

# Jing Woei Li

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/558910/publications.pdf>

Version: 2024-02-01

94  
papers

3,922  
citations

136950

32  
h-index

138484

58  
g-index

95  
all docs

95  
docs citations

95  
times ranked

6345  
citing authors

#	ARTICLE	IF	CITATIONS
1	A tRNA-derived fragment from Chinese yew suppresses ovarian cancer growth via targeting TRPA1. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 27, 718-732.	5.1	19
2	Type 2 innate immunity drives distinct neonatal immune profile conducive for heart regeneration. <i>Theranostics</i> , 2022, 12, 1161-1172.	10.0	6
3	The Identification of MATE Antisense Transcripts in Soybean Using Strand-Specific RNA-Seq Datasets. <i>Genes</i> , 2022, 13, 228.	2.4	1
4	Genetic architecture of wild soybean ( <i>Glycine soja</i> Sieb. and Zucc.) populations originating from different East Asian regions. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 1577-1588.	1.6	2
5	Pan-cancer investigation reveals mechanistic insights of planar cell polarity gene Fuz in carcinogenesis. <i>Aging</i> , 2021, 13, 7259-7283.	3.1	10
6	Authentication of Hedyotis products by adaptor ligation-mediated PCR and metabarcoding. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 196, 113920.	2.8	7
7	RNA G-quadruplexes (rG4s): genomics and biological functions. <i>Nucleic Acids Research</i> , 2021, 49, 5426-5450.	14.5	86
8	Differentially expressed microRNAs that target functional genes in mature soybean nodules. <i>Plant Genome</i> , 2021, 14, e20103.	2.8	8
9	CAG RNAs induce DNA damage and apoptosis by silencing <i>NUDT16</i> expression in polyglutamine degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	17
10	Increased copy number of <i>gibberellin 2-oxidase 8</i> genes reduced trailing growth and shoot length during soybean domestication. <i>Plant Journal</i> , 2021, 107, 1739-1755.	5.7	24
11	Identification of Smad3-related transcriptomes in type 2 diabetic nephropathy by whole transcriptome RNA sequencing. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 2052-2068.	3.6	5
12	Toward haplotype studies in polyploid plants to assist breeding. <i>Molecular Plant</i> , 2021, 14, 1969-1972.	8.3	6
13	Integratome analysis of adipose tissues reveals abnormal epigenetic regulation of adipogenesis, inflammation, and insulin signaling in obese individuals with type 2 diabetes. <i>Clinical and Translational Medicine</i> , 2021, 11, e596.	4.0	4
14	Terpenes and Terpenoids in Plants: Interactions with Environment and Insects. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7382.	4.1	172
15	Advances in optical mapping for genomic research. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2051-2062.	4.1	71
16	Extracellular Vesicles in Head and Neck Cancer: A Potential New Trend in Diagnosis, Prognosis, and Treatment. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8260.	4.1	13
17	rG4-seeker enables high-confidence identification of novel and non-canonical rG4 motifs from rG4-seq experiments. <i>RNA Biology</i> , 2020, 17, 903-917.	3.1	14
18	Transcriptomic analysis reveals the oncogenic role of S6K1 in hepatocellular carcinoma. <i>Journal of Cancer</i> , 2020, 11, 2645-2655.	2.5	8

