Chung-Yen Lin

List of Publications by Year
in descending order

70 papers	5,211 citations	279798 23 h-index	138484 58 g-index
76 all docs	76 docs citations	76 times ranked	6017 citing authors

#	ARTICLE	IF	CITATIONS
1	cytoHubba: identifying hub objects and sub-networks from complex interactome. BMC Systems Biology, 2014, 8, S11.	3.0	3,371
2	Hubba: hub objects analyzer—a framework of interactome hubs identification for network biology. Nucleic Acids Research, 2008, 36, W438-W443.	14.5	239
3	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. Scientific Reports, 2014, 4, 4942.	3.3	147
4	Characterization of FN1–FGFR1 and novel FN1–FGF1 fusion genes in a large series of phosphaturic mesenchymal tumors. Modern Pathology, 2016, 29, 1335-1346.	5.5	139
5	Identification of a novel *FN1-FGFR1* genetic fusion as a frequent event in phosphaturic mesenchymal tumour. Journal of Pathology, 2015, 235, 539-545.	4.5	120
6	Compartment–specific transcriptomics in a reef–building coral exposed to elevated temperatures. Molecular Ecology, 2014, 23, 5816-5830.	3.9	73
7	A Quantitative High-Resolution Genetic Profile Rapidly Identifies Sequence Determinants of Hepatitis C Viral Fitness and Drug Sensitivity. PLoS Pathogens, 2014, 10, e1004064.	4.7	66
8	Over-expression of *AURKA*, *SKA3* and *DSN1* contributes to colorectal adenoma to carcinoma progression. Oncotarget, 2016, 7, 45803-45818.	1.8	63
9	Primer Design Assistant (PDA): a web-based primer design tool. Nucleic Acids Research, 2003, 31, 3751-3754.	14.5	51
10	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. Marine Biotechnology, 2011, 13, 608-621.	2.4	49
11	POWER: PhylOgenetic WEb Repeater--an integrated and user-optimized framework for biomolecular phylogenetic analysis. Nucleic Acids Research, 2005, 33, W553-W556.	14.5	45
12	A hub-attachment based method to detect functional modules from confidence-scored protein interactions and expression profiles. BMC Bioinformatics, 2010, 11, S25.	2.6	40
13	PALM: A Paralleled and Integrated Framework for Phylogenetic Inference with Automatic Likelihood Model Selectors. PLoS ONE, 2009, 4, e8116.	2.5	36
14	Temporal Transcription Program of Recombinant Autographa californica Multiple Nucleopolyhedrosis Virus. Journal of Virology, 2006, 80, 8989-8999.	3.4	35
15	Ectopic and high CXCL13 chemokine expression in myasthenia gravis with thymic lymphoid hyperplasia. Journal of Neuroimmunology, 2010, 221, 101-106.	2.3	34
16	Dual–compartmental transcriptomic+proteomic analysis of a marine endosymbiosis exposed to environmental change. Molecular Ecology, 2016, 25, 5944-5958.	3.9	34
17	Reconstruction of human protein interolog network using evolutionary conserved network. BMC Bioinformatics, 2007, 8, 152.	2.6	33
18	The effect of red light and far-red light conditions on secondary metabolism in Agarwood. BMC Plant Biology, 2015, 15, 139.	3.6	33

