

Miguel Arenas

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

2,178
citations

236833

25
h-index

265120

42
g-index

76
all docs

76
docs citations

76
times ranked

2739
citing authors

#	ARTICLE	IF	CITATIONS
1	Recombination in viruses: Mechanisms, methods of study, and evolutionary consequences. <i>Infection, Genetics and Evolution</i> , 2015, 30, 296-307.	1.0	255
2	Consequences of Range Contractions and Range Shifts on Molecular Diversity. <i>Molecular Biology and Evolution</i> , 2012, 29, 207-218.	3.5	204
3	Genetic consequences of habitat fragmentation during a range expansion. <i>Heredity</i> , 2014, 112, 291-299.	1.2	128
4	Trends in substitution models of molecular evolution. <i>Frontiers in Genetics</i> , 2015, 6, 319.	1.1	115
5	Coalescent Simulation of Intracodon Recombination. <i>Genetics</i> , 2010, 184, 429-437.	1.2	72
6	The Effect of Recombination on the Reconstruction of Ancestral Sequences. <i>Genetics</i> , 2010, 184, 1133-1139.	1.2	72
7	Forensic genetics and genomics: Much more than just a human affair. <i>PLoS Genetics</i> , 2017, 13, e1006960.	1.5	71
8	Ecological connectivity shapes quasispecies structure of <scp>RNA</scp> viruses in an Antarctic lake. <i>Molecular Ecology</i> , 2015, 24, 4812-4825.	2.0	56
9	Simulation of Molecular Data under Diverse Evolutionary Scenarios. <i>PLoS Computational Biology</i> , 2012, 8, e1002495.	1.5	55
10	Microbial sequence typing in the genomic era. <i>Infection, Genetics and Evolution</i> , 2018, 63, 346-359.	1.0	50
11	Recodon: Coalescent simulation of coding DNA sequences with recombination, migration and demography. <i>BMC Bioinformatics</i> , 2007, 8, 458.	1.2	49
12	Protein evolution along phylogenetic histories under structurally constrained substitution models. <i>Bioinformatics</i> , 2013, 29, 3020-3028.	1.8	48
13	Influence of Admixture and Paleolithic Range Contractions on Current European Diversity Gradients. <i>Molecular Biology and Evolution</i> , 2013, 30, 57-61.	3.5	48
14	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. <i>Molecular Biology and Evolution</i> , 2015, 32, 2195-2207.	3.5	48
15	Survey of Crimean-Congo Hemorrhagic Fever Enzootic Focus, Spain, 2011â€“2015. <i>Emerging Infectious Diseases</i> , 2019, 25, 1177-1184.	2.0	42
16	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. <i>Bioinformatics</i> , 2019, 35, 4480-4483.	1.8	41
17	Simulation of Genome-Wide Evolution under Heterogeneous Substitution Models and Complex Multispecies Coalescent Histories. <i>Molecular Biology and Evolution</i> , 2014, 31, 1295-1301.	3.5	39
18	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. <i>Molecular Biology and Evolution</i> , 2016, 33, 946-958.	3.5	36

