

# Jian-Rong Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

30  
papers

2,706  
citations

430874

18  
h-index

501196

28  
g-index

35  
all docs

35  
docs citations

35  
times ranked

3884  
citing authors

#	ARTICLE	IF	CITATIONS
1	MicroRNA-101, Down-regulated in Hepatocellular Carcinoma, Promotes Apoptosis and Suppresses Tumorigenicity. <i>Cancer Research</i> , 2009, 69, 1135-1142.	0.9	586
2	A functional polymorphism in the miR-146a gene is associated with the risk for hepatocellular carcinoma. <i>Carcinogenesis</i> , 2008, 29, 2126-2131.	2.8	326
3	Determinants of the rate of protein sequence evolution. <i>Nature Reviews Genetics</i> , 2015, 16, 409-420.	16.3	294
4	Balanced Codon Usage Optimizes Eukaryotic Translational Efficiency. <i>PLoS Genetics</i> , 2012, 8, e1002603.	3.5	263
5	MicroRNA-26a/b and their host genes cooperate to inhibit the G1/S transition by activating the pRb protein. <i>Nucleic Acids Research</i> , 2012, 40, 4615-4625.	14.5	195
6	Pseudogenization of the Umami Taste Receptor Gene <i>Tas1r1</i> in the Giant Panda Coincided with its Dietary Switch to Bamboo. <i>Molecular Biology and Evolution</i> , 2010, 27, 2669-2673.	8.9	186
7	Protein misinteraction avoidance causes highly expressed proteins to evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E831-40.	7.1	160
8	Impact of translational error-induced and error-free misfolding on the rate of protein evolution. <i>Molecular Systems Biology</i> , 2010, 6, 421.	7.2	116
9	Differential requirements for mRNA folding partially explain why highly expressed proteins evolve slowly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E678-86.	7.1	110
10	Codon-by-Codon Modulation of Translational Speed and Accuracy Via mRNA Folding. <i>PLoS Biology</i> , 2014, 12, e1001910.	5.6	101
11	Dissimilation of synonymous codon usage bias in virus-host coevolution due to translational selection. <i>Nature Ecology and Evolution</i> , 2020, 4, 589-600.	7.8	79
12	Deciphering the Genic Basis of Yeast Fitness Variation by Simultaneous Forward and Reverse Genetics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2486-2502.	8.9	42
13	Human Long Noncoding RNAs Are Substantially Less Folded than Messenger RNAs. <i>Molecular Biology and Evolution</i> , 2015, 32, 970-977.	8.9	32
14	Intra and Interspecific Variations of Gene Expression Levels in Yeast Are Largely Neutral: (Nei Lecture,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	8.9	28
15	In vitro and in vivo growth inhibition of human cervical cancer cells via human papillomavirus E6/E7 mRNAs' cleavage by CRISPR/Cas13a system. <i>Antiviral Research</i> , 2020, 178, 104794.	4.1	27
16	Expression level is a major modifier of the fitness landscape of a protein coding gene. <i>Nature Ecology and Evolution</i> , 2022, 6, 103-115.	7.8	24
17	MtiBase: a database for decoding microRNA target sites located within CDS and 5'UTR regions from CLIP-Seq and expression profile datasets. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav102.	3.0	23
18	Alignment of Cell Lineage Trees Elucidates Genetic Programs for the Development and Evolution of Cell Types. <i>IScience</i> , 2020, 23, 101273.	4.1	23

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19	Nascent RNA folding mitigates transcription-associated mutagenesis. <i>Genome Research</i> , 2016, 26, 50-59.	5.5	21
20	Risk stratification of cervical lesions using capture sequencing and machine learning method based on HPV and human integrated genomic profiles. <i>Carcinogenesis</i> , 2019, 40, 1220-1228.	2.8	19
21	Determinative Developmental Cell Lineages Are Robust to Cell Deaths. <i>PLoS Genetics</i> , 2014, 10, e1004501.	3.5	9
22	Distinct codon usage bias evolutionary patterns between weakly and strongly virulent respiratory viruses. <i>IScience</i> , 2022, 25, 103682.	4.1	9
23	Does mRNA structure contain genetic information for regulating co-translational protein folding?. <i>Zoological Research</i> , 2017, 38, 36-43.	2.1	8
24	Dosage sensitivity of X-linked genes in human embryonic single cells. <i>BMC Genomics</i> , 2019, 20, 42.	2.8	7
25	The evolution of sex chromosome dosage compensation in animals. <i>Journal of Genetics and Genomics</i> , 2020, 47, 681-693.	3.9	7
26	Bidirectional Genetic Control of Phenotypic Heterogeneity and Its Implication for Cancer Drug Resistance. <i>Molecular Biology and Evolution</i> , 2021, 38, 1874-1887.	8.9	5
27	Prediction of Antibiotic Resistance Evolution by Growth Measurement of All Proximal Mutants of Beta-Lactamase. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	3
28	Identification of medium-sized genomic deletions with low coverage, mate-paired restricted tags. <i>BMC Genomics</i> , 2013, 14, 51.	2.8	1
29	The expression tractability of biological traits shaped by natural selection. <i>Journal of Genetics and Genomics</i> , 2019, 46, 397-404.	3.9	0
30	Specificity of mRNA Folding and Its Association with Evolutionarily Adaptive mRNA Secondary Structures. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 882-900.	6.9	0