

Dmitri A Petrov

List of Publications by Year in descending order

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Version: 2024-02-01

152
papers

17,269
citations

16451

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20961

115
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204
all docs

204
docs citations

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times ranked

17382
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a <i>Pitx1</i> Enhancer. <i>Science</i> , 2010, 327, 302-305. | 12.6 | 901 |
| 2 | Selection on Codon Bias. <i>Annual Review of Genetics</i> , 2008, 42, 287-299. | 7.6 | 827 |
| 3 | High Functional Diversity in <i>Mycobacterium tuberculosis</i> Driven by Genetic Drift and Human Demography. <i>PLoS Biology</i> , 2008, 6, e311. | 5.6 | 507 |
| 4 | Genomic Evidence of Rapid and Stable Adaptive Oscillations over Seasonal Time Scales in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2014, 10, e1004775. | 3.5 | 473 |
| 5 | Population genomics of rapid adaptation by soft selective sweeps. <i>Trends in Ecology and Evolution</i> , 2013, 28, 659-669. | 8.7 | 471 |
| 6 | The Large Genome Constraint Hypothesis: Evolution, Ecology and Phenotype. <i>Annals of Botany</i> , 2005, 95, 177-190. | 2.9 | 429 |
| 7 | Recent Selective Sweeps in North American <i>Drosophila melanogaster</i> Show Signatures of Soft Sweeps. <i>PLoS Genetics</i> , 2015, 11, e1005004. | 3.5 | 392 |
| 8 | Evidence That Mutation Is Universally Biased towards AT in Bacteria. <i>PLoS Genetics</i> , 2010, 6, e1001115. | 3.5 | 386 |
| 9 | Evolution of genome size: new approaches to an old problem. <i>Trends in Genetics</i> , 2001, 17, 23-28. | 6.7 | 378 |
| 10 | High intrinsic rate of DNA loss in <i>Drosophila</i> . <i>Nature</i> , 1996, 384, 346-349. | 27.8 | 374 |
| 11 | Quantitative evolutionary dynamics using high-resolution lineage tracking. <i>Nature</i> , 2015, 519, 181-186. | 27.8 | 372 |
| 12 | Precise estimates of mutation rate and spectrum in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2310-8. | 7.1 | 362 |
| 13 | Pervasive Natural Selection in the <i>Drosophila</i> Genome?. <i>PLoS Genetics</i> , 2009, 5, e1000495. | 3.5 | 329 |
| 14 | Viruses are a dominant driver of protein adaptation in mammals. <i>ELife</i> , 2016, 5, . | 6.0 | 267 |
| 15 | Evidence that Adaptation in <i>Drosophila</i> Is Not Limited by Mutation at Single Sites. <i>PLoS Genetics</i> , 2010, 6, e1000924. | 3.5 | 255 |
| 16 | Mutational Equilibrium Model of Genome Size Evolution. <i>Theoretical Population Biology</i> , 2002, 61, 531-544. | 1.1 | 231 |
| 17 | Frequent adaptation and the McDonald-Kreitman test. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8615-8620. | 7.1 | 231 |
| 18 | Pesticide Resistance via Transposition-Mediated Adaptive Gene Truncation in <i>Drosophila</i> . <i>Science</i> , 2005, 309, 764-767. | 12.6 | 226 |

