

# Shu-Hwa Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6004112/publications.pdf>

Version: 2024-02-01

18  
papers

634  
citations

777949

13  
h-index

939365

18  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1390  
citing authors

#	ARTICLE	IF	CITATIONS
1	Piwi reduction in the aged niche eliminates germline stem cells via Toll-GSK3 signaling. <i>Nature Communications</i> , 2020, 11, 3147.	5.8	18
2	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.	3.9	18
3	SQUAT: a Sequencing Quality Assessment Tool for data quality assessments of genome assemblies. <i>BMC Genomics</i> , 2019, 19, 238.	1.2	29
4	Modeling spinocerebellar ataxias 2 and 3 with iPSCs reveals a role for glutamate in disease pathology. <i>Scientific Reports</i> , 2019, 9, 1166.	1.6	29
5	Revealing the compositions of the intestinal microbiota of three Anguillid eel species using 16S rDNA sequencing. <i>Aquaculture Research</i> , 2018, 49, 2404-2415.	0.9	12
6	A gene profiling deconvolution approach to estimating immune cell composition from complex tissues. <i>BMC Bioinformatics</i> , 2018, 19, 154.	1.2	14
7	TEA: the epigenome platform for <i>Arabidopsis</i> methylome study. <i>BMC Genomics</i> , 2016, 17, 1027.	1.2	3
8	Characterization of FN1-EGFR1 and novel FN1-EGF1 fusion genes in a large series of phosphaturic mesenchymal tumors. <i>Modern Pathology</i> , 2016, 29, 1335-1346.	2.9	139
9	Over-expression of <i>AURKA</i> , <i>SKA3</i> and <i>DSN1</i> contributes to colorectal adenoma to carcinoma progression. <i>Oncotarget</i> , 2016, 7, 45803-45818.	0.8	63
10	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.	1.1	23
11	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, 239-248.	1.0	10
12	The effect of red light and far-red light conditions on secondary metabolism in Agarwood. <i>BMC Plant Biology</i> , 2015, 15, 139.	1.6	33
13	A Comprehensive Functional Map of the Hepatitis C Virus Genome Provides a Resource for Probing Viral Proteins. <i>MBio</i> , 2014, 5, e01469-14.	1.8	16
14	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.	0.4	16
15	High-throughput profiling of influenza A virus hemagglutinin gene at single-nucleotide resolution. <i>Scientific Reports</i> , 2014, 4, 4942.	1.6	147
16	Membrane Labeling of Coral Gastrodermal Cells by Biotinylation: The Proteomic Identification of Surface Proteins Involving Cnidaria-Dinoflagellate Endosymbiosis. <i>PLoS ONE</i> , 2014, 9, e85119.	1.1	8
17	UPS 2.0: unique probe selector for probe design and oligonucleotide microarrays at the pangenomic/genomic level. <i>BMC Genomics</i> , 2010, 11, S6.	1.2	20
18	PALM: A Paralleled and Integrated Framework for Phylogenetic Inference with Automatic Likelihood Model Selectors. <i>PLoS ONE</i> , 2009, 4, e8116.	1.1	36