

# Wei-Hua Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/76762/publications.pdf>

Version: 2024-02-01

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  | Consistent Alterations of Human Fecal Microbes After Transplantation into Germ-free Mice. Genomics, Proteomics and Bioinformatics, 2022, 20, 382-393.  | 3.0 | 6         |
| 2  | 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        |
| 3  | 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        |
| 4  | The microbiome of the buffalo digestive tract. Nature Communications, 2022, 13, 823.   | 5.8 | 30        |
| 5  | STAB: a spatio-temporal cell atlas of the human brain. Nucleic Acids Research, 2021, 49, D1029-D1037.  | 6.5 | 43        |
| 6  | 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        |
| 7  | mMGE: a database for human metagenomic extrachromosomal mobile genetic elements. Nucleic Acids Research, 2021, 49, D783-D791.  | 6.5 | 24        |
| 8  | 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        |
| 9  | Treatment regimens may compromise gut-microbiome-derived signatures for liver cirrhosis. Cell Metabolism, 2021, 33, 455-456.   | 7.2 | 10        |
| 10 | 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         |
| 11 | Metagenomic Analysis of Common Intestinal Diseases Reveals Relationships among Microbial Signatures and Powers Multidisease Diagnostic Models. MSystems, 2021, 6, .  | 1.7 | 12        |
| 12 | 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        |
| 13 | GMrepo: a database of curated and consistently annotated human gut metagenomes. Nucleic Acids Research, 2020, 48, D545-D553.   | 6.5 | 96        |
| 14 | Host DNA contents in fecal metagenomics as a biomarker for intestinal diseases and effective treatment. BMC Genomics, 2020, 21, 348.   | 1.2 | 16        |
| 15 | 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       |
| 16 | Dynamic metabolomic analysis of intestinal ischemia-reperfusion injury in rats. IUBMB Life, 2020, 72, 1001-1011.   | 1.5 | 6         |
| 17 | Evolview v3: a webserver for visualization, annotation, and management of phylogenetic trees. Nucleic Acids Research, 2019, 47, W270-W275.   | 6.5 | 564       |
| 18 | Metabolic Dependencies Underlie Interaction Patterns of Gut Microbiota During Enteropathogenesis. Frontiers in Microbiology, 2019, 10, 1205.   | 1.5 | 13        |

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|----|--|-----|-----------|
| 19 | Molecular Signatures Related to the Virulence of <i>Bacillus cereus</i> Sensu Lato, a Leading Cause of Devastating Endophthalmitis. <i>MSystems</i> , 2019, 4, .   | 1.7 | 4         |
| 20 | Prokaryotic Genome Expansion Is Facilitated by Phages and Plasmids but Impaired by CRISPR. <i>Frontiers in Microbiology</i> , 2019, 10, 2254.  | 1.5 | 6         |
| 21 | MVP: a microbe-phage interaction database. <i>Nucleic Acids Research</i> , 2018, 46, D700-D707.  | 6.5 | 82        |
| 22 | Inhibition of TPL2 by interferon- $\gamma$ suppresses bladder cancer through activation of PDE4D. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 288.                                 | 3.5 | 14        |
| 23 | GAAD: A Gene and Autoimmune Disease Association Database. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 252-261.  | 3.0 | 17        |
| 24 | GEAR: A database of Genomic Elements Associated with drug Resistance. <i>Scientific Reports</i> , 2017, 7, 44085.  | 1.6 | 21        |
| 25 | Selection for energy efficiency drives strand-biased gene distribution in prokaryotes. <i>Scientific Reports</i> , 2017, 7, 10572.   | 1.6 | 20        |
| 26 | OGEE v2: an update of the online gene essentiality database with special focus on differentially essential genes in human cancer cell lines. <i>Nucleic Acids Research</i> , 2017, 45, D940-D944.              | 6.5 | 153       |
| 27 | DRDB: An Online Date Palm Genomic Resource Database. <i>Frontiers in Plant Science</i> , 2017, 8, 1889.  | 1.7 | 20        |
| 28 | Computational Molecular Networks and Network Pharmacology. <i>BioMed Research International</i> , 2017, 2017, 1-1.   | 0.9 | 58        |
| 29 | Integration of multi-omics data of a genome-reduced bacterium: Prevalence of post-transcriptional regulation and its correlation with protein abundances. <i>Nucleic Acids Research</i> , 2016, 44, 1192-1202. | 6.5 | 35        |
| 30 | Energy efficiency trade-offs drive nucleotide usage in transcribed regions. <i>Nature Communications</i> , 2016, 7, 11334.   | 5.8 | 104       |
| 31 | Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016, 14, 253-261.  | 3.0 | 15        |
| 32 | Bacterial antisense RNAs are mainly the product of transcriptional noise. <i>Science Advances</i> , 2016, 2, e1501363.   | 4.7 | 118       |
| 33 | Evolview v2: an online visualization and management tool for customized and annotated phylogenetic trees. <i>Nucleic Acids Research</i> , 2016, 44, W236-W241.   | 6.5 | 610       |
| 34 | Defining a minimal cell: essentiality of small <scp>ORF</scp> s and nc <scp>RNA</scp> s in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2015, 11, 780.                                       | 3.2 | 133       |
| 35 | Gene Transfer from Bacteria and Archaea Facilitated Evolution of an Extremophilic Eukaryote. <i>Science</i> , 2013, 339, 1207-1210.  | 6.0 | 439       |
| 36 | Human Monogenic Disease Genes Have Frequently Functionally Redundant Paralogs. <i>PLoS Computational Biology</i> , 2013, 9, e1003073.  | 1.5 | 49        |