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|----|--|------|-----------|
| 19 | Host Species and Environmental Effects on Bacterial Communities Associated with <i>Drosophila</i> in the Laboratory and in the Natural Environment. <i>PLoS ONE</i> , 2013, 8, e70749. | 2.5 | 216 |
| 20 | Size Matters: Non-LTR Retrotransposable Elements and Ectopic Recombination in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2003, 20, 880-892. | 8.9 | 208 |
| 21 | Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast. <i>Cell</i> , 2016, 166, 1585-1596.e22. | 28.9 | 205 |
| 22 | General Rules for Optimal Codon Choice. <i>PLoS Genetics</i> , 2009, 5, e1000556. | 3.5 | 203 |
| 23 | Genome-wide signals of positive selection in human evolution. <i>Genome Research</i> , 2014, 24, 885-895. | 5.5 | 200 |
| 24 | Strong Purifying Selection at Synonymous Sites in <i>D. melanogaster</i> . <i>PLoS Genetics</i> , 2013, 9, e1003527. | 3.5 | 187 |
| 25 | Pervasive and Persistent Redundancy among Duplicated Genes in Yeast. <i>PLoS Genetics</i> , 2008, 4, e1000113. | 3.5 | 181 |
| 26 | Illumina TruSeq Synthetic Long-Reads Empower De Novo Assembly and Resolve Complex, Highly-Repetitive Transposable Elements. <i>PLoS ONE</i> , 2014, 9, e106689. | 2.5 | 180 |
| 27 | High Rate of Recent Transposable Element-Induced Adaptation in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2008, 6, e251. | 5.6 | 176 |
| 28 | Heterozygote advantage as a natural consequence of adaptation in diploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20666-20671. | 7.1 | 174 |
| 29 | Evidence of Selection against Complex Mitotic-Origin Aneuploidy during Preimplantation Development. <i>PLoS Genetics</i> , 2015, 11, e1005601. | 3.5 | 170 |
| 30 | Evidence that RNA Viruses Drove Adaptive Introgression between Neanderthals and Modern Humans. <i>Cell</i> , 2018, 175, 360-371.e13. | 28.9 | 164 |
| 31 | Population Genomics of Transposable Elements in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2011, 28, 1633-1644. | 8.9 | 160 |
| 32 | Secondary contact and local adaptation contribute to genome-wide patterns of clinal variation in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2016, 25, 1157-1174. | 3.9 | 149 |
| 33 | Population Genomics of Transposable Elements in <i>Drosophila</i> . <i>Annual Review of Genetics</i> , 2014, 48, 561-581. | 7.6 | 144 |
| 34 | <i>Drosophila melanogaster</i> recombination rate calculator. <i>Gene</i> , 2010, 463, 18-20. | 2.2 | 142 |
| 35 | Imperfect drug penetration leads to spatial monotherapy and rapid evolution of multidrug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2874-83. | 7.1 | 142 |
| 36 | The mode and tempo of genome size evolution in eukaryotes. <i>Genome Research</i> , 2007, 17, 594-601. | 5.5 | 140 |

