

Martin Wu

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8661804/martin-wu-publications-by-year.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

65 papers	10,781 citations	41 h-index	73 g-index
73 ext. papers	12,508 ext. citations	9.2 avg, IF	5.76 L-index

#	Paper	IF	Citations
65	Glucocorticoids coordinate changes in gut microbiome composition in wild North American red squirrels.. <i>Scientific Reports</i> , 2022 , 12, 2605	4.9	0
64	Apple cider vinegar soaks do not alter the skin bacterial microbiome in atopic dermatitis. <i>PLoS ONE</i> , 2021 , 16, e0252272	3.7	1
63	Re-evaluating the evidence for a universal genetic boundary among microbial species. <i>Nature Communications</i> , 2021 , 12, 4059	17.4	7
62	Dopamine Signaling in the Suprachiasmatic Nucleus Enables Weight Gain Associated with Hedonic Feeding. <i>Current Biology</i> , 2020 , 30, 196-208.e8	6.3	14
61	Rationale, design and baseline characteristics of the Microbiome and Insulin Longitudinal Evaluation Study (MILES). <i>Diabetes, Obesity and Metabolism</i> , 2020 , 22, 1976-1984	6.7	2
60	Multi-omic meta-analysis identifies functional signatures of airway microbiome in chronic obstructive pulmonary disease. <i>ISME Journal</i> , 2020 , 14, 2748-2765	11.9	15
59	Innate Immune Response and Outcome of Clostridium difficile Infection Are Dependent on Fecal Bacterial Composition in the Aged Host. <i>Journal of Infectious Diseases</i> , 2018 , 217, 188-197	7	16
58	Evidence for the Role of the Cecal Microbiome in Maintenance of Immune Regulation and Homeostasis. <i>Annals of Surgery</i> , 2018 , 268, 541-549	7.8	7
57	Microbiota alteration is associated with the development of stress-induced despair behavior. <i>Scientific Reports</i> , 2017 , 7, 43859	4.9	178
56	Seasonal, spatial, and maternal effects on gut microbiome in wild red squirrels. <i>Microbiome</i> , 2017 , 5, 163	16.6	70
55	A new brain dopamine-deficient Drosophila and its pharmacological and genetic rescue. <i>Genes, Brain and Behavior</i> , 2017 , 16, 394-403	3.6	28
54	Comparative Genomic Analysis of Acanthamoeba Endosymbionts Highlights the Role of Amoebae as a "Melting Pot" Shaping the Rickettsiales Evolution. <i>Genome Biology and Evolution</i> , 2017 , 9, 3214-3224	2.9	29
53	PhyloCore: A phylogenetic approach to identifying core taxa in microbial communities. <i>Gene</i> , 2016 , 593, 330-3	3.8	7
52	Development, diet and dynamism: longitudinal and cross-sectional predictors of gut microbial communities in wild baboons. <i>Environmental Microbiology</i> , 2016 , 18, 1312-25	5.2	41
51	Does adaptive radiation of a host lineage promote ecological diversity of its bacterial communities? A test using gut microbiota of Anolis lizards. <i>Molecular Ecology</i> , 2016 , 25, 4793-804	5.7	34
50	An integrated phylogenomic approach toward pinpointing the origin of mitochondria. <i>Scientific Reports</i> , 2015 , 5, 7949	4.9	87
49	A generation-time effect on the rate of molecular evolution in bacteria. <i>Evolution; International Journal of Organic Evolution</i> , 2015 , 69, 643-52	3.8	42

48	Cytosuclear interactions and relaxed selection accelerate sequence evolution in organelle ribosomes. <i>Molecular Biology and Evolution</i> , 2014 , 31, 673-82	8.3	60
47	A recurring syndrome of accelerated plastid genome evolution in the angiosperm tribe Sileneae (Caryophyllaceae). <i>Molecular Phylogenetics and Evolution</i> , 2014 , 72, 82-9	4.1	76
46	Genomic insights into the uncultured genus <i>Candidatus Magnetobacterium</i> in the phylum Nitrospirae. <i>ISME Journal</i> , 2014 , 8, 2463-77	11.9	63
45	Genomic heterogeneity and ecological speciation within one subspecies of <i>Bacillus subtilis</i> . <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4842-53	4.8	35
44	Species matter: the role of competition in the assembly of congeneric bacteria. <i>ISME Journal</i> , 2014 , 8, 531-540	11.9	31
43	Phylogenomic reconstruction indicates mitochondrial ancestor was an energy parasite. <i>PLoS ONE</i> , 2014 , 9, e110685	3.7	38
42	Complete Genome Sequence of the Endosymbiont of <i>Acanthamoeba</i> Strain UWC8, an <i>Amoeba</i> Endosymbiont Belonging to the "Candidatus Midichloriaceae" Family in Rickettsiales. <i>Genome Announcements</i> , 2014 , 2,		8
41	NtERF32: a non-NIC2 locus AP2/ERF transcription factor required in jasmonate-inducible nicotine biosynthesis in tobacco. <i>Plant Molecular Biology</i> , 2014 , 84, 49-66	4.6	58
40	16S rRNA survey revealed complex bacterial communities and evidence of bacterial interference on human adenoids. <i>Environmental Microbiology</i> , 2013 , 15, 535-47	5.2	27
39	A phylum-level bacterial phylogenetic marker database. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1258-83	8.3	77
38	Surprisingly extensive mixed phylogenetic and ecological signals among bacterial Operational Taxonomic Units. <i>Nucleic Acids Research</i> , 2013 , 41, 5175-88	20.1	81
37	Lineage-dependent ecological coherence in bacteria. <i>FEMS Microbiology Ecology</i> , 2012 , 81, 574-82	4.3	26
36	Phylogenomic analysis of bacterial and archaeal sequences with AMPHORA2. <i>Bioinformatics</i> , 2012 , 28, 1033-4	7.2	317
35	Enteric pathogens through life stages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 114	5.9	44
34	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (<i>Petaurista alborufus</i> lena). <i>BMC Genomics</i> , 2012 , 13, 466	4.5	19
33	Rapid evolution of enormous, multichromosomal genomes in flowering plant mitochondria with exceptionally high mutation rates. <i>PLoS Biology</i> , 2012 , 10, e1001241	9.7	335
32	Accounting for alignment uncertainty in phylogenomics. <i>PLoS ONE</i> , 2012 , 7, e30288	3.7	127
31	Incorporating 16S gene copy number information improves estimates of microbial diversity and abundance. <i>PLoS Computational Biology</i> , 2012 , 8, e1002743	5	303

