

Jianzhi Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

131
papers

10,656
citations

53660

45
h-index

39575

94
g-index

137
all docs

137
docs citations

137
times ranked

12716
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Evaluation of an Improved Branch-Site Likelihood Method for Detecting Positive Selection at the Molecular Level. <i>Molecular Biology and Evolution</i> , 2005, 22, 2472-2479. | 3.5 | 1,650 |
| 2 | Why Do Hubs Tend to Be Essential in Protein Networks?. <i>PLoS Genetics</i> , 2006, 2, e88. | 1.5 | 634 |
| 3 | The pleiotropic structure of the genotype-phenotype map: the evolvability of complex organisms. <i>Nature Reviews Genetics</i> , 2011, 12, 204-213. | 7.7 | 577 |
| 4 | Determinants of the rate of protein sequence evolution. <i>Nature Reviews Genetics</i> , 2015, 16, 409-420. | 7.7 | 294 |
| 5 | Rates of Conservative and Radical Nonsynonymous Nucleotide Substitutions in Mammalian Nuclear Genes. <i>Journal of Molecular Evolution</i> , 2000, 50, 56-68. | 0.8 | 274 |
| 6 | Balanced Codon Usage Optimizes Eukaryotic Translational Efficiency. <i>PLoS Genetics</i> , 2012, 8, e1002603. | 1.5 | 263 |
| 7 | Accuracies of ancestral amino acid sequences inferred by the parsimony, likelihood, and distance methods. <i>Journal of Molecular Evolution</i> , 1997, 44, S139-S146. | 0.8 | 256 |
| 8 | Evolutionary deterioration of the vomeronasal pheromone transduction pathway in catarrhine primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8337-8341. | 3.3 | 240 |
| 9 | Genomic patterns of pleiotropy and the evolution of complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 18034-18039. | 3.3 | 218 |
| 10 | Null mutations in human and mouse orthologs frequently result in different phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 6987-6992. | 3.3 | 217 |
| 11 | Accelerated Protein Evolution and Origins of Human-Specific Features: FOXP2 as an Example. <i>Genetics</i> , 2002, 162, 1825-1835. | 1.2 | 217 |
| 12 | Parallel adaptive origins of digestive RNases in Asian and African leaf monkeys. <i>Nature Genetics</i> , 2006, 38, 819-823. | 9.4 | 189 |
| 13 | Evolution of the Human <i>ASPM</i> Gene, a Major Determinant of Brain Size. <i>Genetics</i> , 2003, 165, 2063-2070. | 1.2 | 184 |
| 14 | Toward a Molecular Understanding of Pleiotropy. <i>Genetics</i> , 2006, 173, 1885-1891. | 1.2 | 182 |
| 15 | The hearing gene Prestin unites echolocating bats and whales. <i>Current Biology</i> , 2010, 20, R55-R56. | 1.8 | 178 |
| 16 | Impact of gene expression noise on organismal fitness and the efficacy of natural selection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, E67-76. | 3.3 | 177 |
| 17 | The Genomic Landscape and Evolutionary Resolution of Antagonistic Pleiotropy in Yeast. <i>Cell Reports</i> , 2012, 2, 1399-1410. | 2.9 | 177 |
| 18 | Rapid evolution of primate antiviral enzyme APOBEC3G. <i>Human Molecular Genetics</i> , 2004, 13, 1785-1791. | 1.4 | 170 |

