

Chung-Yen Lin

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62 papers	2,755 citations	19 h-index	52 g-index
76 ext. papers	4,088 ext. citations	6.1 avg, IF	4.88 L-index

#	Paper	IF	Citations
62	cytoHubba: identifying hub objects and sub-networks from complex interactome. <i>BMC Systems Biology</i> , 2014 , 8 Suppl 4, S11	3.5	1459
61	Hubba: hub objects analyzer--a framework of interactome hubs identification for network biology. <i>Nucleic Acids Research</i> , 2008 , 36, W438-43	20.1	186
60	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. <i>Scientific Reports</i> , 2014 , 4, 4942	4.9	113
59	Characterization of FN1-FGFR1 and novel FN1-FGF1 fusion genes in a large series of phosphaturic mesenchymal tumors. <i>Modern Pathology</i> , 2016 , 29, 1335-1346	9.8	95
58	Identification of a novel FN1-FGFR1 genetic fusion as a frequent event in phosphaturic mesenchymal tumour. <i>Journal of Pathology</i> , 2015 , 235, 539-45	9.4	90
57	A quantitative high-resolution genetic profile rapidly identifies sequence determinants of hepatitis C viral fitness and drug sensitivity. <i>PLoS Pathogens</i> , 2014 , 10, e1004064	7.6	51
56	Over-expression of AURKA, SKA3 and DSN1 contributes to colorectal adenoma to carcinoma progression. <i>Oncotarget</i> , 2016 , 7, 45803-45818	3.3	50
55	Compartment-specific transcriptomics in a reef-building coral exposed to elevated temperatures. <i>Molecular Ecology</i> , 2014 , 23, 5816-30	5.7	48
54	A review of the major penaeid shrimp EST studies and the construction of a shrimp transcriptome database based on the ESTs from four penaeid shrimp. <i>Marine Biotechnology</i> , 2011 , 13, 608-21	3.4	45
53	Primer Design Assistant (PDA): A web-based primer design tool. <i>Nucleic Acids Research</i> , 2003 , 31, 3751-420.1	20.1	40
52	POWER: Phylogenetic WEb Repeater--an integrated and user-optimized framework for biomolecular phylogenetic analysis. <i>Nucleic Acids Research</i> , 2005 , 33, W553-6	20.1	37
51	A hub-attachment based method to detect functional modules from confidence-scored protein interactions and expression profiles. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 1, S25	3.6	34
50	Temporal transcription program of recombinant Autographa californica multiple nucleopolyhedrosis virus. <i>Journal of Virology</i> , 2006 , 80, 8989-99	6.6	33
49	PALM: a paralleled and integrated framework for phylogenetic inference with automatic likelihood model selectors. <i>PLoS ONE</i> , 2009 , 4, e8116	3.7	33
48	Ectopic and high CXCL13 chemokine expression in myasthenia gravis with thymic lymphoid hyperplasia. <i>Journal of Neuroimmunology</i> , 2010 , 221, 101-6	3.5	30
47	Dual-compartmental transcriptomic and proteomic analysis of a marine endosymbiosis exposed to environmental change. <i>Molecular Ecology</i> , 2016 , 25, 5944-5958	5.7	29
46	Reconstruction of human protein interolog network using evolutionary conserved network. <i>BMC Bioinformatics</i> , 2007 , 8, 152	3.6	27

45	The effect of red light and far-red light conditions on secondary metabolism in agarwood. <i>BMC Plant Biology</i> , 2015 , 15, 139	5.3	26
44	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (<i>Petaurista alborufus lena</i>). <i>BMC Genomics</i> , 2012 , 13, 466	4.5	19
43	Systematic identification of anti-interferon function on hepatitis C virus genome reveals p7 as an immune evasion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 2018-2023	11.5	18
42	CloudDOE: a user-friendly tool for deploying Hadoop clouds and analyzing high-throughput sequencing data with MapReduce. <i>PLoS ONE</i> , 2014 , 9, e98146	3.7	18
41	Simultaneous detection of multiple fish pathogens using a naked-eye readable DNA microarray. <i>Sensors</i> , 2012 , 12, 2710-28	3.8	18
40	Sequencing and analysis of the transcriptome of the acorn worm <i>Ptychodera flava</i> , an indirect developing hemichordate. <i>Marine Genomics</i> , 2014 , 15, 35-43	1.9	16
39	Convex feasible set algorithm for constrained trajectory smoothing 2017 ,		16
38	UPS 2.0: unique probe selector for probe design and oligonucleotide microarrays at the pangenomic/genomic level. <i>BMC Genomics</i> , 2010 , 11 Suppl 4, S6	4.5	16
37	SQUAT: a Sequencing Quality Assessment Tool for data quality assessments of genome assemblies. <i>BMC Genomics</i> , 2019 , 19, 238	4.5	15
36	De Novo Assembly of the Whole Transcriptome of the Wild Embryo, Preleptocephalus, Leptocephalus, and Glass Eel of <i>Anguilla japonica</i> and Deciphering the Digestive and Absorptive Capacities during Early Development. <i>PLoS ONE</i> , 2015 , 10, e0139105	3.7	15
35	Statistical Learning Algorithms to Compensate Slow Visual Feedback for Industrial Robots. <i>Journal of Dynamic Systems, Measurement and Control, Transactions of the ASME</i> , 2015 , 137,	1.6	14
34	A comprehensive functional map of the hepatitis C virus genome provides a resource for probing viral proteins. <i>MBio</i> , 2014 , 5, e01469-14	7.8	13
33	Using high-throughput transcriptome sequencing to investigate the biotransformation mechanism of hexabromocyclododecane with <i>Rhodospseudomonas palustris</i> in water. <i>Science of the Total Environment</i> , 2019 , 692, 249-258	10.2	11
32	The role of the bacterial protease Prc in the uropathogenesis of extraintestinal pathogenic <i>Escherichia coli</i> . <i>Journal of Biomedical Science</i> , 2020 , 27, 14	13.3	11
31	A gene profiling deconvolution approach to estimating immune cell composition from complex tissues. <i>BMC Bioinformatics</i> , 2018 , 19, 154	3.6	10
30	Fast planning of well conditioned trajectories for model learning 2014 ,		10
29	hp-DPI: <i>Helicobacter pylori</i> database of protein interactomes--embracing experimental and inferred interactions. <i>Bioinformatics</i> , 2005 , 21, 1288-90	7.2	10
28	The novel white spot syndrome virus-induced gene, PmERP15, encodes an ER stress-responsive protein in black tiger shrimp, <i>Penaeus monodon</i> . <i>Developmental and Comparative Immunology</i> , 2015 , 49, 239-48	3.2	9