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|----|---|------|-----------|
| 37 | Genome-Wide Patterns of Adaptation to Temperate Environments Associated with Transposable Elements in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2010, 6, e1000905. | 3.5 | 137 |
| 38 | High sensitivity to aligner and high rate of false positives in the estimates of positive selection in the 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2011, 21, 863-874. | 5.5 | 137 |
| 39 | Pervasive Hitchhiking at Coding and Regulatory Sites in Humans. <i>PLoS Genetics</i> , 2009, 5, e1000336. | 3.5 | 134 |
| 40 | DNA loss and evolution of genome size in <i>Drosophila</i> . <i>Genetica</i> , 2002, 115, 81-91. | 1.1 | 133 |
| 41 | Widespread introgression across a phylogeny of 155 <i>Drosophila</i> genomes. <i>Current Biology</i> , 2022, 32, 111-123.e5. | 3.9 | 132 |
| 42 | Effects of maternal age on euploidy rates in a large cohort of embryos analyzed with 24-chromosome single-nucleotide polymorphism-based preimplantation genetic screening. <i>Fertility and Sterility</i> , 2016, 105, 1307-1313. | 1.0 | 131 |
| 43 | Whole Genome Analysis of 132 Clinical <i>Saccharomyces cerevisiae</i> Strains Reveals Extensive Ploidy Variation. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2421-2434. | 1.8 | 129 |
| 44 | Comparative population genomics of latitudinal variation in <i>Drosophila simulans</i> and <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2016, 25, 723-740. | 3.9 | 128 |
| 45 | Quantification of GC-biased gene conversion in the human genome. <i>Genome Research</i> , 2015, 25, 1215-1228. | 5.5 | 127 |
| 46 | Characterization of bacteriophage P1 library containing inserts of <i>Drosophila</i> DNA of 75?100 kilobase pairs. <i>Chromosoma</i> , 1991, 100, 487-494. | 2.2 | 117 |
| 47 | Genomewide Spatial Correspondence Between Nonsynonymous Divergence and Neutral Polymorphism Reveals Extensive Adaptation in <i>Drosophila</i> . <i>Genetics</i> , 2007, 177, 2083-2099. | 2.9 | 115 |
| 48 | Evolutionary Biology for the 21st Century. <i>PLoS Biology</i> , 2013, 11, e1001466. | 5.6 | 115 |
| 49 | Rates of DNA Duplication and Mitochondrial DNA Insertion in the Human Genome. <i>Journal of Molecular Evolution</i> , 2003, 57, 343-354. | 1.8 | 112 |
| 50 | Genomic Gigantism: DNA Loss Is Slow in Mountain Grasshoppers. <i>Molecular Biology and Evolution</i> , 2001, 18, 246-253. | 8.9 | 111 |
| 51 | Origins and rates of aneuploidy in human blastomeres. <i>Fertility and Sterility</i> , 2012, 97, 395-401. | 1.0 | 110 |
| 52 | Highly contiguous assemblies of 101 drosophilid genomes. <i>ELife</i> , 2021, 10, . | 6.0 | 108 |
| 53 | Common variants spanning <i>PLK4</i> are associated with mitotic-origin aneuploidy in human embryos. <i>Science</i> , 2015, 348, 235-238. | 12.6 | 106 |
| 54 | A quantitative and multiplexed approach to uncover the fitness landscape of tumor suppression in vivo. <i>Nature Methods</i> , 2017, 14, 737-742. | 19.0 | 105 |

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|----|--|------|-----------|
| 55 | Microbiome composition shapes rapid genomic adaptation of <i>Drosophila melanogaster</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 20025-20032. | 7.1 | 103 |
| 56 | Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice. Nature Genetics, 2018, 50, 483-486. | 21.4 | 101 |
| 57 | Relaxed Purifying Selection and Possibly High Rate of Adaptation in Primate Lineage-Specific Genes. Genome Biology and Evolution, 2010, 2, 393-409. | 2.5 | 100 |
| 58 | Seasonally fluctuating selection can maintain polymorphism at many loci via segregation lift. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9932-E9941. | 7.1 | 100 |
| 59 | Distinct Changes of Genomic Biases in Nucleotide Substitution at the Time of Mammalian Radiation. Molecular Biology and Evolution, 2003, 20, 1887-1896. | 8.9 | 95 |
| 60 | Do disparate mechanisms of duplication add similar genes to the genome?. Trends in Genetics, 2005, 21, 548-551. | 6.7 | 91 |
| 61 | Elevated evolutionary rates in the laboratory strain of <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1092-1097. | 7.1 | 90 |
| 62 | Genomic Heterogeneity of Background Substitutional Patterns in <i>Drosophila melanogaster</i> . Genetics, 2005, 169, 709-722. | 2.9 | 90 |
| 63 | LDx: Estimation of Linkage Disequilibrium from High-Throughput Pooled Resequencing Data. PLoS ONE, 2012, 7, e48588. | 2.5 | 88 |
| 64 | Substantial Regional Variation in Substitution Rates in the Human Genome: Importance of GC Content, Gene Density, and Telomere-Specific Effects. Journal of Molecular Evolution, 2005, 60, 748-763. | 1.8 | 85 |
| 65 | Empirical Validation of Pooled Whole Genome Population Re-Sequencing in <i>Drosophila melanogaster</i> . PLoS ONE, 2012, 7, e41901. | 2.5 | 84 |
| 66 | The adaptive role of transposable elements in the <i>Drosophila</i> genome. Gene, 2009, 448, 124-133. | 2.2 | 82 |
| 67 | Rapid seasonal evolution in innate immunity of wild <i>Drosophila melanogaster</i> . Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172599. | 2.6 | 82 |
| 68 | Multiplexed in vivo homology-directed repair and tumor barcoding enables parallel quantification of Kras variant oncogenicity. Nature Communications, 2017, 8, 2053. | 12.8 | 78 |
| 69 | The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. Nature, 2021, 592, 794-798. | 27.8 | 76 |
| 70 | Direct observation of adaptive tracking on ecological time scales in <i>Drosophila</i> . Science, 2022, 375, eabj7484. | 12.6 | 71 |
| 71 | More effective drugs lead to harder selective sweeps in the evolution of drug resistance in HIV-1. ELife, 2016, 5, . | 6.0 | 70 |
| 72 | Soft Selective Sweeps in Complex Demographic Scenarios. Genetics, 2014, 198, 669-684. | 2.9 | 69 |