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19	High-throughput sequencing (HTS) for the analysis of viral populations. <i>Infection, Genetics and Evolution</i> , 2020, 80, 104208.	1.0	35
20	Phylodynamics of HIV-1 from a Phase III AIDS Vaccine Trial in Bangkok, Thailand. <i>PLoS ONE</i> , 2011, 6, e16902.	1.1	34
21	The importance and application of the ancestral recombination graph. <i>Frontiers in Genetics</i> , 2013, 4, 206.	1.1	32
22	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. <i>Infection, Genetics and Evolution</i> , 2018, 63, 295-306.	1.0	32
23	Influence of mutation and recombination on HIV-1 in vitro fitness recovery. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 264-270.	1.2	31
24	Coestimation of recombination, substitution and molecular adaptation rates by approximate Bayesian computation. <i>Heredity</i> , 2014, 112, 255-264.	1.2	30
25	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. <i>Systematic Biology</i> , 2017, 66, syw121.	2.7	29
26	Computational Design of Centralized HIV-1 Genes. <i>Current HIV Research</i> , 2010, 8, 613-621.	0.2	27
27	Ethnic differences in the adaptation rate of HIV gp120 from a vaccine trial. <i>Retrovirology</i> , 2009, 6, 67.	0.9	26
28	Substitution Rates Predicted by Stability-Constrained Models of Protein Evolution Are Not Consistent with Empirical Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 743-755.	3.5	24
29	Heterogeneous recombination among Hepatitis B virus genotypes. <i>Infection, Genetics and Evolution</i> , 2017, 54, 486-490.	1.0	23
30	Characterization of Reticulate Networks Based on the Coalescent with Recombination. <i>Molecular Biology and Evolution</i> , 2008, 25, 2517-2520.	3.5	22
31	Epiphytic fungal community in <i>Vitis vinifera</i> of the Portuguese wine regions. <i>Letters in Applied Microbiology</i> , 2018, 66, 93-102.	1.0	21
32	CodABC: A Computational Framework to Coestimate Recombination, Substitution, and Molecular Adaptation Rates by Approximate Bayesian Computation. <i>Molecular Biology and Evolution</i> , 2015, 32, 1109-1112.	3.5	20
33	Analysis of selection in protein-coding sequences accounting for common biases. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	20
34	Characterization of rare ABCC8 variants identified in Spanish pulmonary arterial hypertension patients. <i>Scientific Reports</i> , 2020, 10, 15135.	1.6	19
35	Advances in Computer Simulation of Genome Evolution: Toward More Realistic Evolutionary Genomics Analysis by Approximate Bayesian Computation. <i>Journal of Molecular Evolution</i> , 2015, 80, 189-192.	0.8	18
36	ProtASR2: Ancestral reconstruction of protein sequences accounting for folding stability. <i>Methods in Ecology and Evolution</i> , 2020, 11, 248-257.	2.2	17

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37	Evolutionary dynamics of the human pseudoautosomal regions. <i>PLoS Genetics</i> , 2021, 17, e1009532.	1.5	16
38	Spatial and Temporal Simulation of Human Evolution. <i>Methods, Frameworks and Applications. Current Genomics</i> , 2014, 15, 245-255.	0.7	16
39	Computer Programs and Methodologies for the Simulation of DNA Sequence Data with Recombination. <i>Frontiers in Genetics</i> , 2013, 4, 9.	1.1	15
40	The Early Peopling of the Philippines based on mtDNA. <i>Scientific Reports</i> , 2020, 10, 4901.	1.6	15
41	Contrasting evolutionary patterns in populations of demersal sharks throughout the western Mediterranean. <i>Marine Biology</i> , 2018, 165, 1.	0.7	14
42	The Molecular Clock in the Evolution of Protein Structures. <i>Systematic Biology</i> , 2019, 68, 987-1002.	2.7	14
43	Genetic Consequences of Antiviral Therapy on HIV-1. <i>Computational and Mathematical Methods in Medicine</i> , 2015, 2015, 1-9.	0.7	13
44	Evaluating the Neolithic Expansion at Both Shores of the Mediterranean Sea. <i>Molecular Biology and Evolution</i> , 2017, 34, 3232-3242.	3.5	13
45	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
46	Influence of mutation bias and hydrophobicity on the substitution rates and sequence entropies of protein evolution. <i>PeerJ</i> , 2018, 6, e5549.	0.9	12
47	Characterization of phylogenetic networks with NetTest. <i>BMC Bioinformatics</i> , 2010, 11, 268.	1.2	11
48	Consequences of Substitution Model Selection on Protein Ancestral Sequence Reconstruction. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
49	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. <i>Methods in Molecular Biology</i> , 2019, 1851, 215-231.	0.4	9
50	Joint analysis of species and genetic variation to quantify the role of dispersal and environmental constraints in community turnover. <i>Ecography</i> , 2022, 2022, .	2.1	9
51	Consequences of diverse evolutionary processes on american genetic gradients of modern humans. <i>Heredity</i> , 2018, 121, 548-556.	1.2	8
52	Protein Evolution in the Flaviviruses. <i>Journal of Molecular Evolution</i> , 2020, 88, 473-476.	0.8	8
53	Prediction and analysis of binding affinities for chemically diverse HIV PR inhibitors by the modified SAFE_p approach. <i>Journal of Computational Chemistry</i> , 2009, 30, 1229-1240.	1.5	7
54	Analyzing the functional divergence of Slo1 and Slo3 channel subfamilies. <i>Molecular Phylogenetics and Evolution</i> , 2019, 133, 33-41.	1.2	7