27	Fly-DPI: database of protein interactomes for D. melanogaster in the approach of systems biology. <i>BMC Bioinformatics</i> , 2006 , 7 Suppl 5, S18	3.6	9
26	Piwi reduction in the aged niche eliminates germline stem cells via Toll-GSK3 signaling. <i>Nature Communications</i> , 2020 , 11, 3147	17.4	8
25	Precise genotyping and recombination detection of Enterovirus. <i>BMC Genomics</i> , 2015 , 16 Suppl 12, S8	4.5	7
24	The unique probe selector: a comprehensive web service for probe design and oligonucleotide arrays. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 1, S8	3.6	7
23	A Bayes regression approach to array-CGH data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2006 , 5, Article3	1.2	7
22	Revealing the compositions of the intestinal microbiota of three Anguillid eel species using 16S rDNA sequencing. <i>Aquaculture Research</i> , 2018 , 49, 2404-2415	1.9	6
21	Robust principal component analysis for iterative learning control of precision motion systems with non-repetitive disturbances 2015 ,		6
20	Subset selection of high-depth next generation sequencing reads for de novo genome assembly using MapReduce framework. <i>BMC Genomics</i> , 2015 , 16 Suppl 12, S9	4.5	5
19	Index of Cancer-Associated Fibroblasts Is Superior to the Epithelial-Mesenchymal Transition Score in Prognosis Prediction. <i>Cancers</i> , 2020 , 12,	6.6	3
18	Functional Characteristics of the Flying Squirrel's Cecal Microbiota under a Leaf-Based Diet, Based on Multiple Meta-Omic Profiling. <i>Frontiers in Microbiology</i> , 2017 , 8, 2622	5.7	3
17	CloudEC: A MapReduce-based algorithm for correcting errors in next-generation sequencing big data 2017 ,		3
16	Design of kinematic controller for real-time vision guided robot manipulators 2014 ,		3
15	AI4AMP: an Antimicrobial Peptide Predictor Using Physicochemical Property-Based Encoding Method and Deep Learning. <i>MSystems</i> , 2021 , e0029921	7.6	3
14	Gut Fecal Microbiota Transplant in a Mouse Model of Orthotopic Rectal Cancer. <i>Frontiers in Oncology</i> , 2020 , 10, 568012	5.3	3
13	Probabilistic Approach to Modeling and Parameter Learning of Indirect Drive Robots From Incomplete Data. <i>IEEE/ASME Transactions on Mechatronics</i> , 2015 , 20, 1036-1045	5.5	2
12	TEA: the epigenome platform for Arabidopsis methylome study. <i>BMC Genomics</i> , 2016 , 17, 1027	4.5	2
11	The degradation mechanisms of Rhodopseudomonas palustris toward hexabromocyclododecane by time-course transcriptome analysis. <i>Chemical Engineering Journal</i> , 2021 , 425, 130489	14.7	2
10	Spotlight: assembly of protein complexes by integrating graph clustering methods. <i>Gene</i> , 2013 , 518, 42-51	3.8	1

9	Matrix factorization for design of Q-filter in iterative learning control 2015 ,		1
8	Androgenic Sensitivities and Ovarian Gene Expression Profiles Prior to Treatment in Japanese Eel (<i>Anguilla japonica</i>). <i>Marine Biotechnology</i> , 2021 , 23, 430-444	3-4	1
7	Path-constrained trajectory planning for robot service life optimization 2016 ,		1
6	Genetic loci determining total immunoglobulin E levels from birth through adulthood. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2019 , 74, 621-625	9-3	1
5	ATACgraph: Profiling Genome-Wide Chromatin Accessibility From ATAC-seq. <i>Frontiers in Genetics</i> , 2020 , 11, 618478	4-5	1
4	Identification of Genes Related to Cold Tolerance and Novel Genetic Markers for Molecular Breeding in Taiwan Tilapia (spp.) via Transcriptome Analysis.. <i>Animals</i> , 2021 , 11,	3-1	1
3	Investigating the Transcriptomic and Expression Presence-Absence Variation Exist in Japanese Eel (<i>Anguilla japonica</i>), a Primitive Teleost. <i>Marine Biotechnology</i> , 2021 , 23, 943-954	3-4	0
2	EpiMOLAS: an intuitive web-based framework for genome-wide DNA methylation analysis. <i>BMC Genomics</i> , 2020 , 21, 163	4-5	
1	Recapitulation of inflammatory and immune-evasive subtypes of oral cancer cells in immunodeficient mice.. <i>Journal of Clinical Oncology</i> , 2019 , 37, e14199-e14199	2-2	