

# Chung-Yen Lin

## List of Publications by Year in Descending Order

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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	AI4AMP: an Antimicrobial Peptide Predictor Using Physicochemical Property-Based Encoding Method and Deep Learning. <i>MSystems</i> , <b>2021</b> , e0029921	7.6	3
61	Investigating the Transcriptomic and Expression Presence-Absence Variation Exist in Japanese Eel ( <i>Anguilla japonica</i> ), a Primitive Teleost. <i>Marine Biotechnology</i> , <b>2021</b> , 23, 943-954	3.4	0
60	Androgenic Sensitivities and Ovarian Gene Expression Profiles Prior to Treatment in Japanese Eel ( <i>Anguilla japonica</i> ). <i>Marine Biotechnology</i> , <b>2021</b> , 23, 430-444	3.4	1
59	The degradation mechanisms of <i>Rhodopseudomonas palustris</i> toward hexabromocyclododecane by time-course transcriptome analysis. <i>Chemical Engineering Journal</i> , <b>2021</b> , 425, 130489	14.7	2
58	Identification of Genes Related to Cold Tolerance and Novel Genetic Markers for Molecular Breeding in Taiwan Tilapia ( <i>spp.</i> ) via Transcriptome Analysis.. <i>Animals</i> , <b>2021</b> , 11,	3.1	1
57	Piwi reduction in the aged niche eliminates germline stem cells via Toll-GSK3 signaling. <i>Nature Communications</i> , <b>2020</b> , 11, 3147	17.4	8
56	EpiMOLAS: an intuitive web-based framework for genome-wide DNA methylation analysis. <i>BMC Genomics</i> , <b>2020</b> , 21, 163	4.5	
55	Index of Cancer-Associated Fibroblasts Is Superior to the Epithelial-Mesenchymal Transition Score in Prognosis Prediction. <i>Cancers</i> , <b>2020</b> , 12,	6.6	3
54	The role of the bacterial protease Prc in the uropathogenesis of extraintestinal pathogenic <i>Escherichia coli</i> . <i>Journal of Biomedical Science</i> , <b>2020</b> , 27, 14	13.3	11
53	Gut Fecal Microbiota Transplant in a Mouse Model of Orthotopic Rectal Cancer. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 568012	5.3	3
52	ATACgraph: Profiling Genome-Wide Chromatin Accessibility From ATAC-seq. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 618478	4.5	1
51	Using high-throughput transcriptome sequencing to investigate the biotransformation mechanism of hexabromocyclododecane with <i>Rhodopseudomonas palustris</i> in water. <i>Science of the Total Environment</i> , <b>2019</b> , 692, 249-258	10.2	11
50	SQUAT: a Sequencing Quality Assessment Tool for data quality assessments of genome assemblies. <i>BMC Genomics</i> , <b>2019</b> , 19, 238	4.5	15
49	Recapitulation of inflammatory and immune-evasive subtypes of oral cancer cells in immunodeficient mice.. <i>Journal of Clinical Oncology</i> , <b>2019</b> , 37, e14199-e14199	2.2	
48	Genetic loci determining total immunoglobulin E levels from birth through adulthood. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 74, 621-625	9.3	1
47	Revealing the compositions of the intestinal microbiota of three Anguillid eel species using 16S rDNA sequencing. <i>Aquaculture Research</i> , <b>2018</b> , 49, 2404-2415	1.9	6
46	A gene profiling deconvolution approach to estimating immune cell composition from complex tissues. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 154	3.6	10

45	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> , <b>2017</b> , 114, 2018-2023	11.5	18
44	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> , <b>2017</b> , 8, 2622	5.7	3
43	Convex feasible set algorithm for constrained trajectory smoothing <b>2017</b> ,		16
42	CloudEC: A MapReduce-based algorithm for correcting errors in next-generation sequencing big data <b>2017</b> ,		3
41	Characterization of FN1-FGFR1 and novel FN1-FGF1 fusion genes in a large series of phosphaturic mesenchymal tumors. <i>Modern Pathology</i> , <b>2016</b> , 29, 1335-1346	9.8	95
40	Dual-compartmental transcriptomic and proteomic analysis of a marine endosymbiosis exposed to environmental change. <i>Molecular Ecology</i> , <b>2016</b> , 25, 5944-5958	5.7	29
39	Over-expression of AURKA, SKA3 and DSN1 contributes to colorectal adenoma to carcinoma progression. <i>Oncotarget</i> , <b>2016</b> , 7, 45803-45818	3.3	50
38	TEA: the epigenome platform for Arabidopsis methylome study. <i>BMC Genomics</i> , <b>2016</b> , 17, 1027	4.5	2
37	Path-constrained trajectory planning for robot service life optimization <b>2016</b> ,		1
36	The effect of red light and far-red light conditions on secondary metabolism in agarwood. <i>BMC Plant Biology</i> , <b>2015</b> , 15, 139	5.3	26
35	Identification of a novel FN1-FGFR1 genetic fusion as a frequent event in phosphaturic mesenchymal tumour. <i>Journal of Pathology</i> , <b>2015</b> , 235, 539-45	9.4	90
34	Precise genotyping and recombination detection of Enterovirus. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 12, S8	4.5	7
33	Subset selection of high-depth next generation sequencing reads for de novo genome assembly using MapReduce framework. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 12, S9	4.5	5
32	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> , <b>2015</b> , 10, e0139105	3.7	15
31	Probabilistic Approach to Modeling and Parameter Learning of Indirect Drive Robots From Incomplete Data. <i>IEEE/ASME Transactions on Mechatronics</i> , <b>2015</b> , 20, 1036-1045	5.5	2
30	Matrix factorization for design of Q-filter in iterative learning control <b>2015</b> ,		1
29	Robust principal component analysis for iterative learning control of precision motion systems with non-repetitive disturbances <b>2015</b> ,		6
28	Statistical Learning Algorithms to Compensate Slow Visual Feedback for Industrial Robots. <i>Journal of Dynamic Systems, Measurement and Control, Transactions of the ASME</i> , <b>2015</b> , 137,	1.6	14