#	ARTICLE	IF	CITATIONS
19	Analysis of Soybean Long Non-Coding RNAs Reveals a Subset of Small Peptide-Coding Transcripts. <i>Plant Physiology</i> , 2020, 182, 1359-1374.	4.8	46
20	Millipede genomes reveal unique adaptations during myriapod evolution. <i>PLoS Biology</i> , 2020, 18, e3000636.	5.6	18
21	SCRaMBLE-in: A Fast and Efficient Method to Diversify and Improve the Yields of Heterologous Pathways in Synthetic Yeast. <i>Methods in Molecular Biology</i> , 2020, 2205, 305-327.	0.9	0
22	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
23	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
24	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
25	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
26	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
27	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
28	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
29	Millipede genomes reveal unique adaptations during myriapod evolution. , 2020, 18, e3000636.		0
30	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
31	OMMA enables population-scale analysis of complex genomic features and phylogenomic relationships from nanochannel-based optical maps. <i>GigaScience</i> , 2019, 8, .	6.4	5
32	Systematic evaluation and optimization of the experimental steps in RNA G-quadruplex structure sequencing. <i>Scientific Reports</i> , 2019, 9, 8091.	3.3	13
33	Genome maps across 26 human populations reveal population-specific patterns of structural variation. <i>Nature Communications</i> , 2019, 10, 1025.	12.8	123
34	Hypoxia Causes Transgenerational Impairment of Ovarian Development and Hatching Success in Fish. <i>Environmental Science &amp; Technology</i> , 2019, 53, 3917-3928.	10.0	39
35	A Small RNA Transforms the Multidrug Resistance of <i>Pseudomonas aeruginosa</i> to Drug Susceptibility. <i>Molecular Therapy - Nucleic Acids</i> , 2019, 16, 218-228.	5.1	13
36	A reference-grade wild soybean genome. <i>Nature Communications</i> , 2019, 10, 1216.	12.8	183

#	ARTICLE	IF	CITATIONS
37	Reference-Based Identification of Long Noncoding RNAs in Plants with Strand-Specific RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2019, 1933, 245-255.	0.9	1
38	Characterization of Hepatocellular Carcinoma Cell Lines Using a Fractionation-Then-Sequencing Approach Reveals Nuclear-Enriched HCC-Associated lncRNAs. <i>Frontiers in Genetics</i> , 2019, 10, 1081.	2.3	12
39	Replication Study for the Association of GWAS-associated Loci With Adolescent Idiopathic Scoliosis Susceptibility and Curve Progression in a Chinese Population. <i>Spine</i> , 2019, 44, 464-471.	2.0	19
40	Transcriptomic reprogramming in soybean seedlings under salt stress. <i>Plant, Cell and Environment</i> , 2019, 42, 98-114.	5.7	111
41	Comparative transcriptomics of multidrug-resistant <i>Acinetobacter baumannii</i> in response to antibiotic treatments. <i>Scientific Reports</i> , 2018, 8, 3515.	3.3	53
42	A comprehensive web tool for toehold switch design. <i>Bioinformatics</i> , 2018, 34, 2862-2864.	4.1	31
43	Transcriptomic analysis reveals transgenerational effect of hypoxia on the neural control of testicular functions. <i>Aquatic Toxicology</i> , 2018, 195, 41-48.	4.0	11
44	High-quality assembly of <i>Dermatophagoides pteronyssinus</i> genome and transcriptome reveals a wide range of novel allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2268-2271.e8.	2.9	34
45	Fine-tuning carbapenem resistance by reducing porin permeability of bacteria activated in the selection process of conjugation. <i>Scientific Reports</i> , 2018, 8, 15248.	3.3	19
46	miRNA-Mediated Interactions in and between Plants and Insects. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3239.	4.1	23
47	Transcriptomic and methylomic analysis reveal the toxicological effect of 2,3,7,8-Tetrachlorodibenzodioxin on human embryonic stem cell. <i>Chemosphere</i> , 2018, 206, 663-673.	8.2	13
48	Coordinated regulation of core and accessory genes in the multipartite genome of <i>Sinorhizobium fredii</i> . <i>PLoS Genetics</i> , 2018, 14, e1007428.	3.5	50
49	OMBlast: alignment tool for optical mapping using a seed-and-extend approach. <i>Bioinformatics</i> , 2017, 33, 311-319.	4.1	39
50	Transcriptome sequencing reveals prenatal PFOS exposure on liver disorders. <i>Environmental Pollution</i> , 2017, 223, 416-425.	7.5	30
51	Using genetics to inform new therapeutics for diabetes. <i>Expert Review of Endocrinology and Metabolism</i> , 2017, 12, 159-169.	2.4	0
52	Transcriptomic and Functional Analyses on the Effects of Dioxin on Insulin Secretion of Pancreatic Islets and $\beta$ -Cells. <i>Environmental Science &amp; Technology</i> , 2017, 51, 11390-11400.	10.0	8
53	Effects of in Utero PFOS Exposure on Transcriptome, Lipidome, and Function of Mouse Testis. <i>Environmental Science &amp; Technology</i> , 2017, 51, 8782-8794.	10.0	51
54	An iterative algorithm for de novo optical map assembly. , 2017, , .		1

