

# Julio Rozas

## List of Publications by Year in descending order

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93  
papers

35,846  
citations

81900

39  
h-index

39675

94  
g-index

103  
all docs

103  
docs citations

103  
times ranked

36898  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Palaeoceanographic changes in the late Pliocene promoted rapid diversification in pelagic seabirds. <i>Journal of Biogeography</i> , 2022, 49, 171-188.	3.0	5
3	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
4	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
5	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
6	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
7	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
8	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
9	Cryptic species delineation in freshwater planarians of the genus <i>Dugesia</i> (Platyhelminthes, Tj ETQq1 1 0.784314 rgBT /Overlock 10 variability. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106496.	2.7	24
10	Evolutionary History of Major Chemosensory Gene Families across Panarthropoda. <i>Molecular Biology and Evolution</i> , 2020, 37, 3601-3615.	8.9	10
11	Dense sampling of bird diversity increases power of comparative genomics. <i>Nature</i> , 2020, 587, 252-257.	27.8	251
12	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
13	Understanding the Early Evolutionary Stages of a Tandem <i>Drosophilamelanogaster</i> -Specific Gene Family: A Structural and Functional Population Study. <i>Molecular Biology and Evolution</i> , 2020, 37, 2584-2600.	8.9	12
14	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
15	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
16	<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
17	Genome mining and sequence analysis of chemosensory soluble proteins in arthropods. <i>Methods in Enzymology</i> , 2020, 642, 1-20.	1.0	5
18	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>GigaScience</i> , 2019, 8, .	6.4	25

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19	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
20	Gene duplications in the E. coli genome: common themes among pathotypes. <i>BMC Genomics</i> , 2019, 20, 313.	2.8	7
21	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
22	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
23	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
24	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
25	DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. <i>Molecular Biology and Evolution</i> , 2017, 34, 3299-3302.	8.9	4,056
26	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
27	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
28	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
29	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
30	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
31	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
32	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	12.8	450
33	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
34	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
35	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
36	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	2.5	34

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37	Evolutionary Analysis of Mitogenomes from Parasitic and Free-Living Flatworms. PLoS ONE, 2015, 10, e0120081.	2.5	44
38	Genome-Wide Analysis of Adaptive Molecular Evolution in the Carnivorous Plant <i>Utricularia gibba</i> . Genome Biology and Evolution, 2015, 7, 444-456.	2.5	33
39	High Gene Family Turnover Rates and Gene Space Adaptation in the Compact Genome of the Carnivorous Plant <i>Utricularia gibba</i> . Molecular Biology and Evolution, 2015, 32, 1284-1295.	8.9	53
40	<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. Antimicrobial Agents and Chemotherapy, 2015, 59, 2006-2015.	3.2	15
41	Comparative analysis of tissue-specific transcriptomes in the funnel-web spider <i>Macrothele calpeiana</i> (Araneae, Hexathelidae). PeerJ, 2015, 3, e1064.	2.0	14
42	Mycobacterial Phylogenomics: An Enhanced Method for Gene Turnover Analysis Reveals Uneven Levels of Gene Gain and Loss among Species and Gene Families. Genome Biology and Evolution, 2014, 6, 1454-1465.	2.5	13
43	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . PLoS Biology, 2014, 12, e1002005.	5.6	221
44	Family Size Evolution in <i>Drosophila</i> Chemosensory Gene Families: A Comparative Analysis with a Critical Appraisal of Methods. Genome Biology and Evolution, 2014, 6, 1669-1682.	2.5	40
45	Insights into the origin and distribution of biodiversity in the Brazilian Atlantic forest hot spot: a statistical phylogeographic study using a low-dispersal organism. Heredity, 2014, 112, 656-665.	2.6	60
46	The coffee genome provides insight into the convergent evolution of caffeine biosynthesis. Science, 2014, 345, 1181-1184.	12.6	520
47	Uncovering the Functional Constraints Underlying the Genomic Organization of the Odorant-Binding Protein Genes. Genome Biology and Evolution, 2013, 5, 2096-2108.	2.5	6
48	Comment on "The Molecular Evolutionary Patterns of the Insulin/FOXO Signaling Pathway". Evolutionary Bioinformatics, 2013, 9, EBO.S11915.	1.2	2
49	PopDrowser: the Population <i>Drosophila</i> Browser. Bioinformatics, 2012, 28, 595-596.	4.1	20
50	Molecular Population Genetics of the Insulin/TOR Signal Transduction Pathway: A Network-Level Analysis in <i>Drosophila melanogaster</i> . Molecular Biology and Evolution, 2012, 29, 123-132.	8.9	17
51	BadiRate: estimating family turnover rates by likelihood-based methods. Bioinformatics, 2012, 28, 279-281.	4.1	108
52	Functional evidence that a recently evolved <i>Drosophila</i> sperm-specific gene boosts sperm competition. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2043-2048.	7.1	53
53	The <i>Drosophila melanogaster</i> Genetic Reference Panel. Nature, 2012, 482, 173-178.	27.8	1,756
54	Unique Features of Odorant-Binding Proteins of the Parasitoid Wasp <i>Nasonia vitripennis</i> Revealed by Genome Annotation and Comparative Analyses. PLoS ONE, 2012, 7, e43034.	2.5	62

