

Martin Wu

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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	The genome sequence of the malaria mosquito <i>Anopheles gambiae</i> . <i>Science</i> , 2002 , 298, 129-49	33.3	1622
64	A phylogeny-driven genomic encyclopaedia of Bacteria and Archaea. <i>Nature</i> , 2009 , 462, 1056-60	50.4	803
63	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
62	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
61	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
60	Genome of <i>Geobacter sulfurreducens</i> : metal reduction in subsurface environments. <i>Science</i> , 2003 , 302, 1967-9	33.3	573
59	Macronuclear genome sequence of the ciliate <i>Tetrahymena thermophila</i> , a model eukaryote. <i>PLoS Biology</i> , 2006 , 4, e286	9.7	544
58	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
57	A simple, fast, and accurate method of phylogenomic inference. <i>Genome Biology</i> , 2008 , 9, R151	18.3	369
56	Comparative genomics of emerging human ehrlichiosis agents. <i>PLoS Genetics</i> , 2006 , 2, e21	6	363
55	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
54	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
53	Phylogenomic analysis of bacterial and archaeal sequences with AMPHORA2. <i>Bioinformatics</i> , 2012 , 28, 1033-4	7.2	317
52	Incorporating 16S gene copy number information improves estimates of microbial diversity and abundance. <i>PLoS Computational Biology</i> , 2012 , 8, e1002743	5	303
51	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
50	Genomic insights into methanotrophy: the complete genome sequence of <i>Methylococcus capsulatus</i> (Bath). <i>PLoS Biology</i> , 2004 , 2, e303	9.7	236
49	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

48	Microbiota alteration is associated with the development of stress-induced despair behavior. <i>Scientific Reports</i> , 2017 , 7, 43859	4.9	178
47	Accounting for alignment uncertainty in phylogenomics. <i>PLoS ONE</i> , 2012 , 7, e30288	3.7	127
46	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
45	An integrated phylogenomic approach toward pinpointing the origin of mitochondria. <i>Scientific Reports</i> , 2015 , 5, 7949	4.9	87
44	The age of the <i>Arabidopsis thaliana</i> genome duplication. <i>Plant Molecular Biology</i> , 2003 , 51, 859-66	4.6	85
43	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
42	Complete genome sequence of the aerobic CO-oxidizing thermophile <i>Thermomicrobium roseum</i> . <i>PLoS ONE</i> , 2009 , 4, e4207	3.7	82
41	Surprisingly extensive mixed phylogenetic and ecological signals among bacterial Operational Taxonomic Units. <i>Nucleic Acids Research</i> , 2013 , 41, 5175-88	20.1	81
40	A phylum-level bacterial phylogenetic marker database. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1258-63	3.3	77
39	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
38	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
37	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
36	Seasonal, spatial, and maternal effects on gut microbiome in wild red squirrels. <i>Microbiome</i> , 2017 , 5, 163	16.6	70
35	Phylogenetic analysis and gene functional predictions: phylogenomics in action. <i>Theoretical Population Biology</i> , 2002 , 61, 481-7	1.2	68
34	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
33	Cytosuclear interactions and relaxed selection accelerate sequence evolution in organelle ribosomes. <i>Molecular Biology and Evolution</i> , 2014 , 31, 673-82	8.3	60
32	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
31	Visualization of ribosomal RNA operon copy number distribution. <i>BMC Microbiology</i> , 2009 , 9, 208	4.5	48

30	Genomic insights into an obligate epibiotic bacterial predator: <i>Micavibrio aeruginosavorus</i> ARL-13. <i>BMC Genomics</i> , 2011 , 12, 453	4.5	47
29	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
28	Enteric pathogens through life stages. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 114	5.9	44
27	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
26	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
25	Phylogenomic reconstruction indicates mitochondrial ancestor was an energy parasite. <i>PLoS ONE</i> , 2014 , 9, e110685	3.7	38
24	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
23	Mapping arm-DNA-binding domain interactions in AraC. <i>Journal of Molecular Biology</i> , 2001 , 307, 1001-9	6.5	35
22	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
21	Does adaptive radiation of a host lineage promote ecological diversity of its bacterial communities? A test using gut microbiota of <i>Anolis</i> lizards. <i>Molecular Ecology</i> , 2016 , 25, 4793-804	5.7	34
20	Species matter: the role of competition in the assembly of congeneric bacteria. <i>ISME Journal</i> , 2014 , 8, 531-540	11.9	31
19	Comparative Genomic Analysis of <i>Acanthamoeba</i> 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
18	A new brain dopamine-deficient <i>Drosophila</i> and its pharmacological and genetic rescue. <i>Genes, Brain and Behavior</i> , 2017 , 16, 394-403	3.6	28
17	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
16	Lineage-dependent ecological coherence in bacteria. <i>FEMS Microbiology Ecology</i> , 2012 , 81, 574-82	4.3	26
15	Strengthened arm-dimerization domain interactions in AraC. <i>Journal of Biological Chemistry</i> , 2001 , 276, 2562-4	5.4	21
14	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
13	Innate Immune Response and Outcome of <i>Clostridium difficile</i> Infection Are Dependent on Fecal Bacterial Composition in the Aged Host. <i>Journal of Infectious Diseases</i> , 2018 , 217, 188-197	7	16

12	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
11	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
10	Complete Genome Sequence of the Endosymbiont of Acanthamoeba Strain UWC8, an Amoeba Endosymbiont Belonging to the "Candidatus Midichloriaceae" Family in Rickettsiales. <i>Genome Announcements</i> , 2014 , 2,		8
9	PhyloCore: A phylogenetic approach to identifying core taxa in microbial communities. <i>Gene</i> , 2016 , 593, 330-3	3.8	7
8	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
7	Re-evaluating the evidence for a universal genetic boundary among microbial species. <i>Nature Communications</i> , 2021 , 12, 4059	17.4	7
6	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
5	Life in Hot Carbon Monoxide: the Complete Genome Sequence of Carboxydotherrmus hydrogenofomans Z-2901. <i>PLoS Genetics</i> , 2005 , preprint, e65	6	1
4	Microbial trait evolution is dominated by frequent and rare pulsed evolution		1
3	Apple cider vinegar soaks do not alter the skin bacterial microbiome in atopic dermatitis. <i>PLoS ONE</i> , 2021 , 16, e0252272	3.7	1
2	Glucocorticoids coordinate changes in gut microbiome composition in wild North American red squirrels.. <i>Scientific Reports</i> , 2022 , 12, 2605	4.9	0
1	Towards Automated Phylogenomic Inference 2011 , 205-215		