

Julio Rozas

List of Publications by Year in descending order

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93
papers

35,846
citations

81900

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39675

94
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103
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103
docs citations

103
times ranked

36898
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. <i>Bioinformatics</i> , 2009, 25, 1451-1452. | 4.1 | 13,645 |
| 2 | DnaSP, DNA polymorphism analyses by the coalescent and other methods. <i>Bioinformatics</i> , 2003, 19, 2496-2497. | 4.1 | 5,561 |
| 3 | DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. <i>Molecular Biology and Evolution</i> , 2017, 34, 3299-3302. | 8.9 | 4,056 |
| 4 | Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218. | 27.8 | 1,886 |
| 5 | Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2002, 19, 2092-2100. | 8.9 | 1,770 |
| 6 | The <i>Drosophila melanogaster</i> Genetic Reference Panel. <i>Nature</i> , 2012, 482, 173-178. | 27.8 | 1,756 |
| 7 | Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313. | 5.6 | 913 |
| 8 | The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. <i>Science</i> , 2014, 345, 1181-1184. | 12.6 | 520 |
| 9 | Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12168-12173. | 7.1 | 482 |
| 10 | Comparative Genomics of the Odorant-Binding and Chemosensory Protein Gene Families across the Arthropoda: Origin and Evolutionary History of the Chemosensory System. <i>Genome Biology and Evolution</i> , 2011, 3, 476-490. | 2.5 | 468 |
| 11 | Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507. | 12.8 | 450 |
| 12 | Molecular evolution of the major chemosensory gene families in insects. <i>Heredity</i> , 2009, 103, 208-216. | 2.6 | 430 |
| 13 | DNA Sequence Polymorphism Analysis Using DnaSP. <i>Methods in Molecular Biology</i> , 2009, 537, 337-350. | 0.9 | 293 |
| 14 | Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257. | 27.8 | 251 |
| 15 | Statistical Power Analysis of Neutrality Tests Under Demographic Expansions, Contractions and Bottlenecks With Recombination. <i>Genetics</i> , 2008, 179, 555-567. | 2.9 | 242 |
| 16 | The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005. | 5.6 | 221 |
| 17 | Comparative genomic analysis of the odorant-binding protein family in 12 <i>Drosophila</i> genomes: purifying selection and birth-and-death evolution. <i>Genome Biology</i> , 2007, 8, R235. | 9.6 | 170 |
| 18 | Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, <i>Manduca sexta</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2016, 76, 118-147. | 2.7 | 154 |