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|----|---|-----|-----------|
| 37 | OGEE: an online gene essentiality database. <i>Nucleic Acids Research</i> , 2012, 40, D901-D906.  | 6.5 | 187       |
| 38 | EvoView, an online tool for visualizing, annotating and managing phylogenetic trees. <i>Nucleic Acids Research</i> , 2012, 40, W569-W572.   | 6.5 | 400       |
| 39 | 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. <i>Molecular Biology and Evolution</i> , 2012, 29, 1703-1706. | 3.5 | 90        |
| 40 | Transcription start site associated RNAs in bacteria. <i>Molecular Systems Biology</i> , 2012, 8, 585.  | 3.2 | 40        |
| 41 | Minimal regulatory spaces in yeast genomes. <i>BMC Genomics</i> , 2011, 12, 320.  | 1.2 | 6         |
| 42 | Orthology prediction methods: A quality assessment using curated protein families. <i>BioEssays</i> , 2011, 33, 769-780.  | 1.2 | 121       |
| 43 | Human functional genetic studies are biased against the medically most relevant primate-specific genes. <i>BMC Evolutionary Biology</i> , 2010, 10, 316.  | 3.2 | 16        |
| 44 | Assessing the Influence of Adjacent Gene Orientation on the Evolution of Gene Upstream Regions in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2010, 185, 695-701.   | 1.2 | 4         |
| 45 | ColorTree: a batch customization tool for phylogenetic trees. <i>BMC Research Notes</i> , 2009, 2, 155.   | 0.6 | 12        |
| 46 | Impact of Genome Reduction on Bacterial Metabolism and Its Regulation. <i>Science</i> , 2009, 326, 1263-1268.   | 6.0 | 267       |
| 47 | Proteome Organization in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1235-1240.   | 6.0 | 440       |
| 48 | Transcriptome Complexity in a Genome-Reduced Bacterium. <i>Science</i> , 2009, 326, 1268-1271.  | 6.0 | 394       |
| 49 | Systematic analysis of alternative first exons in plant genomes. <i>BMC Plant Biology</i> , 2007, 7, 55.  | 1.6 | 24        |
| 50 | Deguelin inhibits expression of IkappaBalpha protein in Raji and U937 cells <sup>1</sup> . <i>Acta Pharmacologica Sinica</i> , 2006, 27, 485-490.   | 2.8 | 15        |