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|----|--|------|-----------|
| 73 | Fitness variation across subtle environmental perturbations reveals local modularity and global pleiotropy of adaptation. <i>ELife</i> , 2020, 9, . | 6.0 | 69 |
| 74 | Broker Genes in Human Disease. <i>Genome Biology and Evolution</i> , 2010, 2, 815-825. | 2.5 | 68 |
| 75 | Trash DNA is what gets thrown away: high rate of DNA loss in <i>Drosophila</i> . <i>Gene</i> , 1997, 205, 279-289. | 2.2 | 67 |
| 76 | Broad geographic sampling reveals the shared basis and environmental correlates of seasonal adaptation in <i>Drosophila</i> . <i>ELife</i> , 2021, 10, . | 6.0 | 66 |
| 77 | Reduced selection leads to accelerated gene loss in <i>Shigella</i> . <i>Genome Biology</i> , 2007, 8, R164. | 9.6 | 64 |
| 78 | Stress response, behavior, and development are shaped by transposable element-induced mutations in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2019, 15, e1007900. | 3.5 | 64 |
| 79 | Hidden Complexity of Yeast Adaptation under Simple Evolutionary Conditions. <i>Current Biology</i> , 2018, 28, 515-525.e6. | 3.9 | 63 |
| 80 | T-lex2: genotyping, frequency estimation and re-annotation of transposable elements using single or pooled next-generation sequencing data. <i>Nucleic Acids Research</i> , 2015, 43, e22-e22. | 14.5 | 61 |
| 81 | X-Linked Genes Evolve Higher Codon Bias in <i>Drosophila</i> and <i>Caenorhabditis</i> . <i>Genetics</i> , 2005, 171, 145-155. | 2.9 | 60 |
| 82 | Single nucleotide mapping of trait space reveals Pareto fronts that constrain adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 1539-1551. | 7.8 | 60 |
| 83 | Global Transcriptional Profiling of Diapause and Climatic Adaptation in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2016, 33, 707-720. | 8.9 | 59 |
| 84 | Genetic Determinants of EGFR-Driven Lung Cancer Growth and Therapeutic Response <i>In Vivo</i> . <i>Cancer Discovery</i> , 2021, 11, 1736-1753. | 9.4 | 59 |
| 85 | A Recent Adaptive Transposable Element Insertion Near Highly Conserved Developmental Loci in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1949-1961. | 8.9 | 58 |
| 86 | Tripolar chromosome segregation drives the association between maternal genotype at variants spanning PLK4 and aneuploidy in human preimplantation embryos. <i>Human Molecular Genetics</i> , 2018, 27, 2573-2585. | 2.9 | 55 |
| 87 | A combined molecular and cytogenetic approach to genome evolution in <i>Drosophila</i> using large-fragment DNA cloning. <i>Chromosoma</i> , 1993, 102, 253-266. | 2.2 | 54 |
| 88 | Protein Evolution in the Context of <i>Drosophila</i> Development. <i>Journal of Molecular Evolution</i> , 2005, 60, 774-785. | 1.8 | 54 |
| 89 | Paucity of chimeric gene-transposable element transcripts in the <i>Drosophila melanogaster</i> genome. <i>BMC Biology</i> , 2005, 3, 24. | 3.8 | 54 |
| 90 | A repetitive DNA element, associated with telomeric sequences in <i>Drosophila melanogaster</i> , contains open reading frames. <i>Chromosoma</i> , 1992, 102, 32-40. | 2.2 | 53 |