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|----|---|------|-----------|
| 19 | The Estimation of the Number and the Length Distribution of Gene Conversion Tracts From Population DNA Sequence Data. <i>Genetics</i> , 1997, 146, 89-99. | 2.9 | 135 |
| 20 | The avocado genome informs deep angiosperm phylogeny, highlights introgressive hybridization, and reveals pathogen-influenced gene space adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17081-17089. | 7.1 | 134 |
| 21 | VariScan: Analysis of evolutionary patterns from large-scale DNA sequence polymorphism data. <i>Bioinformatics</i> , 2005, 21, 2791-2793. | 4.1 | 120 |
| 22 | DNA Variation at the <i>rp49</i> Gene Region of <i>Drosophila simulans</i> : Evolutionary Inferences From an Unusual Haplotype Structure. <i>Genetics</i> , 2001, 158, 1147-1155. | 2.9 | 116 |
| 23 | Genome-wide DNA polymorphism analyses using VariScan. <i>BMC Bioinformatics</i> , 2006, 7, 409. | 2.6 | 115 |
| 24 | BadiRate: estimating family turnover rates by likelihood-based methods. <i>Bioinformatics</i> , 2012, 28, 279-281. | 4.1 | 108 |
| 25 | Genome of the pitcher plant <i>Cephalotus</i> reveals genetic changes associated with carnivory. <i>Nature Ecology and Evolution</i> , 2017, 1, 59. | 7.8 | 99 |
| 26 | Network-level molecular evolutionary analysis of the insulin/TOR signal transduction pathway across 12 <i>Drosophila</i> genomes. <i>Genome Research</i> , 2009, 19, 234-242. | 5.5 | 74 |
| 27 | Gene conversion is involved in the transfer of genetic information between naturally occurring inversions of <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11517-11521. | 7.1 | 72 |
| 28 | Land planarians (Platyhelminthes) as a model organism for fine-scale phylogeographic studies: understanding patterns of biodiversity in the Brazilian Atlantic Forest hotspot. <i>Journal of Evolutionary Biology</i> , 2011, 24, 887-896. | 1.7 | 69 |
| 29 | Molecular characterization of <i>Botrytis ourmia</i> -like virus, a mycovirus close to the plant pathogenic genus <i>Ourmiavirus</i> . <i>Virology</i> , 2016, 489, 158-164. | 2.4 | 65 |
| 30 | Unique Features of Odorant-Binding Proteins of the Parasitoid Wasp <i>Nasonia vitripennis</i> Revealed by Genome Annotation and Comparative Analyses. <i>PLoS ONE</i> , 2012, 7, e43034. | 2.5 | 62 |
| 31 | Insights into the origin and distribution of biodiversity in the Brazilian Atlantic forest hot spot: a statistical phylogeographic study using a low-dispersal organism. <i>Heredity</i> , 2014, 112, 656-665. | 2.6 | 60 |
| 32 | Genomic adaptations to aquatic and aerial life in mayflies and the origin of insect wings. <i>Nature Communications</i> , 2020, 11, 2631. | 12.8 | 57 |
| 33 | Chromosomal Inversion Polymorphism Leads to Extensive Genetic Structure. <i>Genetics</i> , 2005, 169, 1573-1581. | 2.9 | 55 |
| 34 | Molecular Population Genetics of the <i>rp49</i> Gene Region in Different Chromosomal Inversions of <i>Drosophila subobscura</i> . <i>Genetics</i> , 1999, 151, 189-202. | 2.9 | 54 |
| 35 | Functional evidence that a recently evolved <i>Drosophila</i> sperm-specific gene boosts sperm competition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2043-2048. | 7.1 | 53 |
| 36 | High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant <i>Utricularia gibba</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1284-1295. | 8.9 | 53 |