27	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> , <b>2015</b> , 49, 239-48	3.2	9
26	Sequencing and analysis of the transcriptome of the acorn worm <i>Ptychodera flava</i> , an indirect developing hemichordate. <i>Marine Genomics</i> , <b>2014</b> , 15, 35-43	1.9	16
25	cytoHubba: identifying hub objects and sub-networks from complex interactome. <i>BMC Systems Biology</i> , <b>2014</b> , 8 Suppl 4, S11	3.5	1459
24	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. <i>Scientific Reports</i> , <b>2014</b> , 4, 4942	4.9	113
23	CloudDOE: a user-friendly tool for deploying Hadoop clouds and analyzing high-throughput sequencing data with MapReduce. <i>PLoS ONE</i> , <b>2014</b> , 9, e98146	3.7	18
22	A quantitative high-resolution genetic profile rapidly identifies sequence determinants of hepatitis C viral fitness and drug sensitivity. <i>PLoS Pathogens</i> , <b>2014</b> , 10, e1004064	7.6	51
21	A comprehensive functional map of the hepatitis C virus genome provides a resource for probing viral proteins. <i>MBio</i> , <b>2014</b> , 5, e01469-14	7.8	13
20	Design of kinematic controller for real-time vision guided robot manipulators <b>2014</b> ,		3
19	Compartment-specific transcriptomics in a reef-building coral exposed to elevated temperatures. <i>Molecular Ecology</i> , <b>2014</b> , 23, 5816-30	5.7	48
18	Fast planning of well conditioned trajectories for model learning <b>2014</b> ,		10
17	Spotlight: assembly of protein complexes by integrating graph clustering methods. <i>Gene</i> , <b>2013</b> , 518, 42-51	3.8	1
16	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> , <b>2012</b> , 13, 466	4.5	19
15	Simultaneous detection of multiple fish pathogens using a naked-eye readable DNA microarray. <i>Sensors</i> , <b>2012</b> , 12, 2710-28	3.8	18
14	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> , <b>2011</b> , 13, 608-21	3.4	45
13	Ectopic and high CXCL13 chemokine expression in myasthenia gravis with thymic lymphoid hyperplasia. <i>Journal of Neuroimmunology</i> , <b>2010</b> , 221, 101-6	3.5	30
12	A hub-attachment based method to detect functional modules from confidence-scored protein interactions and expression profiles. <i>BMC Bioinformatics</i> , <b>2010</b> , 11 Suppl 1, S25	3.6	34
11	UPS 2.0: unique probe selector for probe design and oligonucleotide microarrays at the pangenomic/genomic level. <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 4, S6	4.5	16
10	PALM: a paralleled and integrated framework for phylogenetic inference with automatic likelihood model selectors. <i>PLoS ONE</i> , <b>2009</b> , 4, e8116	3.7	33

9	The unique probe selector: a comprehensive web service for probe design and oligonucleotide arrays. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 1, S8	3.6	7
8	Hubba: hub objects analyzer--a framework of interactome hubs identification for network biology. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W438-43	20.1	186
7	Reconstruction of human protein interolog network using evolutionary conserved network. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 152	3.6	27
6	Fly-DPI: database of protein interactomes for <i>D. melanogaster</i> in the approach of systems biology. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 5, S18	3.6	9
5	Temporal transcription program of recombinant <i>Autographa californica</i> multiple nucleopolyhedrosis virus. <i>Journal of Virology</i> , <b>2006</b> , 80, 8989-99	6.6	33
4	A Bayes regression approach to array-CGH data. <i>Statistical Applications in Genetics and Molecular Biology</i> , <b>2006</b> , 5, Article3	1.2	7
3	POWER: Phylogenetic WEb Repeater--an integrated and user-optimized framework for biomolecular phylogenetic analysis. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W553-6	20.1	37
2	hp-DPI: <i>Helicobacter pylori</i> database of protein interactomes--embracing experimental and inferred interactions. <i>Bioinformatics</i> , <b>2005</b> , 21, 1288-90	7.2	10
1	Primer Design Assistant (PDA): A web-based primer design tool. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3751-4	20.1	40