## **B Franz Lang**

List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	An ancestral mitochondrial DNA resembling a eubacterial genome in miniature. Nature, 1997, 387, 493-497.	27.8	658
2	Mitochondrial Genome Evolution and the Origin of Eukaryotes. Annual Review of Genetics, 1999, 33, 351-397.	7.6	603
3	Phylogenomic analyses support the monophyly of Excavata and resolve relationships among eukaryotic "supergroups― Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3859-3864.	7.1	444
4	<i>Cyanophora paradoxa</i> Genome Elucidates Origin of Photosynthesis in Algae and Plants. Science, 2012, 335, 843-847.	12.6	371
5	Genomic Analysis of the Basal Lineage Fungus Rhizopus oryzae Reveals a Whole-Genome Duplication. PLoS Genetics, 2009, 5, e1000549.	3.5	332
6	Mitochondrial introns: a critical view. Trends in Genetics, 2007, 23, 119-125.	6.7	313
7	Mitochondria of Protists. Annual Review of Genetics, 2004, 38, 477-524.	7.6	295
8	Detecting and Overcoming Systematic Errors in Genome-Scale Phylogenies. Systematic Biology, 2007, 56, 389-399.	5.6	288
9	A Phylogenomic Investigation into the Origin of Metazoa. Molecular Biology and Evolution, 2008, 25, 664-672.	8.9	259
10	The Capsaspora genome reveals a complex unicellular prehistory of animals. Nature Communications, 2013, 4, 2325.	12.8	244
11	Strikingly Bacteria-Like and Gene-Rich Mitochondrial Genomes throughout Jakobid Protists. Genome Biology and Evolution, 2013, 5, 418-438.	2.5	222
12	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate Salpingoeca rosetta. Genome Biology, 2013, 14, R15.	9.6	219
13	The origins of multicellularity: a multi-taxon genome initiative. Trends in Genetics, 2007, 23, 113-118.	6.7	201
14	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
15	Whirly proteins maintain plastid genome stability in <i>Arabidopsis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14693-14698.	7.1	177
16	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
17	Unexpected Repertoire of Metazoan Transcription Factors in the Unicellular Holozoan Capsaspora owczarzaki. Molecular Biology and Evolution, 2011, 28, 1241-1254.	8.9	172
18	Toward Resolving the Eukaryotic Tree: The Phylogenetic Positions of Jakobids and Cercozoans. Current Biology, 2007, 17, 1420-1425.	3.9	170

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19	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
20	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
21	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
22	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. Nature Communications, 2014, 5, 4471.	12.8	133
23	Widespread occurrence of organelle genome-encoded 5S rRNAs including permuted molecules. Nucleic Acids Research, 2014, 42, 13764-13777.	14.5	129
24	Rooting the Eukaryotic Tree with Mitochondrial and Bacterial Proteins. Molecular Biology and Evolution, 2012, 29, 1277-1289.	8.9	121
25	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
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	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
28	Phylogenomic Analyses Support the Monophyly of Taphrinomycotina, including <i>Schizosaccharomyces</i> Fission Yeasts. Molecular Biology and Evolution, 2009, 26, 27-34.	8.9	91
29	An updated phylogeny of the Alphaproteobacteria reveals that the parasitic Rickettsiales and Holosporales have independent origins. ELife, 2019, 8, .	6.0	91
30	A Broad Phylogenetic Survey Unveils the Diversity and Evolution of Telomeres in Eukaryotes. Genome Biology and Evolution, 2013, 5, 468-483.	2.5	89
31	Sequencing complete mitochondrial and plastid genomes. Nature Protocols, 2007, 2, 603-614.	12.0	84
32	TBestDB: a taxonomically broad database of expressed sequence tags (ESTs). Nucleic Acids Research, 2007, 35, D445-D451.	14.5	81
33	A Comparative Genomics Approach to the Evolution of Eukaryotes and their Mitochondria. Journal of Eukaryotic Microbiology, 1999, 46, 320-326.	1.7	79
34	Group I-intron trans-splicing and mRNA editing in the mitochondria of placozoan animals. Trends in Genetics, 2009, 25, 381-386.	6.7	79
35	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
36	Insights into the Origin of Metazoan Filopodia and Microvilli. Molecular Biology and Evolution, 2013, 30, 2013-2023.	8.9	78

