Wei-Hua Chen

List of Publications by Year
in descending order

50 papers	5,371 citations	236833 25 h-index	189801 50 g-index
57 all docs	57 docs citations	57 times ranked	8173 citing authors

#	Article	IF	Citations
1	Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. Nucleic Acids Research, 2016, 44, W236-W241.	6.5	610
2	Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. Nucleic Acids Research, 2019, 47, W270-W275.	6.5	564
3	Proteome Organization in a Genome-Reduced Bacterium. Science, 2009, 326, 1235-1240.	6.0	440
4	Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. Science, 2013, 339, 1207-1210.	6.0	439
5	EvolView, an online tool for visualizing, annotating and managing phylogenetic trees. Nucleic Acids Research, 2012, 40, W569-W572.	6.5	400
6	Transcriptome Complexity in a Genome-Reduced Bacterium. Science, 2009, 326, 1268-1271.	6.0	394
7	Rapid Detection of COVID-19 Coronavirus Using a Reverse Transcriptional Loop-Mediated Isothermal Amplification (RT-LAMP) Diagnostic Platform. Clinical Chemistry, 2020, 66, 975-977.	1.5	372
8	Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. Science, 2009, 326, 1263-1268.	6.0	267
9	OGEE: an online gene essentiality database. Nucleic Acids Research, 2012, 40, D901-D906.	6.5	187
10	OGEE v2: an update of the online gene essentiality database with special focus on differentially essential genes in human cancer cell lines. Nucleic Acids Research, 2017, 45, D940-D944.	6.5	153
11	Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genomeâ€reduced bacterium. Molecular Systems Biology, 2015, 11, 780.	3.2	133
12	Orthology prediction methods: A quality assessment using curated protein families. BioEssays, 2011, 33, 769-780.	1.2	121
13	Bacterial antisense RNAs are mainly the product of transcriptional noise. Science Advances, 2016, 2, e1501363.	4.7	118
14	Energy efficiency trade-offs drive nucleotide usage in transcribed regions. Nature Communications, 2016, 7, 11334.	5.8	104
15	GMrepo: a database of curated and consistently annotated human gut metagenomes. Nucleic Acids Research, 2020, 48, D545-D553.	6.5	96
16	Younger Genes Are Less Likely to Be Essential than Older Genes, and Duplicates Are Less Likely to Be Essential than Singletons of the Same Age. Molecular Biology and Evolution, 2012, 29, 1703-1706.	3.5	90
17	MVP: a microbeâ€"phage interaction database. Nucleic Acids Research, 2018, 46, D700-D707.	6.5	82
18	Computational Molecular Networks and Network Pharmacology. BioMed Research International, 2017, 2017, 1-1.	0.9	58