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19	AI4AMP: an Antimicrobial Peptide Predictor Using Physicochemical Property-Based Encoding Method and Deep Learning. MSystems, 2021, 6, e0029921.	3.8	33
20	Systematic identification of anti-interferon function on hepatitis C virus genome reveals p7 as an immune evasion protein. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2018-2023.	7.1	29
21	SQUAT: a Sequencing Quality Assessment Tool for data quality assessments of genome assemblies. BMC Genomics, 2019, 19, 238.	2.8	29
22	Metagenomic analysis reveals a functional signature for biomass degradation by cecal microbiota in the leaf-eating flying squirrel (Petaurista alborufus lena). BMC Genomics, 2012, 13, 466.	2.8	27
23	Convex feasible set algorithm for constrained trajectory smoothing. , 2017, , .		27
24	Simultaneous Detection of Multiple Fish Pathogens Using a Naked-Eye Readable DNA Microarray. Sensors, 2012, 12, 2710-2728.	3.8	26
25	CloudDOE: A User-Friendly Tool for Deploying Hadoop Clouds and Analyzing High-Throughput Sequencing Data with MapReduce. PLoS ONE, 2014, 9, e98146.	2.5	24
26	The role of the bacterial protease Prc in the uropathogenesis of extraintestinal pathogenic Escherichia coli. Journal of Biomedical Science, 2020, 27, 14.	7.0	24
27	De Novo Assembly of the Whole Transcriptome of the Wild Embryo, Preleptocephalus, Leptocephalus, and Glass Eel of Anguilla japonica and Deciphering the Digestive and Absorptive Capacities during Early Development. PLoS ONE, 2015, 10, e0139105.	2.5	23
28	UPS 2.0: unique probe selector for probe design and oligonucleotide microarrays at the pangenomic/genomic level. BMC Genomics, 2010, 11, S6.	2.8	20
29	Statistical Learning Algorithms to Compensate Slow Visual Feedback for Industrial Robots. Journal of Dynamic Systems, Measurement and Control, Transactions of the ASME, 2015, 137, .	1.6	20
30	Using high-throughput transcriptome sequencing to investigate the biotransformation mechanism of hexabromocyclododecane with Rhodopseudomonas palustris in water. Science of the Total Environment, 2019, 692, 249-258.	8.0	18
31	Piwi reduction in the aged niche eliminates germline stem cells via Toll-GSK3 signaling. Nature Communications, 2020, 11, 3147.	12.8	18
32	Index of Cancer-Associated Fibroblasts Is Superior to the Epithelial–Mesenchymal Transition Score in Prognosis Prediction. Cancers, 2020, 12, 1718.	3.7	18
33	A Comprehensive Functional Map of the Hepatitis C Virus Genome Provides a Resource for Probing Viral Proteins. MBio, 2014, 5, e01469-14.	4.1	16
34	Sequencing and analysis of the transcriptome of the acorn worm Ptychodera flava, an indirect developing hemichordate. Marine Genomics, 2014, 15, 35-43.	1.1	16
35	A gene profiling deconvolution approach to estimating immune cell composition from complex tissues. BMC Bioinformatics, 2018, 19, 154.	2.6	14
36	Galectin-1 orchestrates an inflammatory tumor-stroma crosstalk in hepatoma by enhancing TNFR1 protein stability and signaling in carcinoma-associated fibroblasts. Oncogene, 2022, 41, 3011-3023.	5.9	14