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37	GOBASE: an organelle genome database. Nucleic Acids Research, 2009, 37, D946-D950.	14.5	74
38	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
39	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
40	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
41	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. Nucleic Acids Research, 2011, 39, 4202-4219.	14.5	69
42	Purification of mitochondrial and plastid DNA. Nature Protocols, 2007, 2, 652-660.	12.0	58
43	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
44	Group I Intron–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
45	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
46	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
47	The RNA structure alignment ontology. Rna, 2009, 15, 1623-1631.	3.5	34
48	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
49	Diversity and dispersal of a ubiquitous protein family: acyl-CoA dehydrogenases. Nucleic Acids Research, 2009, 37, 5619-5631.	14.5	26
50	New Insights Into Acidithiobacillus thiooxidans Sulfur Metabolism Through Coupled Gene Expression, Solution Chemistry, Microscopy, and Spectroscopy Analyses. Frontiers in Microbiology, 2020, 11, 411.	<b>3.</b> 5	24
51	Distribution and Phylogeny of EFL and EF-1α in Euglenozoa Suggest Ancestral Co-Occurrence Followed by Differential Loss. PLoS ONE, 2009, 4, e5162.	2.5	24
52	Natural reassignment of CUU and CUA sense codons to alanine in Ashbya mitochondria. Nucleic Acids Research, 2014, 42, 499-508.	14.5	23
53	Mitochondrial tRNA Structure, Identity, and Evolution of the Genetic Code., 2012,, 431-474.		22
54	Sequence and structure of the linear mitochondrial genome of Pneumocystis carinii. Molecular Genetics and Genomics, 2010, 283, 63-72.	2.1	20

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55	Plastid Genomes of Algae. Advances in Photosynthesis and Respiration, 2012, , 59-87.	1.0	20
56	Genome Sequence of <i>Spizellomyces punctatus</i> . Genome Announcements, 2016, 4, .	0.8	20
57	UTILITY OF THE MITOCHONDRIAL nad4L GENE FOR ALGAL AND PROTISTAN PHYLOGENETIC ANALYSIS1. Journal of Phycology, 1996, 32, 452-456.	2.3	19
58	Programmed translational bypassing elements in mitochondria: structure, mobility, and evolutionary origin. Trends in Genetics, 2015, 31, 187-194.	6.7	19
59	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
60	A second eukaryotic group with mitochondrion-encoded tmRNA. RNA Biology, 2013, 10, 1117-1124.	3.1	18
61	Construction of cDNA Libraries: Focus on Protists and Fungi. Methods in Molecular Biology, 2009, 533, 33-47.	0.9	18
62	Mitochondrial Genomics in Protists, an Approach to Probing Eukaryotic Evolution. Protist, 1998, 149, 313-322.	1.5	17
63	The complete <i>Glomus intraradices</i> mitochondrial genome sequence – a milestone in mycorrhizal research. New Phytologist, 2009, 183, 3-6.	7.3	17
64	Daily Changes in the Phosphoproteome of the Dinoflagellate Lingulodinium. Protist, 2012, 163, 746-754.	1.5	17
65	Evolution of tRNA Repertoires in Bacillus Inferred with OrthoAlign. Molecular Biology and Evolution, 2015, 32, 1643-1656.	8.9	16
66	Mitochondrial and Eukaryotic Origins. Advances in Botanical Research, 2012, , 1-20.	1.1	14
67	Genome sequence of the opportunistic human pathogen Magnusiomyces capitatus. Current Genetics, 2019, 65, 539-560.	1.7	14
68	Accounting for Gene Rate Heterogeneity in Phylogenetic Inference. Systematic Biology, 2007, 56, 194-205.	5.6	12
69	Mitochondrial Genomes in Fungi. , 2018, , 722-728.		12
70	Evolution of the Fungi and their Mitochondrial Genomes. Applied Mycology and Biotechnology, 2003, 3, 133-159.	0.3	10
71	Analysis of genes encoding highly conserved lysine-rich proteins in Aplysia californica and Saccharomyces cerevisiae. FEBS Journal, 1994, 220, 997-1003.	0.2	8
72	An Unexpectedly Complex Mitoribosome 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

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73	Mitochondrial genomes of the human pathogens <i> Coccidioides immitis </i> > and <i> Coccidioides posadasii   G3: Genes, Genomes, Genetics, 2021, 11, .</i>	1.8	8
74	Mitochondrial Genomes in Fungi., 2014,, 1-7.		4
75	Endosymbionts in cranberry: Diversity, effect on plant growth, and pathogen biocontrol. Plants People Planet, 2022, 4, 511-522.	3.3	4
76	Mitochondrial Genomes in Unicellular Relatives of Animals. , 2014, , 1-4.		2
77	EST Databases and Web Tools for EST Projects. Methods in Molecular Biology, 2009, 533, 241-256.	0.9	2
78	Mitochondrial Genomes in Unicellular Relatives of Animals. , 2018, , 742-745.		0