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|-----|--|------|-----------|
| 91 | T-lex: a program for fast and accurate assessment of transposable element presence using next-generation sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, e36-e36. | 14.5 | 53 |
| 92 | Codon Bias and Noncoding GC Content Correlate Negatively with Recombination Rate on the <i>Drosophila</i> X Chromosome. <i>Journal of Molecular Evolution</i> , 2005, 61, 315-324. | 1.8 | 50 |
| 93 | Rapid Sequence Turnover at an Intergenic Locus in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2004, 21, 670-680. | 8.9 | 48 |
| 94 | Comparative population genomics: power and principles for the inference of functionality. <i>Trends in Genetics</i> , 2014, 30, 133-139. | 6.7 | 48 |
| 95 | Transposable elements in clonal lineages: lethal hangover from sex. <i>Biological Journal of the Linnean Society</i> , 2003, 79, 33-41. | 1.6 | 46 |
| 96 | Similar Levels of X-linked and Autosomal Nucleotide Variation in African and non-African populations of <i>Drosophila melanogaster</i> . <i>BMC Evolutionary Biology</i> , 2007, 7, 202. | 3.2 | 46 |
| 97 | Human-chimpanzee fused cells reveal cis-regulatory divergence underlying skeletal evolution. <i>Nature Genetics</i> , 2021, 53, 467-476. | 21.4 | 46 |
| 98 | Similarly Strong Purifying Selection Acts on Human Disease Genes of All Evolutionary Ages. <i>Genome Biology and Evolution</i> , 2009, 1, 131-144. | 2.5 | 45 |
| 99 | Deep sequencing of natural and experimental populations of <i>Drosophila melanogaster</i> reveals biases in the spectrum of new mutations. <i>Genome Research</i> , 2017, 27, 1988-2000. | 5.5 | 45 |
| 100 | Elevated Linkage Disequilibrium and Signatures of Soft Sweeps Are Common in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2016, 203, 863-880. | 2.9 | 44 |
| 101 | Exploiting selection at linked sites to infer the rate and strength of adaptation. <i>Nature Ecology and Evolution</i> , 2019, 3, 977-984. | 7.8 | 43 |
| 102 | Pervasive Strong Selection at the Level of Codon Usage Bias in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2020, 214, 511-528. | 2.9 | 42 |
| 103 | Evolution of Genome Content: Population Dynamics of Transposable Elements in Flies and Humans. <i>Methods in Molecular Biology</i> , 2012, 855, 361-383. | 0.9 | 41 |
| 104 | Soft Selective Sweeps in Evolutionary Rescue. <i>Genetics</i> , 2017, 205, 1573-1586. | 2.9 | 41 |
| 105 | Genomic inference accurately predicts the timing and severity of a recent bottleneck in a nonmodel insect population. <i>Molecular Ecology</i> , 2014, 23, 136-150. | 3.9 | 40 |
| 106 | Empowering conservation practice with efficient and economical genotyping from poor quality samples. <i>Methods in Ecology and Evolution</i> , 2019, 10, 853-859. | 5.2 | 40 |
| 107 | Heterozygote Advantage Is a Common Outcome of Adaptation in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2016, 203, 1401-1413. | 2.9 | 38 |
| 108 | High rate of adaptation of mammalian proteins that interact with <i>Plasmodium</i> and related parasites. <i>PLoS Genetics</i> , 2017, 13, e1007023. | 3.5 | 37 |