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|----|--|-----|-----------|
| 37 | Molecular and Chromosomal Phylogeny in the Obscure Group of <i>Drosophila</i> Inferred from Sequences of the <i>rp49</i> Gene Region. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 33-41. | 2.7 | 52 |
| 38 | Evolutionary Analysis of Mitogenomes from Parasitic and Free-Living Flatworms. <i>PLoS ONE</i> , 2015, 10, e0120081. | 2.5 | 44 |
| 39 | <i>bitacora</i> : A comprehensive tool for the identification and annotation of gene families in genome assemblies. <i>Molecular Ecology Resources</i> , 2020, 20, 1445-1452. | 4.8 | 44 |
| 40 | Evolution of chemosensory gene families in arthropods: Insight from the first inclusive comparative transcriptome analysis across spider appendages. <i>Genome Biology and Evolution</i> , 2017, 9, eww296. | 2.5 | 43 |
| 41 | Comparative Genomics of the Vertebrate Insulin/TOR Signal Transduction Pathway: A Network-Level Analysis of Selective Pressures. <i>Genome Biology and Evolution</i> , 2011, 3, 87-101. | 2.5 | 40 |
| 42 | Family Size Evolution in <i>Drosophila</i> Chemosensory Gene Families: A Comparative Analysis with a Critical Appraisal of Methods. <i>Genome Biology and Evolution</i> , 2014, 6, 1669-1682. | 2.5 | 40 |
| 43 | The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , 2020, 18, 90. | 3.8 | 40 |
| 44 | TRUFA: A User-Friendly Web Server for <i>de novo</i> RNA-seq Analysis Using Cluster Computing. <i>Evolutionary Bioinformatics</i> , 2015, 11, EBO.S23873. | 1.2 | 37 |
| 45 | Unexpected High Polymorphism at the <i>FABP4</i> Gene Unveils a Complex History for Pig Populations. <i>Genetics</i> , 2006, 174, 2119-2127. | 2.9 | 35 |
| 46 | Comparative Genomics Reveals Thousands of Novel Chemosensory Genes and Massive Changes in Chemoreceptor Repertoires across Chelicerates. <i>Genome Biology and Evolution</i> , 2018, 10, 1221-1236. | 2.5 | 35 |
| 47 | Assessing Associations between the <i>AURKA-HMMR-TPX2-TUBG1</i> Functional Module and Breast Cancer Risk in <i>BRCA1/2</i> Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020. | 2.5 | 34 |
| 48 | <i>RPS4Y</i> gene family evolution in primates. <i>BMC Evolutionary Biology</i> , 2008, 8, 142. | 3.2 | 33 |
| 49 | Genome-Wide Analysis of Adaptive Molecular Evolution in the Carnivorous Plant <i>Utricularia gibba</i> . <i>Genome Biology and Evolution</i> , 2015, 7, 444-456. | 2.5 | 33 |
| 50 | The role of historical factors and natural selection in the evolution of breeding systems of <i>Oxalis alpina</i> in the Sonoran desert "Sky Islands". <i>Journal of Evolutionary Biology</i> , 2010, 23, 2163-2175. | 1.7 | 29 |
| 51 | Transfer of genetic information in the <i>rp49</i> region of <i>Drosophila subobscura</i> between different chromosomal gene arrangements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 8083-8087. | 7.1 | 27 |
| 52 | Large-Scale Adaptive Hitchhiking Upon High Recombination in <i>Drosophila simulans</i> . <i>Genetics</i> , 2003, 165, 895-900. | 2.9 | 27 |
| 53 | The draft genome sequence of the spider <i>Dysdera silvatica</i> (Araneae, Dysderidae): A valuable resource for functional and evolutionary genomic studies in chelicerates. <i>CigaScience</i> , 2019, 8, . | 6.4 | 25 |
| 54 | Cryptic species delineation in freshwater planarians of the genus <i>Dugesia</i> (Platyhelminthes). <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106496. | 2.7 | 24 |