#	ARTICLE	IF	CITATIONS
19	GMrepo v2: a curated human gut microbiome database with special focus on disease markers and cross-dataset comparison. Nucleic Acids Research, 2022, 50, D777-D784.	6.5	50
20	Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. PLoS Computational Biology, 2013, 9, e1003073.	1.5	49
21	STAB: a spatio-temporal cell atlas of the human brain. Nucleic Acids Research, 2021, 49, D1029-D1037.	6.5	43
22	OGEE v3: Online GEne Essentiality database with increased coverage of organisms and human cell lines. Nucleic Acids Research, 2021, 49, D998-D1003.	6.5	42
23	Transcription start site associated RNAs in bacteria. Molecular Systems Biology, 2012, 8, 585.	3.2	40
24	Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. Nucleic Acids Research, 2016, 44, 1192-1202.	6.5	35
25	Optimization of scleroglucan production by Sclerotium rolfsii by lowering pH during fermentation via oxalate metabolic pathway manipulation using CRISPR/Cas9. Fungal Biology and Biotechnology, 2021, 8, 1.	2.5	35
26	The microbiome of the buffalo digestive tract. Nature Communications, 2022, 13, 823.	5.8	30
27	Alterations of the Human Lung and Gut Microbiomes in Non-Small Cell Lung Carcinomas and Distant Metastasis. Microbiology Spectrum, 2021, 9, e0080221.	1.2	28
28	mBodyMap: a curated database for microbes across human body and their associations with health and diseases. Nucleic Acids Research, 2022, 50, D808-D816.	6.5	26
29	Systematic analysis of alternative first exons in plant genomes. BMC Plant Biology, 2007, 7, 55.	1.6	24
30	mMGE: a database for human metagenomic extrachromosomal mobile genetic elements. Nucleic Acids Research, 2021, 49, D783-D791.	6.5	24
31	GEAR: A database of Genomic Elements Associated with drug Resistance. Scientific Reports, 2017, 7, 44085.	1.6	21
32	Selection for energy efficiency drives strand-biased gene distribution in prokaryotes. Scientific Reports, 2017, 7, 10572.	1.6	20
33	DRDB: An Online Date Palm Genomic Resource Database. Frontiers in Plant Science, 2017, 8, 1889.	1.7	20
34	GAAD: A Gene and Autoimmiune Disease Association Database. Genomics, Proteomics and Bioinformatics, 2018, 16, 252-261.	3.0	17
35	Human functional genetic studies are biased against the medically most relevant primate-specific genes. BMC Evolutionary Biology, 2010, 10, 316.	3.2	16
36	Host DNA contents in fecal metagenomics as a biomarker for intestinal diseases and effective treatment. BMC Genomics, 2020, 21, 348.	1.2	16

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37	Deguelin inhibits expression of IkappaBalpha protein in Raji and U937 cells1. Acta Pharmacologica Sinica, 2006, 27, 485-490.	2.8	15
38	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	3.0	15
39	Inhibition of TPL2 by interferon-Î± suppresses bladder cancer through activation of PDE4D. Journal of Experimental and Clinical Cancer Research, 2018, 37, 288.	3.5	14
40	Metabolic Dependencies Underlie Interaction Patterns of Gut Microbiota During Enteropathogenesis. Frontiers in Microbiology, 2019, 10, 1205.	1.5	13
41	ColorTree: a batch customization tool for phylogenic trees. BMC Research Notes, 2009, 2, 155.	0.6	12
42	Metagenomic Analysis of Common Intestinal Diseases Reveals Relationships among Microbial Signatures and Powers Multidisease Diagnostic Models. MSystems, 2021, 6, .	1.7	12
43	Treatment regimens may compromise gut-microbiome-derived signatures for liver cirrhosis. Cell Metabolism, 2021, 33, 455-456.	7.2	10
44	Minimal regulatory spaces in yeast genomes. BMC Genomics, 2011, 12, 320.	1.2	6
45	Prokaryotic Genome Expansion Is Facilitated by Phages and Plasmids but Impaired by CRISPR. Frontiers in Microbiology, 2019, 10, 2254.	1.5	6
46	Consistent Alterations of Human Fecal Microbes After Transplantation into Germ-free Mice. Genomics, Proteomics and Bioinformatics, 2022, 20, 382-393.	3.0	6
47	Dynamic metabolomic analysis of intestinal ischemiaâ€"reperfusion injury in rats. IUBMB Life, 2020, 72, 1001-1011.	1.5	6
48	Assessing the Influence of Adjacent Gene Orientation on the Evolution of Gene Upstream Regions in Arabidopsis thaliana. Genetics, 2010, 185, 695-701.	1.2	4
49	Molecular Signatures Related to the Virulence of Bacillus cereus Sensu Lato, a Leading Cause of Devastating Endophthalmitis. MSystems, 2019, 4, .	1.7	4
50	Selection for Cheaper Amino Acids Drives Nucleotide Usage at the Start of Translation in Eukaryotic Genes. Genomics, Proteomics and Bioinformatics, 2021, 19, 949-957.	3.0	4