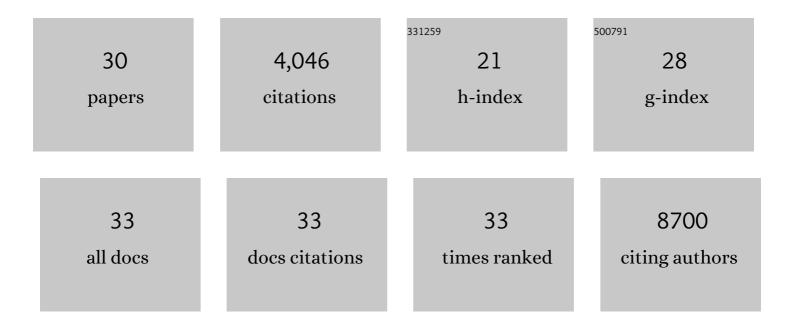
Wen-Chi Chou

List of Publications by Year in descending order

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WEN-CHI CHOU

#	Article	IF	CITATIONS
1	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. Nature Microbiology, 2022, 7, 630-639.	5.9	54
2	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. BMC Microbiology, 2021, 21, 53.	1.3	21
3	A novel computational framework for genome-scale alternative transcription units prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	0
4	Spatially distinct physiology of Bacteroides fragilis within the proximal colon of gnotobiotic mice. Nature Microbiology, 2020, 5, 746-756.	5.9	57
5	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
6	rSeqTU—A Machine-Learning Based R Package for Prediction of Bacterial Transcription Units. Frontiers in Genetics, 2019, 10, 374.	1.1	7
7	Gut microbiota utilize immunoglobulin A for mucosal colonization. Science, 2018, 360, 795-800.	6.0	447
8	SeqTU: A Web Server for Identification of Bacterial Transcription Units. Scientific Reports, 2017, 7, 43925.	1.6	13
9	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. Science Translational Medicine, 2017, 9, .	5.8	139
10	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
11	A combined reference panel from the 1000 Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. Scientific Reports, 2016, 6, 39313.	1.6	32
12	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	3.0	51
13	Novel Genetic Variants Associated With Increased Vertebral Volumetric BMD, Reduced Vertebral Fracture Risk, and Increased Expression of <i>SLC1A3</i> and <i>EPHB2</i> . Journal of Bone and Mineral Research, 2016, 31, 2085-2097.	3.1	42
14	Targeted sequencing of genome wide significant loci associated with bone mineral density (BMD) reveals significant novel and rare variants: the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) targeted sequencing study. Human Molecular Genetics, 2016, 25, ddw289.	1.4	7
15	Comprehensive characterization of the genomic alterations in human gastric cancer. International Journal of Cancer, 2015, 137, 86-95.	2.3	67
16	Analysis of strand-specific RNA-seq data using machine learning reveals the structures of transcription units in Clostridium thermocellum. Nucleic Acids Research, 2015, 43, e67-e67.	6.5	24
17	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
18	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582

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#	Article	IF	CITATIONS
19	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass (<i>Panicum virgatum</i> L.). Plant Journal, 2013, 74, 160-173.	2.8	70
20	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769.	9.4	785
21	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (Artibeus jamaicensis). PLoS ONE, 2012, 7, e48472.	1.1	77
22	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
23	An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer. Nucleic Acids Research, 2011, 39, 1197-1207.	6.5	188
24	GolgiP: prediction of Golgi-resident proteins in plants. Bioinformatics, 2010, 26, 2464-2465.	1.8	12
25	Genome Sequence of the Anaerobic, Thermophilic, and Cellulolytic Bacterium " <i>Anaerocellum thermophilum</i> ―DSM 6725. Journal of Bacteriology, 2009, 191, 3760-3761.	1.0	78
26	pDAWG: An Integrated Database for Plant Cell Wall Genes. Bioenergy Research, 2009, 2, 209-216.	2.2	13
27	BESearch: A Supervised Learning Approach to Search for Molecular Event Participants. , 2007, , .		2
28	BIOSMILE: A semantic role labeling system for biomedical verbs using a maximum-entropy model with automatically generated template features. BMC Bioinformatics, 2007, 8, 325.	1.2	45
29	Integrating linguistic knowledge into a conditional random fieldframework to identify biomedical named entities. Expert Systems With Applications, 2006, 30, 117-128.	4.4	39
30	Various criteria in the evaluation of biomedical named entity recognition. BMC Bioinformatics, 2006, 7, 92.	1.2	80