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|----|--|------|-----------|
| 19 | The fitness landscape of a tRNA gene. <i>Science</i> , 2016, 352, 837-840. | 6.0 | 168 |
| 20 | 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. | 3.3 | 160 |
| 21 | Synonymous mutations in representative yeast genes are mostly strongly non-neutral. <i>Nature</i> , 2022, 606, 725-731. | 13.7 | 157 |
| 22 | Frequent False Detection of Positive Selection by the Likelihood Method with Branch-Site Models. <i>Molecular Biology and Evolution</i> , 2004, 21, 1332-1339. | 3.5 | 155 |
| 23 | Prevalent positive epistasis in <i>Escherichia coli</i> and <i>Saccharomyces cerevisiae</i> metabolic networks. <i>Nature Genetics</i> , 2010, 42, 272-276. | 9.4 | 134 |
| 24 | Human coding RNA editing is generally nonadaptive. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 3769-3774. | 3.3 | 128 |
| 25 | Are Convergent and Parallel Amino Acid Substitutions in Protein Evolution More Prevalent Than Neutral Expectations?. <i>Molecular Biology and Evolution</i> , 2015, 32, 2085-2096. | 3.5 | 124 |
| 26 | Significant Impact of Protein Dispensability on the Instantaneous Rate of Protein Evolution. <i>Molecular Biology and Evolution</i> , 2005, 22, 1147-1155. | 3.5 | 114 |
| 27 | Positive selection for elevated gene expression noise in yeast. <i>Molecular Systems Biology</i> , 2009, 5, 299. | 3.2 | 112 |
| 28 | Genomic evidence for adaptation by gene duplication. <i>Genome Research</i> , 2014, 24, 1356-1362. | 2.4 | 107 |
| 29 | Phylostratigraphic Bias Creates Spurious Patterns of Genome Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 258-267. | 3.5 | 107 |
| 30 | Codon-by-Codon Modulation of Translational Speed and Accuracy Via mRNA Folding. <i>PLoS Biology</i> , 2014, 12, e1001910. | 2.6 | 101 |
| 31 | Evolutionary adaptations to new environments generally reverse plastic phenotypic changes. <i>Nature Communications</i> , 2018, 9, 350. | 5.8 | 96 |
| 32 | No Genome-Wide Protein Sequence Convergence for Echolocation. <i>Molecular Biology and Evolution</i> , 2015, 32, 1237-1241. | 3.5 | 94 |
| 33 | Human RNase 7: a new cationic ribonuclease of the RNase A superfamily. <i>Nucleic Acids Research</i> , 2003, 31, 602-607. | 6.5 | 83 |
| 34 | Evaluating Phylostratigraphic Evidence for Widespread De Novo Gene Birth in Genome Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1245-1256. | 3.5 | 83 |
| 35 | Yeast Spontaneous Mutation Rate and Spectrum Vary with Environment. <i>Current Biology</i> , 2019, 29, 1584-1591.e3. | 1.8 | 82 |
| 36 | Dissimilation of synonymous codon usage bias in virus-host coevolution due to translational selection. <i>Nature Ecology and Evolution</i> , 2020, 4, 589-600. | 3.4 | 79 |