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55	Simulation of coding sequence evolution. , 2012, , 126-132.		7
56	HIV Protease and Integrase Empirical Substitution Models of Evolution: Protein-Specific Models Outperform Generalist Models. <i>Genes</i> , 2022, 13, 61.	1.0	6
57	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. <i>Scientific Reports</i> , 2019, 9, 7825.	1.6	5
58	Molecular Evolution of DNA Topoisomerase III Beta (TOP3B) in Metazoa. <i>Journal of Molecular Evolution</i> , 2021, 89, 384-395.	0.8	5
59	Evolutionary History of TOPIIA Topoisomerases in Animals. <i>Journal of Molecular Evolution</i> , 2022, 90, 149-165.	0.8	5
60	Selecting among Alternative Scenarios of Human Evolution by Simulated Genetic Gradients. <i>Genes</i> , 2018, 9, 506.	1.0	4
61	Gradual Distance Dispersal Shapes the Genetic Structure in an Alpine Grasshopper. <i>Genes</i> , 2019, 10, 590.	1.0	4
62	Risk Variants in Three Alzheimer's Disease Genes Show Association with EEG Endophenotypes. <i>Journal of Alzheimer's Disease</i> , 2021, 80, 209-223.	1.2	4
63	Influence of Paleolithic range contraction, admixture and long-distance dispersal on genetic gradients of modern humans in Asia. <i>Molecular Ecology</i> , 2020, 29, 2150-2159.	2.0	4
64	Evaluating Causes of Current Genetic Gradients of Modern Humans of the Iberian Peninsula. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
65	ProteinEvolverABC: coestimation of recombination and substitution rates in protein sequences by approximate Bayesian computation. <i>Bioinformatics</i> , 2021, 38, 58-64.	1.8	3
66	Consequences of the Last Glacial Period on the Genetic Diversity of Southeast Asians. <i>Genes</i> , 2022, 13, 384.	1.0	3
67	Immunoescape of HIV-1 in Env-EL9 CD8 ⁺ T cell response restricted by HLA-B*14:02 in a Non progressor who lost twenty-seven years of HIV-1 control. <i>Retrovirology</i> , 2022, 19, 6.	0.9	3
68	Applications of the Coalescent for the Evolutionary Analysis of Genetic Data. , 2019, , 746-758.		2
69	The influence of heterogeneous codon frequencies along sequences on the estimation of molecular adaptation. <i>Bioinformatics</i> , 2020, 36, 430-436.	1.8	2
70	Computational Analysis of Recombination in Viral Nucleotide Sequences. , 2021, , 108-115.		2
71	Genome-Wide Scan for Five Brain Oscillatory Phenotypes Identifies a New QTL Associated with Theta EEG Band. <i>Brain Sciences</i> , 2020, 10, 870.	1.1	1
72	General considerations for online teaching practices in bioinformatics in the time of COVID 19. <i>Biochemistry and Molecular Biology Education</i> , 2021, 49, 683-684.	0.5	1