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|----|--|-----|-----------|
| 55 | Divergent evolution and molecular adaptation in the <i>Drosophila</i> odorant-binding protein family: inferences from sequence variation at the OS-E and OS-F genes. <i>BMC Evolutionary Biology</i> , 2008, 8, 323. | 3.2 | 23 |
| 56 | Chance and predictability in evolution: The genomic basis of convergent dietary specializations in an adaptive radiation. <i>Molecular Ecology</i> , 2019, 28, 4028-4045. | 3.9 | 21 |
| 57 | Nucleotide Polymorphism at the rp49 region of <i>Drosophila subobscura</i> : Lack of geographic subdivision within chromosomal arrangements in Europe. <i>Journal of Evolutionary Biology</i> , 1995, 8, 355-367. | 1.7 | 20 |
| 58 | PopDrowser: the Population <i>Drosophila</i> Browser. <i>Bioinformatics</i> , 2012, 28, 595-596. | 4.1 | 20 |
| 59 | Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2006, 23, 1642-1642. | 8.9 | 19 |
| 60 | Molecular Population Genetics of the Insulin/TOR Signal Transduction Pathway: A Network-Level Analysis in <i>Drosophila melanogaster</i> . <i>Molecular Biology and Evolution</i> , 2012, 29, 123-132. | 8.9 | 17 |
| 61 | 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 |
| 62 | <i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> from Human and Animal Origins: Genetic Diversity, Antimicrobial Susceptibility, and Characterization of a Vancomycin-Resistant Calf Isolate Carrying a <i>vanA</i> -Tn 1546-Like Element. <i>Antimicrobial Agents and Chemotherapy</i> , 2015, 59, 2006-2015. | 3.2 | 15 |
| 63 | Comparative analysis of tissue-specific transcriptomes in the funnel-web spider <i>Macrothele calpeiana</i> (Araneae, Hexathelidae). <i>PeerJ</i> , 2015, 3, e1064. | 2.0 | 14 |
| 64 | Nucleotide Polymorphism in the Rpl215 Gene Region of the Insular Species <i>Drosophila guanche</i> : Reduced Efficacy of Weak Selection on Synonymous Variation. <i>Molecular Biology and Evolution</i> , 2003, 20, 1867-1875. | 8.9 | 13 |
| 65 | Mycobacterial Phylogenomics: An Enhanced Method for Gene Turnover Analysis Reveals Uneven Levels of Gene Gain and Loss among Species and Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 1454-1465. | 2.5 | 13 |
| 66 | Understanding the Early Evolutionary Stages of a Tandem <i>Drosophila melanogaster</i> -Specific Gene Family: A Structural and Functional Population Study. <i>Molecular Biology and Evolution</i> , 2020, 37, 2584-2600. | 8.9 | 12 |
| 67 | Integrating Sequence Capture and Restriction Site-Associated DNA Sequencing to Resolve Recent Radiations of Pelagic Seabirds. <i>Systematic Biology</i> , 2021, 70, 976-996. | 5.6 | 12 |
| 68 | Chromosome-Level Genome Assembly of the Common Chaffinch (Aves: <i>Fringilla coelebs</i>): A Valuable Resource for Evolutionary Biology. <i>Genome Biology and Evolution</i> , 2021, 13, . | 2.5 | 12 |
| 69 | The chromosome-scale assembly of the Canary Islands endemic spider <i>Dysdera silvatica</i> (Arachnida, Araneae) sheds light on the origin and genome structure of chemoreceptor gene families in chelicerates. <i>Molecular Ecology Resources</i> , 2022, 22, 375-390. | 4.8 | 12 |
| 70 | Comparative Genomics Uncovers Unique Gene Turnover and Evolutionary Rates in a Gene Family Involved in the Detection of Insect Cuticular Pheromones. <i>Genome Biology and Evolution</i> , 2016, 8, 1734-1747. | 2.5 | 11 |
| 71 | Rapid Functional and Sequence Differentiation of a Tandemly Repeated Species-Specific Multigene Family in <i>Drosophila</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 51-65. | 8.9 | 11 |
| 72 | Molecular population genetics of the OBP83 genomic region in <i>Drosophila subobscura</i> and <i>D. guanche</i> : contrasting the effects of natural selection and gene arrangement expansion in the patterns of nucleotide variation. <i>Heredity</i> , 2011, 106, 191-201. | 2.6 | 10 |