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|-----|---|------|-----------|
| 109 | Tissue-Specific cis-Regulatory Divergence Implicates eIoF in Inhibiting Interspecies Mating in <i>Drosophila</i> . <i>Current Biology</i> , 2018, 28, 3969-3975.e3. | 3.9 | 37 |
| 110 | Ancient RNA virus epidemics through the lens of recent adaptation in human genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190575. | 4.0 | 37 |
| 111 | <i>Drosophila</i> Evolution over Space and Time (DEST): A New Population Genomics Resource. <i>Molecular Biology and Evolution</i> , 2021, 38, 5782-5805. | 8.9 | 37 |
| 112 | Enhancer Choice in Cis and in Trans in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2004, 167, 1739-1747. | 2.9 | 36 |
| 113 | The cis-regulatory effects of modern human-specific variants. <i>ELife</i> , 2021, 10, . | 6.0 | 36 |
| 114 | Recent Evolutionary History of Tigers Highlights Contrasting Roles of Genetic Drift and Selection. <i>Molecular Biology and Evolution</i> , 2021, 38, 2366-2379. | 8.9 | 35 |
| 115 | A Functional Taxonomy of Tumor Suppression in Oncogenic KRAS-Driven Lung Cancer. <i>Cancer Discovery</i> , 2021, 11, 1754-1773. | 9.4 | 35 |
| 116 | Detection of hard and soft selective sweeps from <i>Drosophila melanogaster</i> population genomic data. <i>PLoS Genetics</i> , 2021, 17, e1009373. | 3.5 | 35 |
| 117 | Obstruction of adaptation in diploids by recessive, strongly deleterious alleles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2658-66. | 7.1 | 34 |
| 118 | Long live the king: chromosome-level assembly of the lion (<i>Panthera leo</i>) using linked-read, Hi-C, and long-read data. <i>BMC Biology</i> , 2020, 18, 3. | 3.8 | 34 |
| 119 | Functional biology in its natural context: A search for emergent simplicity. <i>ELife</i> , 2021, 10, . | 6.0 | 34 |
| 120 | An Intrinsically Disordered Region of the DNA Repair Protein Nbs1 Is a Species-Specific Barrier to Herpes Simplex Virus 1 in Primates. <i>Cell Host and Microbe</i> , 2016, 20, 178-188. | 11.0 | 33 |
| 121 | Spatiotemporal dynamics and genome-wide association analysis of desiccation tolerance in <i>Drosophila melanogaster</i> . <i>Molecular Ecology</i> , 2018, 27, 3525-3540. | 3.9 | 33 |
| 122 | Faster than Neutral Evolution of Constrained Sequences: The Complex Interplay of Mutational Biases and Weak Selection. <i>Genome Biology and Evolution</i> , 2011, 3, 383-395. | 2.5 | 30 |
| 123 | Accurate Allele Frequencies from Ultra-low Coverage Pool-Seq Samples in Evolve-and-Resequencing Experiments. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 4159-4168. | 1.8 | 29 |
| 124 | Inferring the Strength of Selection in <i>Drosophila</i> under Complex Demographic Models. <i>Molecular Biology and Evolution</i> , 2008, 26, 513-526. | 8.9 | 28 |
| 125 | The clarifying role of time series data in the population genetics of HIV. <i>PLoS Genetics</i> , 2021, 17, e1009050. | 3.5 | 26 |
| 126 | A spatio-temporal assessment of simian/human immunodeficiency virus (SHIV) evolution reveals a highly dynamic process within the host. <i>PLoS Pathogens</i> , 2017, 13, e1006358. | 4.7 | 25 |

