Wen-Chi Chou

List of Publications by Year
in descending order

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	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769.	9.4	785
2	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
3	Whole‐genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
4	Gut microbiota utilize immunoglobulin A for mucosal colonization. Science, 2018, 360, 795-800.	6.0	447
5	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
6	An integrated transcriptomic and computational analysis for biomarker identification in gastric cancer. Nucleic Acids Research, 2011, 39, 1197-1207.	6.5	188
7	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147
8	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
9	Various criteria in the evaluation of biomedical named entity recognition. BMC Bioinformatics, 2006, 7, 92.	1.2	80
10	Genome Sequence of the Anaerobic, Thermophilic, and Cellulolytic Bacterium â€œ <i>Anaerocellum thermophilum</i> â€•DSM 6725. Journal of Bacteriology, 2009, 191, 3760-3761.	1.0	78
11	Transcriptome Sequencing and Annotation for the Jamaican Fruit Bat (Artibeus jamaicensis). PLoS ONE, 2012, 7, e48472.	1.1	77
12	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
13	Comprehensive characterization of the genomic alterations in human gastric cancer. International Journal of Cancer, 2015, 137, 86-95.	2.3	67
14	Spatially distinct physiology of Bacteroides fragilis within the proximal colon of gnotobiotic mice. Nature Microbiology, 2020, 5, 746-756.	5.9	57
15	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. Nature Microbiology, 2022, 7, 630-639.	5.9	54
16	<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
17	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
18	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

#	Article	IF	Citations
19	Integrating linguistic knowledge into a conditional random field framework to identify biomedical named entities. Expert Systems With Applications, 2006, 30, 117-128.	4.4	39
20	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
21	A combined reference panel from the 1000â€‰Genomes and UK10K projects improved rare variant imputation in European and Chinese samples. Scientific Reports, 2016, 6, 39313.	1.6	32
22	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
23	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
24	pDAWG: An Integrated Database for Plant Cell Wall Genes. Bioenergy Research, 2009, 2, 209-216.	2.2	13
25	SeqTU: A Web Server for Identification of Bacterial Transcription Units. Scientific Reports, 2017, 7, 43925.	1.6	13
26	GolgiP: prediction of Golgi-resident proteins in plants. Bioinformatics, 2010, 26, 2464-2465.	1.8	12
27	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
28	rSeqTUâ€"A Machine-Learning Based R Package for Prediction of Bacterial Transcription Units. Frontiers in Genetics, 2019, 10, 374.	1.1	7
29	BESearch: A Supervised Learning Approach to Search for Molecular Event Participants. , 2007, , .		2
30	A novel computational framework for genome-scale alternative transcription units prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	0