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|----|---|-----|-----------|
| 37 | The Genomic Landscape of Position Effects on Protein Expression Level and Noise in Yeast. <i>Cell Systems</i> , 2016, 2, 347-354. | 2.9 | 78 |
| 38 | Abundant Indispensable Redundancies in Cellular Metabolic Networks. <i>Genome Biology and Evolution</i> , 2009, 1, 23-33. | 1.1 | 72 |
| 39 | Why Is the Correlation between Gene Importance and Gene Evolutionary Rate So Weak?. <i>PLoS Genetics</i> , 2009, 5, e1000329. | 1.5 | 64 |
| 40 | Multi-environment fitness landscapes of a tRNA gene. <i>Nature Ecology and Evolution</i> , 2018, 2, 1025-1032. | 3.4 | 62 |
| 41 | Stop-codon read-through arises largely from molecular errors and is generally nonadaptive. <i>PLoS Genetics</i> , 2019, 15, e1008141. | 1.5 | 59 |
| 42 | Human C-to-U Coding RNA Editing Is Largely Nonadaptive. <i>Molecular Biology and Evolution</i> , 2018, 35, 963-969. | 3.5 | 56 |
| 43 | Morphological and molecular convergences in mammalian phylogenetics. <i>Nature Communications</i> , 2016, 7, 12758. | 5.8 | 55 |
| 44 | Testing the Chromosomal Speciation Hypothesis for Humans and Chimpanzees. <i>Genome Research</i> , 2004, 14, 845-851. | 2.4 | 52 |
| 45 | Is Phylotranscriptomics as Reliable as Phylogenomics?. <i>Molecular Biology and Evolution</i> , 2020, 37, 3672-3683. | 3.5 | 52 |
| 46 | Genetic Redundancies and Their Evolutionary Maintenance. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 279-300. | 0.8 | 51 |
| 47 | Molecular evidence for the loss of three basic tastes in penguins. <i>Current Biology</i> , 2015, 25, R141-R142. | 1.8 | 51 |
| 48 | Measuring the evolutionary rate of protein-protein interaction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 8725-8730. | 3.3 | 50 |
| 49 | Are Human Translated Pseudogenes Functional?. <i>Molecular Biology and Evolution</i> , 2016, 33, 755-760. | 3.5 | 48 |
| 50 | Idiosyncratic epistasis creates universals in mutational effects and evolutionary trajectories. <i>Nature Ecology and Evolution</i> , 2020, 4, 1685-1693. | 3.4 | 48 |
| 51 | Mammalian circular RNAs result largely from splicing errors. <i>Cell Reports</i> , 2021, 36, 109439. | 2.9 | 48 |
| 52 | Parallel Functional Changes in the Digestive RNases of Ruminants and Colobines by Divergent Amino Acid Substitutions. <i>Molecular Biology and Evolution</i> , 2003, 20, 1310-1317. | 3.5 | 47 |
| 53 | Further Simulations and Analyses Demonstrate Open Problems of Phylostratigraphy. <i>Genome Biology and Evolution</i> , 2017, 9, 1519-1527. | 1.1 | 47 |
| 54 | No X-Chromosome Dosage Compensation in Human Proteomes. <i>Molecular Biology and Evolution</i> , 2015, 32, 1456-1460. | 3.5 | 46 |

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|----|---|-----|-----------|
| 55 | Evidence that alternative transcriptional initiation is largely nonadaptive. <i>PLoS Biology</i> , 2019, 17, e3000197. | 2.6 | 46 |
| 56 | Antagonistic pleiotropy conceals molecular adaptations in changing environments. <i>Nature Ecology and Evolution</i> , 2020, 4, 461-469. | 3.4 | 46 |
| 57 | He et al. reply. <i>Nature Genetics</i> , 2011, 43, 1171-1172. | 9.4 | 45 |
| 58 | Correlation Between the Substitution Rate and Rate Variation Among Sites in Protein Evolution. <i>Genetics</i> , 1998, 149, 1615-1625. | 1.2 | 44 |
| 59 | Most m6A RNA Modifications in Protein-Coding Regions Are Evolutionarily Unconserved and Likely Nonfunctional. <i>Molecular Biology and Evolution</i> , 2018, 35, 666-675. | 3.5 | 43 |
| 60 | Deciphering the Genic Basis of Yeast Fitness Variation by Simultaneous Forward and Reverse Genetics. <i>Molecular Biology and Evolution</i> , 2017, 34, 2486-2502. | 3.5 | 42 |
| 61 | Evolution of DMY, a Newly Emergent Male Sex-Determination Gene of Medaka Fish. <i>Genetics</i> , 2004, 166, 1887-1895. | 1.2 | 41 |
| 62 | Coexpression of Linked Genes in Mammalian Genomes Is Generally Disadvantageous. <i>Molecular Biology and Evolution</i> , 2008, 25, 1555-1565. | 3.5 | 40 |
| 63 | Testing the neutral hypothesis of phenotypic evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12219-12224. | 3.3 | 38 |
| 64 | Neutral Theory and Phenotypic Evolution. <i>Molecular Biology and Evolution</i> , 2018, 35, 1327-1331. | 3.5 | 38 |
| 65 | Alternative Polyadenylation of Mammalian Transcripts Is Generally Deleterious, Not Adaptive. <i>Cell Systems</i> , 2018, 6, 734-742.e4. | 2.9 | 38 |
| 66 | The preponderance of nonsynonymous A-to-I RNA editing in coleoids is nonadaptive. <i>Nature Communications</i> , 2019, 10, 5411. | 5.8 | 38 |
| 67 | The Genotype-Phenotype Map of Yeast Complex Traits: Basic Parameters and the Role of Natural Selection. <i>Molecular Biology and Evolution</i> , 2014, 31, 1568-1580. | 3.5 | 36 |
| 68 | Patterns and Mechanisms of Diminishing Returns from Beneficial Mutations. <i>Molecular Biology and Evolution</i> , 2019, 36, 1008-1021. | 3.5 | 36 |
| 69 | Disulfide-Bond Reshuffling in the Evolution of an Ape Placental Ribonuclease. <i>Molecular Biology and Evolution</i> , 2007, 24, 505-512. | 3.5 | 33 |
| 70 | Human Long Noncoding RNAs Are Substantially Less Folded than Messenger RNAs. <i>Molecular Biology and Evolution</i> , 2015, 32, 970-977. | 3.5 | 32 |
| 71 | Adaptive Genetic Robustness of <i>Escherichia coli</i> Metabolic Fluxes. <i>Molecular Biology and Evolution</i> , 2016, 33, 1164-1176. | 3.5 | 32 |
| 72 | Genetic Gene Expression Changes during Environmental Adaptations Tend to Reverse Plastic Changes Even after the Correction for Statistical Nonindependence. <i>Molecular Biology and Evolution</i> , 2019, 36, 604-612. | 3.5 | 32 |