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|----|---|-----|-----------|
| 73 | Evolutionary History of Major Chemosensory Gene Families across Panarthropoda. <i>Molecular Biology and Evolution</i> , 2020, 37, 3601-3615. | 8.9 | 10 |
| 74 | Patterns of Nucleotide Polymorphism and Divergence in the Odorant-Binding Protein Genes <i>OS-E</i> and <i>OS-F</i> : Analysis in the <i>Melanogaster</i> Species Subgroup of <i>Drosophila</i> . <i>Genetics</i> , 2003, 165, 1279-1288. | 2.9 | 10 |
| 75 | The nature of introns 4-7 largely reflects the lineage specificity of HLA-A alleles. <i>Immunogenetics</i> , 2002, 54, 447-462. | 2.4 | 9 |
| 76 | Smelling in the dark: Phylogenomic insights into the chemosensory system of a subterranean beetle. <i>Molecular Ecology</i> , 2021, 30, 2573-2590. | 3.9 | 9 |
| 77 | Weak Polygenic Selection Drives the Rapid Adaptation of the Chemosensory System: Lessons from the Upstream Regions of the Major Gene Families. <i>Genome Biology and Evolution</i> , 2016, 8, 2493-2504. | 2.5 | 8 |
| 78 | DOMINO: development of informative molecular markers for phylogenetic and genome-wide population genetic studies in non-model organisms. <i>Bioinformatics</i> , 2016, 32, 3753-3759. | 4.1 | 8 |
| 79 | DNA variation at the <i>rp49</i> gene region in <i>Drosophila madeirensis</i> and <i>D. subobscura</i> from Madeira: inferences about the origin of an insular endemic species. <i>Journal of Evolutionary Biology</i> , 2001, 14, 379-387. | 1.7 | 7 |
| 80 | Gene duplications in the <i>E. coli</i> genome: common themes among pathotypes. <i>BMC Genomics</i> , 2019, 20, 313. | 2.8 | 7 |
| 81 | A Program to Optimize the Design of Oligonucleotides for PCR Amplification. <i>Journal of Heredity</i> , 1991, 82, 84-84. | 2.4 | 6 |
| 82 | Unusual Pattern of Nucleotide Sequence Variation at the <i>OS-E</i> and <i>OS-F</i> Genomic Regions of <i>Drosophila simulans</i> . <i>Genetics</i> , 2007, 175, 1923-1935. | 2.9 | 6 |
| 83 | Uncovering the Functional Constraints Underlying the Genomic Organization of the Odorant-Binding Protein Genes. <i>Genome Biology and Evolution</i> , 2013, 5, 2096-2108. | 2.5 | 6 |
| 84 | Latitudinal differences in sex chromosome inversions, sex linked allozymes, and mitochondrial DNA variation in <i>Drosophila subobscura</i> . <i>Genetica</i> , 1993, 92, 67-74. | 1.1 | 5 |
| 85 | Genome mining and sequence analysis of chemosensory soluble proteins in arthropods. <i>Methods in Enzymology</i> , 2020, 642, 1-20. | 1.0 | 5 |
| 86 | On the shoulder of giants: Mitogenome recovery from non-targeted genome projects for phylogenetic inference and molecular evolution studies. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 5-30. | 1.4 | 5 |
| 87 | Palaeoceanographic changes in the late Pliocene promoted rapid diversification in pelagic seabirds. <i>Journal of Biogeography</i> , 2022, 49, 171-188. | 3.0 | 5 |
| 88 | The First Genome of the Balearic Shearwater (<i>Puffinus mauretanicus</i>) Provides a Valuable Resource for Conservation Genomics and Sheds Light on Adaptation to a Pelagic lifestyle. <i>Genome Biology and Evolution</i> , 2022, 14, . | 2.5 | 4 |
| 89 | Positive Selection Versus Demography: Evolutionary Inferences Based on an Unusual Haplotype Structure in <i>Drosophila simulans</i> . <i>Molecular Biology and Evolution</i> , 2006, 23, 1643-1647. | 8.9 | 3 |
| 90 | Positive selection in extra cellular domains in the diversification of <i>Strigamia maritima</i> chemoreceptors. <i>Frontiers in Ecology and Evolution</i> , 2015, 3, . | 2.2 | 3 |

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|----|--|-----|-----------|
| 91 | The chloroplast genome of the pincushion cactus <i>Mammillaria haageana</i> subsp. <i>san-angelensis</i> , a Mexican endangered species. <i>Mitochondrial DNA Part B: Resources</i> , 2020, 5, 2038-2039. | 0.4 | 3 |
| 92 | Comment on "The Molecular Evolutionary Patterns of the Insulin/FOXO Signaling Pathway". <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S11915. | 1.2 | 2 |
| 93 | Computational prediction of the phenotypic effects of genetic variants: basic concepts and some application examples in <i>Drosophila</i> nervous system genes. <i>Journal of Neurogenetics</i> , 2017, 31, 307-319. | 1.4 | 2 |