

# Shiheng Tao

## List of Publications by Year in descending order

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26  
papers

363  
citations

1040056

9  
h-index

888059

17  
g-index

26  
all docs

26  
docs citations

26  
times ranked

374  
citing authors

#	ARTICLE	IF	CITATIONS
1	A detailed comparative analysis of codon usage bias in Alongshan virus. <i>Virus Research</i> , 2022, 308, 198646.	2.2	11
2	RSVdb: a comprehensive database of transcriptome RNA structure. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	5
3	Altered Metabolic Strategies: Elaborate Mechanisms Adopted by <i>Oenococcus oeni</i> in Response to Acid Stress. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 2906-2918.	5.2	14
4	Analysis of codon usage patterns and influencing factors in rice tungro bacilliform virus. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104750.	2.3	11
5	Edging on Mutational Bias, Induced Natural Selection From Host and Natural Reservoirs Predominates Codon Usage Evolution in Hantaan Virus. <i>Frontiers in Microbiology</i> , 2021, 12, 699788.	3.5	10
6	Genome-wide characterization, evolution, structure, and expression analysis of the F-box genes in <i>Caenorhabditis</i> . <i>BMC Genomics</i> , 2021, 22, 889.	2.8	6
7	Exploring the evolutionary dynamics of <i>Rhizobium</i> plasmids through bipartite network analysis. <i>Environmental Microbiology</i> , 2020, 22, 934-951.	3.8	7
8	CRISPR-CBEI: a Designing and Analyzing Tool Kit for Cytosine Base Editor-Mediated Gene Inactivation. <i>MSystems</i> , 2020, 5, .	3.8	20
9	Codon Usage Bias Analysis of Bluetongue Virus Causing Livestock Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 655.	3.5	20
10	Deciphering the rules of mRNA structure differentiation in <i>Saccharomyces cerevisiae</i> in vivo and in vitro with deep neural networks. <i>RNA Biology</i> , 2019, 16, 1044-1054.	3.1	8
11	CellSim: a novel software to calculate cell similarity and identify their co-regulation networks. <i>BMC Bioinformatics</i> , 2019, 20, 111.	2.6	3
12	Evolutionary Analysis of the F-Box Gene Family in Saccharomycetaceae. <i>DNA and Cell Biology</i> , 2019, 38, 333-340.	1.9	1
13	Genomic insight into the taxonomy of <i>Rhizobium</i> genospecies that nodulate <i>Phaseolus vulgaris</i> . <i>Systematic and Applied Microbiology</i> , 2018, 41, 300-310.	2.8	44
14	Analysis of codon usage bias of Crimean-Congo hemorrhagic fever virus and its adaptation to hosts. <i>Infection, Genetics and Evolution</i> , 2018, 58, 1-16.	2.3	40
15	Rapid Identification of Major QTLs Associated With Near-Freezing Temperature Tolerance in <i>Saccharomyces cerevisiae</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2110.	3.5	16
16	A Novel Strategy for Detecting Recent Horizontal Gene Transfer and Its Application to <i>Rhizobium</i> Strains. <i>Frontiers in Microbiology</i> , 2018, 9, 973.	3.5	36
17	miRNA editing landscape reveals miR-34c regulated spermatogenesis through structure and target change in pig and mouse. <i>Biochemical and Biophysical Research Communications</i> , 2018, 502, 486-492.	2.1	9
18	Codon usage bias and evolutionary analyses of Zika virus genomes. <i>Genes and Genomics</i> , 2017, 39, 855-866.	1.4	17

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19	Codon usage bias in 5' terminal coding sequences reveals distinct enrichment of gene functions. <i>Genomics</i> , 2017, 109, 506-513.	2.9	11
20	Influences of Dominance and Evolution of Sex in Finite Diploid Populations. <i>PLoS ONE</i> , 2015, 10, e0128459.	2.5	0
21	Physiologically Shrinking the Solution Space of a <i>Saccharomyces cerevisiae</i> Genome-Scale Model Suggests the Role of the Metabolic Network in Shaping Gene Expression Noise. <i>PLoS ONE</i> , 2015, 10, e0139590.	2.5	1
22	Codon Usage in Signal Sequences Affects Protein Expression and Secretion Using Baculovirus/Insect Cell Expression System. <i>PLoS ONE</i> , 2015, 10, e0145887.	2.5	10
23	Genome-Wide Identification and Evolution of HECT Genes in Soybean. <i>International Journal of Molecular Sciences</i> , 2015, 16, 8517-8535.	4.1	15
24	Training Set Selection for the Prediction of Essential Genes. <i>PLoS ONE</i> , 2014, 9, e86805.	2.5	38
25	Evolution of the F-Box Gene Family in Euarchontoglires: Gene Number Variation and Selection Patterns. <i>PLoS ONE</i> , 2014, 9, e94899.	2.5	6
26	Neighbor Preferences of Amino Acids and Context-Dependent Effects of Amino Acid Substitutions in Human, Mouse, and Dog. <i>International Journal of Molecular Sciences</i> , 2014, 15, 15963-15980.	4.1	4