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|----|---|-----|-----------|
| 73 | Deep Residual Neural Networks Resolve Quartet Molecular Phylogenies. <i>Molecular Biology and Evolution</i> , 2020, 37, 1495-1507. | 3.5 | 32 |
| 74 | The optimal mating distance resulting from heterosis and genetic incompatibility. <i>Science Advances</i> , 2018, 4, eaau5518. | 4.7 | 30 |
| 75 | Intra and Interspecific Variations of Gene Expression Levels in Yeast Are Largely Neutral: (Nei Lecture,) <i>Tj ETQq1 1 0,784314 rgBT /Ove</i> | 3.5 | 28 |
| 76 | Genome-Wide Evolutionary Conservation of N-Glycosylation Sites. <i>Molecular Biology and Evolution</i> , 2011, 28, 2351-2357. | 3.5 | 27 |
| 77 | In Search of Beneficial Coding RNA Editing. <i>Molecular Biology and Evolution</i> , 2015, 32, 536-541. | 3.5 | 26 |
| 78 | EVOLUTION:Molecular Origin of Species. , 1998, 282, 1428-1429. | | 25 |
| 79 | Why Are Genes Encoded on the Lagging Strand of the Bacterial Genome?. <i>Genome Biology and Evolution</i> , 2013, 5, 2436-2439. | 1.1 | 25 |
| 80 | Evolution of the Yeast Recombination Landscape. <i>Molecular Biology and Evolution</i> , 2019, 36, 412-422. | 3.5 | 24 |
| 81 | Phenotypic plasticity as a long-term memory easing readaptations to ancestral environments. <i>Science Advances</i> , 2020, 6, eaba3388. | 4.7 | 24 |
| 82 | On the Evolution of Codon Volatility. <i>Genetics</i> , 2005, 169, 495-501. | 1.2 | 23 |
| 83 | Yeast mutation accumulation experiment supports elevated mutation rates at highly transcribed sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4062. | 3.3 | 23 |
| 84 | Why Human Disease-Associated Residues Appear as the Wild-Type in Other Species: Genome-Scale Structural Evidence for the Compensation Hypothesis. <i>Molecular Biology and Evolution</i> , 2014, 31, 1787-1792. | 3.5 | 23 |
| 85 | A Simple Method for Estimating the Strength of Natural Selection on Overlapping Genes. <i>Genome Biology and Evolution</i> , 2015, 7, 381-390. | 1.1 | 23 |
| 86 | Allele-specific single-cell RNA sequencing reveals different architectures of intrinsic and extrinsic gene expression noises. <i>Nucleic Acids Research</i> , 2020, 48, 533-547. | 6.5 | 23 |
| 87 | Population Genomic Analysis Reveals Contrasting Demographic Changes of Two Closely Related Dolphin Species in the Last Glacial. <i>Molecular Biology and Evolution</i> , 2018, 35, 2026-2033. | 3.5 | 22 |
| 88 | Nascent RNA folding mitigates transcription-associated mutagenesis. <i>Genome Research</i> , 2016, 26, 50-59. | 2.4 | 21 |
| 89 | Toward Reducing Phylostratigraphic Errors and Biases. <i>Genome Biology and Evolution</i> , 2018, 10, 2037-2048. | 1.1 | 20 |
| 90 | Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. <i>PLoS Genetics</i> , 2019, 15, e1008389. | 1.5 | 20 |