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55	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
56	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
57	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
58	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
59	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
60	Genome Sequence of the Pea Aphid <i>Acyrtosiphon pisum</i> . <i>PLoS Biology</i> , 2010, 8, e1000313.	5.6	913
61	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
62	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
63	Molecular evolution of the major chemosensory gene families in insects. <i>Heredity</i> , 2009, 103, 208-216.	2.6	430
64	DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. <i>Bioinformatics</i> , 2009, 25, 1451-1452.	4.1	13,645
65	DNA Sequence Polymorphism Analysis Using DnaSP. <i>Methods in Molecular Biology</i> , 2009, 537, 337-350.	0.9	293
66	RPS4Y gene family evolution in primates. <i>BMC Evolutionary Biology</i> , 2008, 8, 142.	3.2	33
67	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
68	Statistical Power Analysis of Neutrality Tests Under Demographic Expansions, Contractions and Bottlenecks With Recombination. <i>Genetics</i> , 2008, 179, 555-567.	2.9	242
69	Unusual Pattern of Nucleotide Sequence Variation at the OS-E and OS-F Genomic Regions of <i>Drosophila simulans</i> . <i>Genetics</i> , 2007, 175, 1923-1935.	2.9	6
70	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
71	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
72	Genome-wide DNA polymorphism analyses using VariScan. <i>BMC Bioinformatics</i> , 2006, 7, 409.	2.6	115

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73	Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2006, 23, 1642-1642.	8.9	19
74	Unexpected High Polymorphism at the FABP4 Gene Unveils a Complex History for Pig Populations. <i>Genetics</i> , 2006, 174, 2119-2127.	2.9	35
75	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
76	Chromosomal Inversion Polymorphism Leads to Extensive Genetic Structure. <i>Genetics</i> , 2005, 169, 1573-1581.	2.9	55
77	VariScan: Analysis of evolutionary patterns from large-scale DNA sequence polymorphism data. <i>Bioinformatics</i> , 2005, 21, 2791-2793.	4.1	120
78	DnaSP, DNA polymorphism analyses by the coalescent and other methods. <i>Bioinformatics</i> , 2003, 19, 2496-2497.	4.1	5,561
79	Nucleotide Polymorphism in the Rpl215 Gene Region of the Insular Species <i>Drosophila guanache</i> : Reduced Efficacy of Weak Selection on Synonymous Variation. <i>Molecular Biology and Evolution</i> , 2003, 20, 1867-1875.	8.9	13
80	Large-Scale Adaptive Hitchhiking Upon High Recombination in <i>Drosophila simulans</i> . <i>Genetics</i> , 2003, 165, 895-900.	2.9	27
81	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
82	Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2002, 19, 2092-2100.	8.9	1,770
83	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
84	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
85	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
86	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
87	Molecular and Chromosomal Phylogeny in the <i>Obscura</i> 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
88	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
89	Nucleotide Polymorphism at the <i>rp49</i> 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
90	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

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91	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
92	Transfer of genetic information in the rp49 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
93	A Program to Optimize the Design of Oligonucleotides for PCR Amplification. <i>Journal of Heredity</i> , 1991, 82, 84-84.	2.4	6