#	ARTICLE	IF	CITATIONS
55	Systematic Selection of Reference Genes for the Normalization of Circulating RNA Transcripts in Pregnant Women Based on RNA-Seq Data. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1709.	4.1	26
56	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. <i>Genome Biology</i> , 2017, 18, 230.	8.8	28
57	Comparison of Small RNA Profiles of <i>Glycine max</i> and <i>Glycine soja</i> at Early Developmental Stages. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2043.	4.1	7
58	Transcriptomic alterations in <i>Daphnia magna</i> embryos from mothers exposed to hypoxia. <i>Aquatic Toxicology</i> , 2016, 177, 454-463.	4.0	13
59	Interactome-transcriptome analysis discovers signatures complementary to GWAS Loci of Type 2 Diabetes. <i>Scientific Reports</i> , 2016, 6, 35228.	3.3	20
60	Pathogenesis of POLR1C-dependent Type 3 Treacher Collins Syndrome revealed by a zebrafish model. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 1147-1158.	3.8	38
61	Fatty liver disease induced by perfluorooctane sulfonate: Novel insight from transcriptome analysis. <i>Chemosphere</i> , 2016, 159, 166-177.	8.2	43
62	Transcriptomic responses of marine medaka's ovary to hypoxia. <i>Aquatic Toxicology</i> , 2016, 177, 476-483.	4.0	21
63	Hypoxia alters testicular functions of marine medaka through microRNAs regulation. <i>Aquatic Toxicology</i> , 2016, 180, 266-273.	4.0	34
64	Hypoxia causes transgenerational impairments in reproduction of fish. <i>Nature Communications</i> , 2016, 7, 12114.	12.8	134
65	Discovery and functional characterization of novel miRNAs in the marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2016, 175, 106-116.	4.0	13
66	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. <i>Genetics</i> , 2016, 202, 351-362.	2.9	126
67	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	14.5	113
68	Differential responses of female and male brains to hypoxia in the marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2016, 172, 36-43.	4.0	13
69	Hypoxia alters steroidogenesis in female marine medaka through miRNAs regulation. <i>Aquatic Toxicology</i> , 2016, 172, 1-8.	4.0	49
70	Transcriptomic analysis reveals specific osmoregulatory adaptive responses in gill mitochondria-rich cells and pavement cells of the Japanese eel. <i>BMC Genomics</i> , 2015, 16, 1072.	2.8	28
71	Small RNAs in Plant Responses to Abiotic Stresses: Regulatory Roles and Study Methods. <i>International Journal of Molecular Sciences</i> , 2015, 16, 24532-24554.	4.1	42
72	The draft genome, transcriptome, and microbiome of <i>Dermatophagoides farinae</i> reveal a broad spectrum of dust mite allergens. <i>Journal of Allergy and Clinical Immunology</i> , 2015, 135, 539-548.	2.9	172