30	Lactic acid production by <i>Streptococcus thermophilus</i> alters <i>Clostridium difficile</i> infection and in vitro Toxin A production. <i>Gut Microbes</i> , 2012 , 3, 523-9	8.8	34
29	Recent acceleration of plastid sequence and structural evolution coincides with extreme mitochondrial divergence in the angiosperm genus <i>Silene</i> . <i>Genome Biology and Evolution</i> , 2012 , 4, 294-306	3.9	83
28	Towards Automated Phylogenomic Inference 2011 , 205-215		
27	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. <i>Genome Biology</i> , 2011 , 12, R100	18.3	89
26	Stalking the fourth domain in metagenomic data: searching for, discovering, and interpreting novel, deep branches in marker gene phylogenetic trees. <i>PLoS ONE</i> , 2011 , 6, e18011	3.7	72
25	Genomic insights into an obligate epibiotic bacterial predator: <i>Micavibrio aeruginosavorus</i> ARL-13. <i>BMC Genomics</i> , 2011 , 12, 453	4.5	47
24	Visualization of ribosomal RNA operon copy number distribution. <i>BMC Microbiology</i> , 2009 , 9, 208	4.5	48
23	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
22	Three genomes from the phylum Acidobacteria provide insight into the lifestyles of these microorganisms in soils. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2046-56	4.8	590
21	Complete genome sequence of the aerobic CO-oxidizing thermophile <i>Thermomicrobium roseum</i> . <i>PLoS ONE</i> , 2009 , 4, e4207	3.7	82
20	A simple, fast, and accurate method of phylogenomic inference. <i>Genome Biology</i> , 2008 , 9, R151	18.3	369
19	Identification of a fourth family of lycopene cyclases in photosynthetic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11784-9	11.5	71
18	Macronuclear genome sequence of the ciliate <i>Tetrahymena thermophila</i> , a model eukaryote. <i>PLoS Biology</i> , 2006 , 4, e286	9.7	544
17	Comparative genomics of emerging human ehrlichiosis agents. <i>PLoS Genetics</i> , 2006 , 2, e21	6	363
16	Genome sequence of <i>Aeromonas hydrophila</i> ATCC 7966T: jack of all trades. <i>Journal of Bacteriology</i> , 2006 , 188, 8272-82	3.5	275
15	Life in hot carbon monoxide: the complete genome sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005 , 1, e65	6	184
14	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 10913-8	11.5	430
13	Life in Hot Carbon Monoxide: the Complete Genome Sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005 , preprint, e65	6	1

12	Phylogenomics of the reproductive parasite <i>Wolbachia pipientis</i> wMel: a streamlined genome overrun by mobile genetic elements. <i>PLoS Biology</i> , 2004 , 2, E69	9.7	613
11	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
10	The age of the <i>Arabidopsis thaliana</i> genome duplication. <i>Plant Molecular Biology</i> , 2003 , 51, 859-66	4.6	85
9	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria. <i>Nature</i> , 2003 , 423, 81-6	50.4	692
8	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , 2003 , 302, 1967-9	33.3	573
7	The complete genome sequence of <i>Chlorobium tepidum</i> TLS, a photosynthetic, anaerobic, green-sulfur bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 9509-14	11.5	321
6	Phylogenetic analysis and gene functional predictions: phylogenomics in action. <i>Theoretical Population Biology</i> , 2002 , 61, 481-7	1.2	68
5	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
4	Strengthened arm-dimerization domain interactions in AraC. <i>Journal of Biological Chemistry</i> , 2001 , 276, 2562-4	5.4	21
3	The role of rigidity in DNA looping-unlooping by AraC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 427-31	11.5	47
2	Mapping arm-DNA-binding domain interactions in AraC. <i>Journal of Molecular Biology</i> , 2001 , 307, 1001-9	6.5	35
1	Microbial trait evolution is dominated by frequent and rare pulsed evolution		1