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37	Robust principal component analysis for iterative learning control of precision motion systems with non-repetitive disturbances. , 2015, , .		12
38	Revealing the compositions of the intestinal microbiota of three Anguillid eel species using 16S rDNA sequencing. Aquaculture Research, 2018, 49, 2404-2415.	1.8	12
39	Fly-DPI: database of protein interactomes for D. melanogaster in the approach of systems biology. BMC Bioinformatics, 2006, 7, S18.	2.6	11
40	Fast planning of well conditioned trajectories for model learning. , 2014, , .		11
41	A Yes-Associated Protein (YAP) and Insulin-Like Growth Factor 1 Receptor (IGF-1R) Signaling Loop Is Involved in Sorafenib Resistance in Hepatocellular Carcinoma. Cancers, 2021, 13, 3812.	3.7	11
42	hp-DPI: Helicobacter pylori Database of Protein Interactomes--embracing experimental and inferred interactions. Bioinformatics, 2005, 21, 1288-1290.	4.1	10
43	The novel white spot syndrome virus-induced gene, PmERP15, encodes an ER stress-responsive protein in black tiger shrimp, Penaeus monodon. Developmental and Comparative Immunology, 2015, 49, 239-248.	2.3	10
44	Precise genotyping and recombination detection of Enterovirus. BMC Genomics, 2015, 16, S8.	2.8	9
45	The degradation mechanisms of Rhodopseudomonas palustris toward hexabromocyclododecane by time-course transcriptome analysis. Chemical Engineering Journal, 2021, 425, 130489.	12.7	9
46	Development of Disease-Resistance-Associated Microsatellite DNA Markers for Selective Breeding of Tilapia (Oreochromis spp.) Farmed in Taiwan. Genes, 2022, 13, 99.	2.4	9
47	A Bayes Regression Approach to Array-CGH Data. Statistical Applications in Genetics and Molecular Biology, 2006, 5, Article3.	0.6	8
48	ATACgraph: Profiling Genome-Wide Chromatin Accessibility From ATAC-seq. Frontiers in Genetics, 2020, 11, 618478.	2.3	8
49	The unique probe selector: a comprehensive web service for probe design and oligonucleotide arrays. BMC Bioinformatics, 2008, 9, S8.	2.6	7
50	CloudEC: A MapReduce-based algorithm for correcting errors in next-generation sequencing big data. , 2017, , .		7
51	Peptide-Based Drug Predictions for Cancer Therapy Using Deep Learning. Pharmaceuticals, 2022, 15, 422.	3.8	7
52	Subset selection of high-depth next generation sequencing reads for de novo genome assembly using MapReduce framework. BMC Genomics, 2015, 16, S9.	2.8	6
53	Gut Fecal Microbiota Transplant in a Mouse Model of Orthotopic Rectal Cancer. Frontiers in Oncology, 2020, 10, 568012.	2.8	6
54	MetaSquare: an integrated metadatabase of 16S rRNA gene amplicon for microbiome taxonomic classification. Bioinformatics, 2022, 38, 2930-2931.	4.1	6

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55	Functional Characteristics of the Flying Squirrel's Cecal Microbiota under a Leaf-Based Diet, Based on Multiple Meta-Omic Profiling. Frontiers in Microbiology, 2017, 8, 2622.	3.5	5
56	Identification of Genes Related to Cold Tolerance and Novel Genetic Markers for Molecular Breeding in Taiwan Tilapia (Oreochromis spp.) via Transcriptome Analysis. Animals, 2021, 11, 3538.	2.3	5
57	Visual tracking with sensing dynamics compensation using the Expectation-Maximization algorithm. , 2013, , .		4
58	Design of kinematic controller for real-time vision guided robot manipulators. , 2014, , .		4
59	Probabilistic Approach to Modeling and Parameter Learning of Indirect Drive Robots From Incomplete Data. IEEE/ASME Transactions on Mechatronics, 2015, 20, 1036-1045.	5.8	3
60	TEA: the epigenome platform for Arabidopsis methylome study. BMC Genomics, 2016, 17, 1027.	2.8	3
61	Androgenic Sensitivities and Ovarian Gene Expression Profiles Prior to Treatment in Japanese Eel (Anguilla japonica). Marine Biotechnology, 2021, 23, 430-444.	2.4	3
62	Investigating the Transcriptomic and Expression Presence-Absence Variation Exist in Japanese Eel (Anguilla japonica), a Primitive Teleost. Marine Biotechnology, 2021, 23, 943-954.	2.4	3
63	Matrix factorization for design of Q-filter in iterative learning control. , 2015, , .		2
64	Genetic loci determining total immunoglobulin E levels from birth through adulthood. Allergy: European Journal of Allergy and Clinical Immunology, 2019, 74, 621-625.	5.7	2
65	Spotlight: Assembly of protein complexes by integrating graph clustering methods. Gene, 2013, 518, 42-51.	2.2	1
66	Path-constrained trajectory planning for robot service life optimization. , 2016, , .		1
67	Learning control for task specific industrial robots. , 2016, , .		0
68	EpiMOLAS: an intuitive web-based framework for genome-wide DNA methylation analysis. BMC Genomics, 2020, 21, 163.	2.8	0
69	Recapitulation of inflammatory and immune-evasive subtypes of oral cancer cells in immunodeficient mice.. Journal of Clinical Oncology, 2019, 37, e14199-e14199.	1.6	0
70	Elegancy: Digitizing the wisdom from laboratories to the cloud with free no-code platform. IScience, 2022, 25, 104710.	4.1	0