

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 | Variances and covariances of linear summary statistics of segregating sites. <i>Theoretical Population Biology</i> , 2022, 145, 95-108. | 1.1 | 5 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | Stairway Plot 2: demographic history inference with folded SNP frequency spectra. <i>Genome Biology</i> , 2020, 21, 280. | 8.8 | 125 |
| 6 | <i>Mycobacterium tuberculosis</i> clinical isolates carry mutational signatures of host immune environments. <i>Science Advances</i> , 2020, 6, eaba4901. | 10.3 | 33 |
| 7 | 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 |
| 8 | Drivers of Mating Type Composition in <i>Tetrahymena thermophila</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 2328-2343. | 2.5 | 8 |
| 9 | eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. <i>National Science Review</i> , 2019, 6, 867-869. | 9.5 | 29 |
| 10 | Common variants in SIRT1 and human longevity in a Chinese population. <i>BMC Medical Genetics</i> , 2016, 17, 31. | 2.1 | 16 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Efficient Estimation of Mutation Rates during Individual Development by Minimization of Chi-Square. <i>PLoS ONE</i> , 2015, 10, e0135398. | 2.5 | 0 |
| 15 | Exploring population size changes using SNP frequency spectra. <i>Nature Genetics</i> , 2015, 47, 555-559. | 21.4 | 332 |
| 16 | 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 |
| 17 | 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 |
| 18 | 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 |

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|----|---|-----|-----------|
| 19 | Statistical Methods for Analyzing <i>Drosophila</i> Germline Mutation Rates. <i>Genetics</i> , 2013, 194, 927-936. | 2.9 | 3 |
| 20 | 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 |
| 21 | A High Polymorphism Level in <i>Rhinopithecus roxellana</i> . <i>International Journal of Primatology</i> , 2009, 30, 337-351. | 1.9 | 15 |
| 22 | Statistical Tests for Detecting Positive Selection by Utilizing High-Frequency Variants. <i>Genetics</i> , 2006, 174, 1431-1439. | 2.9 | 294 |
| 23 | Exact coalescent for the Wright-Fisher model. <i>Theoretical Population Biology</i> , 2006, 69, 385-394. | 1.1 | 52 |
| 24 | Ranking analysis of microarray data: A powerful method for identifying differentially expressed genes. <i>Genomics</i> , 2006, 88, 846-854. | 2.9 | 25 |
| 25 | Estimating Mutation Rate: How to Count Mutations?. <i>Genetics</i> , 2003, 164, 797-805. | 2.9 | 17 |
| 26 | Inferring the major genomic mode of dominance and overdominance. <i>Genetica</i> , 1998, 102/103, 559-567. | 1.1 | 8 |
| 27 | On the three methods for estimating deleterious genomic mutation parameters. <i>Genetical Research</i> , 1998, 71, 223-236. | 0.9 | 25 |
| 28 | Conditions for Positive and Negative Correlations Between Fitness and Heterozygosity in Equilibrium Populations. <i>Genetics</i> , 1998, 148, 1333-1340. | 2.9 | 22 |
| 29 | Simultaneous Estimation of All the Parameters of a Stepwise Mutation Model. <i>Genetics</i> , 1998, 150, 487-497. | 2.9 | 36 |
| 30 | Statistical Tests of Neutrality of Mutations Against Population Growth, Hitchhiking and Background Selection. <i>Genetics</i> , 1997, 147, 915-925. | 2.9 | 5,823 |
| 31 | New Statistical Tests of Neutrality for DNA Samples From a Population. <i>Genetics</i> , 1996, 143, 557-570. | 2.9 | 261 |
| 32 | 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 |