

# Yun-Xin Fu

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

7,279  
citations

516710

16  
h-index

434195

31  
g-index

34  
all docs

34  
docs citations

34  
times ranked

9525  
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical Tests of Neutrality of Mutations Against Population Growth, Hitchhiking and Background Selection. <i>Genetics</i> , 1997, 147, 915-925.	2.9	5,823
2	Exploring population size changes using SNP frequency spectra. <i>Nature Genetics</i> , 2015, 47, 555-559.	21.4	332
3	Statistical Tests for Detecting Positive Selection by Utilizing High-Frequency Variants. <i>Genetics</i> , 2006, 174, 1431-1439.	2.9	294
4	New Statistical Tests of Neutrality for DNA Samples From a Population. <i>Genetics</i> , 1996, 143, 557-570.	2.9	261
5	Stairway Plot 2: demographic history inference with folded SNP frequency spectra. <i>Genome Biology</i> , 2020, 21, 280.	8.8	125
6	Exact coalescent for the Wright-Fisher model. <i>Theoretical Population Biology</i> , 2006, 69, 385-394.	1.1	52
7	Estimating the Age of the Common Ancestor of a DNA Sample Using the Number of Segregating Sites. <i>Genetics</i> , 1996, 144, 829-838.	2.9	41
8	Simultaneous Estimation of All the Parameters of a Stepwise Mutation Model. <i>Genetics</i> , 1998, 150, 487-497.	2.9	36
9	<i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901.	10.3	33
10	eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. <i>National Science Review</i> , 2019, 6, 867-869.	9.5	29
11	On the three methods for estimating deleterious genomic mutation parameters. <i>Genetical Research</i> , 1998, 71, 223-236.	0.9	25
12	Ranking analysis of microarray data: A powerful method for identifying differentially expressed genes. <i>Genomics</i> , 2006, 88, 846-854.	2.9	25
13	Highly variable recessive lethal or nearly lethal mutation rates during germ-line development of male <i>Drosophila melanogaster</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15914-15919.	7.1	22
14	Conditions for Positive and Negative Correlations Between Fitness and Heterozygosity in Equilibrium Populations. <i>Genetics</i> , 1998, 148, 1333-1340.	2.9	22
15	Association of common variants in TOMM40/APOE/APOC1 region with human longevity in a Chinese population. <i>Journal of Human Genetics</i> , 2016, 61, 323-328.	2.3	20
16	Estimating Mutation Rate: How to Count Mutations?. <i>Genetics</i> , 2003, 164, 797-805.	2.9	17
17	Common variants in SIRT1 and human longevity in a Chinese population. <i>BMC Medical Genetics</i> , 2016, 17, 31.	2.1	16
18	A High Polymorphism Level in <i>Rhinopithecus roxellana</i> . <i>International Journal of Primatology</i> , 2009, 30, 337-351.	1.9	15

#	ARTICLE	IF	CITATIONS
19	Pattern of Mutation Rates in the Germline of <i>Drosophila melanogaster</i> Males from a Large-Scale Mutation Screening Experiment. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1503-1514.	1.8	15
20	Insight Derived from Molecular Dynamics Simulations into Molecular Motions, Thermodynamics and Kinetics of HIV-1 gp120. <i>PLoS ONE</i> , 2014, 9, e104714.	2.5	12
21	Molecular dynamics simulations reveal distinct differences in conformational dynamics and thermodynamics between the unliganded and CD4-bound states of HIV-1 gp120. <i>Physical Chemistry Chemical Physics</i> , 2020, 22, 5548-5560.	2.8	12
22	Inferring the major genomic mode of dominance and overdominance. <i>Genetica</i> , 1998, 102/103, 559-567.	1.1	8
23	Drivers of Mating Type Composition in <i>Tetrahymena thermophila</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2328-2343.	2.5	8
24	Lack of association between polymorphisms in the SIRT6 gene and longevity in a Chinese population. <i>Molecular and Cellular Probes</i> , 2016, 30, 79-82.	2.1	5
25	Identification and Characterization of Base-Substitution Mutations in the Macronuclear Genome of the Ciliate <i>Tetrahymena thermophila</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	5
26	Genetic Association Analysis of Common Variants in FOXO3 Related to Longevity in a Chinese Population. <i>PLoS ONE</i> , 2016, 11, e0167918.	2.5	5
27	A Deep Learning Approach for Predicting Antigenic Variation of Influenza A H3N2. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-10.	1.3	5
28	Variances and covariances of linear summary statistics of segregating sites. <i>Theoretical Population Biology</i> , 2022, 145, 95-108.	1.1	5
29	Statistical Methods for Analyzing <i>Drosophila</i> Germline Mutation Rates. <i>Genetics</i> , 2013, 194, 927-936.	2.9	3
30	An Efficient Estimator of the Mutation Parameter and Analysis of Polymorphism from the 1000 Genomes Project. <i>Genes</i> , 2014, 5, 561-575.	2.4	2
31	Efficient Estimation of Mutation Rates during Individual Development by Minimization of Chi-Square. <i>PLoS ONE</i> , 2015, 10, e0135398.	2.5	0
32	Amitosis as a strategy of cell division—Insight from the proliferation of <i>Tetrahymena thermophila</i> macronuclei. <i>Theoretical Population Biology</i> , 2022, 145, 52-62.	1.1	0