#	ARTICLE	IF	CITATIONS
73	Transcriptomic responses of corpuscle of Stannius gland of Japanese eels ( <i>Anguilla japonica</i> ) to Changes in Water Salinity. <i>Scientific Reports</i> , 2015, 5, 9836.	3.3	21
74	A new <i>mib</i> allele with a chromosomal deletion covering <i>foxc1a</i> exhibits anterior somite specification defect. <i>Scientific Reports</i> , 2015, 5, 10673.	3.3	10
75	Hypoxia induces miR-210, leading to anti-apoptosis in ovarian follicular cells of marine medaka <i>Oryzias melastigma</i> . <i>Aquatic Toxicology</i> , 2015, 165, 189-196.	4.0	29
76	Hepatocellular carcinoma-derived exosomes promote motility of immortalized hepatocyte through transfer of oncogenic proteins and RNAs. <i>Carcinogenesis</i> , 2015, 36, 1008-1018.	2.8	213
77	Tissue-specific transcriptome assemblies of the marine medaka <i>Oryzias melastigma</i> and comparative analysis with the freshwater medaka <i>Oryzias latipes</i> . <i>BMC Genomics</i> , 2015, 16, 135.	2.8	47
78	Draft Genome Sequence of Extensively Drug-Resistant <i>Acinetobacter baumannii</i> Strain CUAB1 from a Patient in Hong Kong, China. <i>Genome Announcements</i> , 2015, 3, .	0.8	1
79	Using RNA-Seq Data to Evaluate Reference Genes Suitable for Gene Expression Studies in Soybean. <i>PLoS ONE</i> , 2015, 10, e0136343.	2.5	64
80	Identification and Expression Profiling of MicroRNAs in the Brain, Liver and Gonads of Marine Medaka ( <i>Oryzias melastigma</i> ) and in Response to Hypoxia. <i>PLoS ONE</i> , 2014, 9, e110698.	2.5	68
81	The Essential Component in DNA-Based Information Storage System: Robust Error-Tolerating Module. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 49.	4.1	18
82	Draft Genome Sequence of <i>Clostridium butyricum</i> Strain NOR 33234, Isolated from an Elderly Patient with Diarrhea. <i>Genome Announcements</i> , 2014, 2, .	0.8	9
83	A novel missense mutation in <i>CCDC88C</i> activates the JNK pathway and causes a dominant form of spinocerebellar ataxia. <i>Journal of Medical Genetics</i> , 2014, 51, 590-595.	3.2	64
84	Viral-Human Chimeric Transcript Predisposes Risk to Liver Cancer Development and Progression. <i>Cancer Cell</i> , 2014, 25, 335-349.	16.8	254
85	Transcriptome sequencing of Chinese and Caucasian population identifies ethnic-associated differential transcript abundance of heterogeneous nuclear ribonucleoprotein K (hnRNPK). <i>Genomics</i> , 2014, 103, 56-64.	2.9	20
86	Integrative Identification of Epstein-Barr Virus-Associated Mutations and Epigenetic Alterations in Gastric Cancer. <i>Gastroenterology</i> , 2014, 147, 1350-1362.e4.	1.3	90
87	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	12.8	332
88	Open Data: A Sustainable Model. <i>Science</i> , 2013, 342, 1042-1042.	12.6	1
89	The NGS WikiBook: a dynamic collaborative online training effort with long-term sustainability. <i>Briefings in Bioinformatics</i> , 2013, 14, 548-555.	6.5	8
90	ViralFusionSeq: accurately discover viral integration events and reconstruct fusion transcripts at single-base resolution. <i>Bioinformatics</i> , 2013, 29, 649-651.	4.1	85

#	ARTICLE	IF	CITATIONS
91	SEQanswers: an open access community for collaboratively decoding genomes. <i>Bioinformatics</i> , 2012, 28, 1272-1273.	4.1	54
92	The SEQanswers wiki: a wiki database of tools for high-throughput sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, D1313-D1317.	14.5	35
93	Detection of splicing events and multiread locations from RNA-seq data based on a geometric-tail (GT) distribution of intron length. <i>BMC Bioinformatics</i> , 2011, 12, S2.	2.6	0
94	Natural variation in four human collagen genes across an ethnically diverse population. <i>Genomics</i> , 2008, 91, 307-314.	2.9	47