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|-----|--|-----|-----------|
| 91 | Environment-dependent pleiotropic effects of mutations on the maximum growth rate r and carrying capacity K of population growth. <i>PLoS Biology</i> , 2019, 17, e3000121. | 2.6 | 20 |
| 92 | Universal pleiotropy is not a valid null hypothesis: reply to Hill and Zhang. <i>Nature Reviews Genetics</i> , 2012, 13, 296-296. | 7.7 | 19 |
| 93 | The Genomic Architecture of Interactions Between Natural Genetic Polymorphisms and Environments in Yeast Growth. <i>Genetics</i> , 2017, 205, 925-937. | 1.2 | 19 |
| 94 | Synchronization of stochastic expressions drives the clustering of functionally related genes. <i>Science Advances</i> , 2019, 5, eaax6525. | 4.7 | 18 |
| 95 | The rate and molecular spectrum of mutation are selectively maintained in yeast. <i>Nature Communications</i> , 2021, 12, 4044. | 5.8 | 18 |
| 96 | Why Phenotype Robustness Promotes Phenotype Evolvability. <i>Genome Biology and Evolution</i> , 2017, 9, 3509-3515. | 1.1 | 15 |
| 97 | The X to Autosome Expression Ratio in Haploid and Diploid Human Embryonic Stem Cells. <i>Molecular Biology and Evolution</i> , 2016, 33, 3104-3107. | 3.5 | 14 |
| 98 | A different perspective on alternative cleavage and polyadenylation. <i>Nature Reviews Genetics</i> , 2020, 21, 63-63. | 7.7 | 14 |
| 99 | Pseudogenization of the tumor-growth promoter angiogenin in a leaf-eating monkey. <i>Gene</i> , 2003, 308, 95-101. | 1.0 | 13 |
| 100 | Amino acid exchangeabilities vary across the tree of life. <i>Science Advances</i> , 2019, 5, eaax3124. | 4.7 | 13 |
| 101 | Mammalian Alternative Translation Initiation Is Mostly Nonadaptive. <i>Molecular Biology and Evolution</i> , 2020, 37, 2015-2028. | 3.5 | 13 |
| 102 | Fly wing evolution explained by a neutral model with mutational pleiotropy. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 2158-2167. | 1.1 | 12 |
| 103 | Are Nonsynonymous Transversions Generally More Deleterious than Nonsynonymous Transitions?. <i>Molecular Biology and Evolution</i> , 2021, 38, 181-191. | 3.5 | 12 |
| 104 | Evolution of DMY, a Newly Emergent Male Sex-Determination Gene of Medaka Fish. <i>Genetics</i> , 2004, 166, 1887-1895. | 1.2 | 11 |
| 105 | Gene Tree Discordance Does Not Explain Away the Temporal Decline of Convergence in Mammalian Protein Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2017, 34, 1682-1688. | 3.5 | 10 |
| 106 | Retesting the influences of mutation accumulation and antagonistic pleiotropy on human senescence and disease. <i>Nature Ecology and Evolution</i> , 2019, 3, 992-993. | 3.4 | 10 |
| 107 | Higher Germline Mutagenesis of Genes with Stronger Testis Expressions Refutes the Transcriptional Scanning Hypothesis. <i>Molecular Biology and Evolution</i> , 2020, 37, 3225-3231. | 3.5 | 10 |
| 108 | Determinative Developmental Cell Lineages Are Robust to Cell Deaths. <i>PLoS Genetics</i> , 2014, 10, e1004501. | 1.5 | 9 |

