

Wen-Chi Chou

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

4,046
citations

331259

21
h-index

500791

28
g-index

33
all docs

33
docs citations

33
times ranked

8700
citing authors

#	ARTICLE	IF	CITATIONS
1	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 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. <i>BMC Microbiology</i> , 2021, 21, 53.	1.3	21
3	A novel computational framework for genome-scale alternative transcription units prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	0
4	Spatially distinct physiology of <i>Bacteroides fragilis</i> within the proximal colon of gnotobiotic mice. <i>Nature Microbiology</i> , 2020, 5, 746-756.	5.9	57
5	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	2.2	38
6	rSeqTU: A Machine-Learning Based R Package for Prediction of Bacterial Transcription Units. <i>Frontiers in Genetics</i> , 2019, 10, 374.	1.1	7
7	Gut microbiota utilize immunoglobulin A for mucosal colonization. <i>Science</i> , 2018, 360, 795-800.	6.0	447
8	SeqTU: A Web Server for Identification of Bacterial Transcription Units. <i>Scientific Reports</i> , 2017, 7, 43925.	1.6	13
9	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	139
10	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 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. <i>Scientific Reports</i> , 2016, 6, 39313.	1.6	32
12	GWAS analysis of handgrip and lower body strength in older adults in the CHARGE consortium. <i>Aging Cell</i> , 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> . <i>Journal of Bone and Mineral Research</i> , 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. <i>Human Molecular Genetics</i> , 2016, 25, ddx289.	1.4	7
15	Comprehensive characterization of the genomic alterations in human gastric cancer. <i>International Journal of Cancer</i> , 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 <i>Clostridium thermocellum</i> . <i>Nucleic Acids Research</i> , 2015, 43, e67-e67.	6.5	24
17	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	13.7	483
18	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582

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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.). <i>Plant Journal</i> , 2013, 74, 160-173.	2.8	70
20	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012, 44, 765-769.	9.4	785
21	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (<i>Artibeus jamaicensis</i>). <i>PLoS ONE</i> , 2012, 7, e48472.	1.1	77
22	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
23	An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer. <i>Nucleic Acids Research</i> , 2011, 39, 1197-1207.	6.5	188
24	GolgiP: prediction of Golgi-resident proteins in plants. <i>Bioinformatics</i> , 2010, 26, 2464-2465.	1.8	12
25	Genome Sequence of the Anaerobic, Thermophilic, and Cellulolytic Bacterium <i>Anaerocellum thermophilum</i> DSM 6725. <i>Journal of Bacteriology</i> , 2009, 191, 3760-3761.	1.0	78
26	pDAWG: An Integrated Database for Plant Cell Wall Genes. <i>Bioenergy Research</i> , 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. <i>BMC Bioinformatics</i> , 2007, 8, 325.	1.2	45
29	Integrating linguistic knowledge into a conditional random field framework to identify biomedical named entities. <i>Expert Systems With Applications</i> , 2006, 30, 117-128.	4.4	39
30	Various criteria in the evaluation of biomedical named entity recognition. <i>BMC Bioinformatics</i> , 2006, 7, 92.	1.2	80