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|-----|--|------|-----------|
| 127 | Evolutionary Dynamics in Structured Populations Under Strong Population Genetic Forces. <i>C3: Genes, Genomes, Genetics</i> , 2019, 9, 3395-3407. | 1.8 | 23 |
| 128 | Cost-effective assembly of the African wild dog (<i>Lycaon pictus</i>) genome using linked reads. <i>GigaScience</i> , 2019, 8, . | 6.4 | 22 |
| 129 | Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021, 24, 186-196. | 14.8 | 22 |
| 130 | How Intron Splicing Affects the Deletion and Insertion Profile in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2002, 162, 1233-1244. | 2.9 | 22 |
| 131 | Nonadaptive Explanations for Signatures of Partial Selective Sweeps in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2008, 25, 1025-1042. | 8.9 | 21 |
| 132 | Genome size as a mutation-selection-drift process.. <i>Genes and Genetic Systems</i> , 1999, 74, 201-207. | 0.7 | 19 |
| 133 | Minor shift in background substitutional patterns in the <i>Drosophila saltans</i> and <i>willistoni</i> lineages is insufficient to explain GC content of coding sequences. <i>BMC Biology</i> , 2006, 4, 37. | 3.8 | 17 |
| 134 | MITEs – The Ultimate Parasites. <i>Science</i> , 2009, 325, 1352-1353. | 12.6 | 17 |
| 135 | Common host variation drives malaria parasite fitness in healthy human red cells. <i>ELife</i> , 2021, 10, . | 6.0 | 17 |
| 136 | On the Limitations of Using Ribosomal Genes as References for the Study of Codon Usage: A Rebuttal. <i>PLoS ONE</i> , 2012, 7, e49060. | 2.5 | 17 |
| 137 | The <i>Tetragnatha kauaiensis</i> Genome Sheds Light on the Origins of Genomic Novelty in Spiders. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 16 |
| 138 | Molecular Evolution of the Testis TAFs of <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2009, 26, 1103-1116. | 8.9 | 15 |
| 139 | Extremely Rare Polymorphisms in <i>Saccharomyces cerevisiae</i> Allow Inference of the Mutational Spectrum. <i>PLoS Genetics</i> , 2017, 13, e1006455. | 3.5 | 13 |
| 140 | Genetic Adaptation in New York City Rats. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 13 |
| 141 | Quantitative <i>In Vivo</i> Analyses Reveal a Complex Pharmacogenomic Landscape in Lung Adenocarcinoma. <i>Cancer Research</i> , 2021, 81, 4570-4580. | 0.9 | 13 |
| 142 | Slow but Steady: Reduction of Genome Size through Biased Mutation [with Reply]. <i>Plant Cell</i> , 1997, 9, 1900. | 6.6 | 10 |
| 143 | A Novel Method Distinguishes Between Mutation Rates and Fixation Biases in Patterns of Single-Nucleotide Substitution. <i>Journal of Molecular Evolution</i> , 2006, 62, 168-175. | 1.8 | 10 |
| 144 | Historical trends and new surveillance of <i>Plasmodium falciparum</i> drug resistance markers in Angola. <i>Malaria Journal</i> , 2021, 20, 175. | 2.3 | 7 |

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|-----|---|------|-----------|
| 145 | Combinatorial Inactivation of Tumor Suppressors Efficiently Initiates Lung Adenocarcinoma with Therapeutic Vulnerabilities. <i>Cancer Research</i> , 2022, 82, 1589-1602. | 0.9 | 7 |
| 146 | Revisiting the malaria hypothesis: accounting for polygenicity and pleiotropy. <i>Trends in Parasitology</i> , 2022, 38, 290-301. | 3.3 | 5 |
| 147 | Richard C. Lewontin (1929–2021). <i>Science</i> , 2021, 373, 745-745. | 12.6 | 2 |
| 148 | Seeking Goldilocks During Evolution of Drug Resistance. <i>PLoS Biology</i> , 2017, 15, e2001872. | 5.6 | 2 |
| 149 | Reply to Chen and Zhang: On interpreting genome-wide trends from yeast mutation accumulation data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4063-E4063. | 7.1 | 0 |
| 150 | Common variants associated with mitotic-origin of aneuploidy in human embryos. <i>Reproductive BioMedicine Online</i> , 2018, 36, e1. | 2.4 | 0 |
| 151 | SNP genotyping to monitor wild tigers for conservation. <i>Canadian Journal of Biotechnology</i> , 2017, 1, 19-19. | 0.3 | 0 |
| 152 | Tumor suppressor pathways shape EGFR-driven lung tumor progression and response to treatment. <i>Molecular and Cellular Oncology</i> , 2022, 9, 1994328. | 0.7 | 0 |