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|-----|---|-----|-----------|
| 109 | Gene product diversity: adaptive or not?. Trends in Genetics, 2022, 38, 1112-1122. | 2.9 | 9 |
| 110 | Rampant False Detection of Adaptive Phenotypic Optimization by ParTI-Based Pareto Front Inference. Molecular Biology and Evolution, 2021, 38, 1653-1664. | 3.5 | 8 |
| 111 | Paleomolecular biology unravels the evolutionary mystery of vertebrate UV vision: Fig. 1.. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8045-8047. | 3.3 | 7 |
| 112 | Epistasis Analysis Goes Genome-Wide. PLoS Genetics, 2017, 13, e1006558. | 1.5 | 7 |
| 113 | Asexual Experimental Evolution of Yeast Does Not Curtail Transposable Elements. Molecular Biology and Evolution, 2021, 38, 2831-2842. | 3.5 | 7 |
| 114 | On the Origin of Frameshift-Robustness of the Standard Genetic Code. Molecular Biology and Evolution, 2021, 38, 4301-4309. | 3.5 | 7 |
| 115 | The drifting human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20147-20148. | 3.3 | 7 |
| 116 | The Coupon Collection Behavior in Human Reproduction. Current Biology, 2020, 30, 3856-3861.e1. | 1.8 | 6 |
| 117 | Natural selection contributes to the myopia epidemic. National Science Review, 2021, 8, . | 4.6 | 6 |
| 118 | Impact of structure space continuity on protein fold classification. Scientific Reports, 2016, 6, 23263. | 1.6 | 5 |
| 119 | Unbiased inference of the fitness landscape ruggedness from imprecise fitness estimates. Evolution; International Journal of Organic Evolution, 2021, 75, 2658-2671. | 1.1 | 5 |
| 120 | Transposon insertional mutagenesis of diverse yeast strains suggests coordinated gene essentiality polymorphisms. Nature Communications, 2022, 13, 1490. | 5.8 | 5 |
| 121 | Is the Genetic Code Optimized for Resource Conservation?. Molecular Biology and Evolution, 2021, 38, 5122-5126. | 3.5 | 4 |
| 122 | Testing the adaptive hypothesis of lagging-strand encoding in bacterial genomes. Nature Communications, 2022, 13, 2628. | 5.8 | 4 |
| 123 | Codon usage bias and nuclear mRNA concentration: Correlation vs. causation. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, . | 3.3 | 3 |
| 124 | Parallel transcriptomic changes in the origins of divergent monogamous vertebrates?. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17627-17628. | 3.3 | 2 |
| 125 | On the Origin of Compositional Features of Ribosomes. Genome Biology and Evolution, 2018, 10, 2010-2016. | 1.1 | 1 |
| 126 | Caution in testing phenotypic selection. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2022180118. | 3.3 | 1 |

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|-----|---|-----|-----------|
| 127 | Toward understanding the evolutionary histories and mechanisms of mangroves. National Science Review, 2017, 4, 737-737. | 4.6 | 0 |
| 128 | Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389. | | 0 |
| 129 | Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389. | | 0 |
| 130 | Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389. | | 0 |
| 131 | Chromosome-wide co-fluctuation of stochastic gene expression in mammalian cells. , 2019, 15, e1008389. | | 0 |