2210.	8.9	49
34	Cyanophora paradoxa Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	12.6	371
35	Rooting the Eukaryotic Tree with Mitochondrial and Bacterial Proteins. Molecular Biology and Evolution, 2012, 29, 1277-1289.	8.9	121
36	Dinoflagellate tandem array gene transcripts are highly conserved and not polycistronic. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15793-15798.	7.1	73

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37	Mitochondrial and Eukaryotic Origins. Advances in Botanical Research, 2012, , 1-20.	1.1	14
38	Plastid Genomes of Algae. Advances in Photosynthesis and Respiration, 2012, , 59-87.	1.0	20
39	Mitochondrial tRNA Structure, Identity, and Evolution of the Genetic Code. , 2012, , 431-474.		22
40	Phylogenetic Relationships within the Opisthokonta Based on Phylogenomic Analyses of Conserved Single-Copy Protein Domains. Molecular Biology and Evolution, 2012, 29, 531-544.	8.9	166
41	Daily Changes in the Phosphoproteome of the Dinoflagellate Lingulodinium. Protist, 2012, 163, 746-754.	1.5	17
42	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. Nucleic Acids Research, 2011, 39, 4202-4219.	14.5	69
43	An unusual tRNAThr derived from tRNAHis reassigns in yeast mitochondria the CUN codons to threonine. Nucleic Acids Research, 2011, 39, 4866-4874.	14.5	35
44	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	8.9	172
45	Sequence and structure of the linear mitochondrial genome of Pneumocystis carinii. Molecular Genetics and Genomics, 2010, 283, 63-72.	2.1	20
46	Phylogenomic Analyses Support the Monophyly of Taphrinomycotina, including Schizosaccharomyces Fission Yeasts. Molecular Biology and Evolution, 2009, 26, 27-34.	8.9	91
47	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic â€œsupergroupsâ€• Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3859-3864.	7.1	444
48	GOBASE: an organelle genome database. Nucleic Acids Research, 2009, 37, D946-D950.	14.5	74
49	Whirly proteins maintain plastid genome stability in Arabidopsis. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14693-14698.	7.1	177
50	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	3.5	34
51	Diversity and dispersal of a ubiquitous protein family: acyl-CoA dehydrogenases. Nucleic Acids Research, 2009, 37, 5619-5631.	14.5	26
52	Genomic Analysis of the Basal Lineage Fungus Rhizopus oryzae Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	3.5	332
53	Group I-intron trans-splicing and mRNA editing in the mitochondria of placozoan animals. Trends in Genetics, 2009, 25, 381-386.	6.7	79
54	Phylogenomic analyses predict sistergroup relationship of nucleariids and Fungi and paraphyly of zygomycetes with significant support. BMC Evolutionary Biology, 2009, 9, 272.	3.2	119

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55	The complete Glomus intraradices mitochondrial genome sequence â€“ a milestone in mycorrhizal research. New Phytologist, 2009, 183, 3-6.	7.3	17
56	EST Databases and Web Tools for EST Projects. Methods in Molecular Biology, 2009, 533, 241-256.	0.9	2
57	Construction of cDNA Libraries: Focus on Protists and Fungi. Methods in Molecular Biology, 2009, 533, 33-47.	0.9	18
58	Distribution and Phylogeny of EFL and EF-1Î± in Euglenozoa Suggest Ancestral Co-Occurrence Followed by Differential Loss. PLoS ONE, 2009, 4, e5162.	2.5	24
59	A Phylogenomic Investigation into the Origin of Metazoa. Molecular Biology and Evolution, 2008, 25, 664-672.	8.9	259
60	Accounting for Gene Rate Heterogeneity in Phylogenetic Inference. Systematic Biology, 2007, 56, 194-205.	5.6	12
61	Glass Sponges and Bilaterian Animals Share Derived Mitochondrial Genomic Features: A Common Ancestry or Parallel Evolution?. Molecular Biology and Evolution, 2007, 24, 1518-1527.	8.9	70
62	TBestDB: a taxonomically broad database of expressed sequence tags (ESTs). Nucleic Acids Research, 2007, 35, D445-D451.	14.5	81
63	Purification of mitochondrial and plastid DNA. Nature Protocols, 2007, 2, 652-660.	12.0	58
64	Sequencing complete mitochondrial and plastid genomes. Nature Protocols, 2007, 2, 603-614.	12.0	84
65	Toward Resolving the Eukaryotic Tree: The Phylogenetic Positions of Jakobids and Cercozoans. Current Biology, 2007, 17, 1420-1425.	3.9	170
66	The origins of multicellularity: a multi-taxon genome initiative. Trends in Genetics, 2007, 23, 113-118.	6.7	201
67	Mitochondrial introns: a critical view. Trends in Genetics, 2007, 23, 119-125.	6.7	313
68	Detecting and Overcoming Systematic Errors in Genome-Scale Phylogenies. Systematic Biology, 2007, 56, 389-399.	5.6	288
69	Mitochondria of Protists. Annual Review of Genetics, 2004, 38, 477-524.	7.6	295
70	Evolution of the Fungi and their Mitochondrial Genomes. Applied Mycology and Biotechnology, 2003, 3, 133-159.	0.3	10
71	Complete Sequence of the Mitochondrial DNA of the Red Alga Porphyra purpurea: Cyanobacterial Introns and Shared Ancestry of Red and Green Algae. Plant Cell, 1999, 11, 1675-1694.	6.6	178
72	The Complete Mitochondrial DNA Sequences of Nephroselmis olivacea and Pedinomonas minor: Two Radically Different Evolutionary Patterns within Green Algae. Plant Cell, 1999, 11, 1717-1729.	6.6	154

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73	A Comparative Genomics Approach to the Evolution of Eukaryotes and their Mitochondria. Journal of Eukaryotic Microbiology, 1999, 46, 320-326.	1.7	79
74	Mitochondrial Genome Evolution and the Origin of Eukaryotes. Annual Review of Genetics, 1999, 33, 351-397.	7.6	603
75	Mitochondrial Genomics in Protists, an Approach to Probing Eukaryotic Evolution. Protist, 1998, 149, 313-322.	1.5	17
76	An ancestral mitochondrial DNA resembling a eubacterial genome in miniature. Nature, 1997, 387, 493-497.	27.8	658
77	UTILITY OF THE MITOCHONDRIAL nad4L GENE FOR ALGAL AND PROTISTAN PHYLOGENETIC ANALYSIS1. Journal of Phycology, 1996, 32, 452-456.	2.3	19
78	Analysis of genes encoding highly conserved lysine-rich proteins in Aplysia californica and Saccharomyces cerevisiae. FEBS Journal, 1994, 220, 997-1003.	0.2	8