Miguel Arenas

List of Publications by Year in descending order

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MICHEL ADENAS

#	Article	IF	CITATIONS
1	Consequences of the Last Glacial Period on the Genetic Diversity of Southeast Asians. Genes, 2022, 13, 384.	2.4	3
2	Evolutionary History of TOPIIA Topoisomerases in Animals. Journal of Molecular Evolution, 2022, 90, 149-165.	1.8	5
3	Joint analysis of species and genetic variation to quantify the role of dispersal and environmental constraints in community turnover. Ecography, 2022, 2022, .	4.5	9
4	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. Retrovirology, 2022, 19, 6.	2.0	3
5	HIV Protease and Integrase Empirical Substitution Models of Evolution: Protein-Specific Models Outperform Generalist Models. Genes, 2022, 13, 61.	2.4	6
6	Consequences of Substitution Model Selection on Protein Ancestral Sequence Reconstruction. Molecular Biology and Evolution, 2022, 39, .	8.9	10
7	Computational Analysis of Recombination in Viral Nucleotide Sequences. , 2021, , 108-115.		2
8	Risk Variants in Three Alzheimer's Disease Genes Show Association with EEG Endophenotypes. Journal of Alzheimer's Disease, 2021, 80, 209-223.	2.6	4
9	Evaluating Causes of Current Genetic Gradients of Modern Humans of the Iberian Peninsula. Genome Biology and Evolution, 2021, 13, .	2.5	3
10	Evolutionary dynamics of the human pseudoautosomal regions. PLoS Genetics, 2021, 17, e1009532.	3.5	16
11	Molecular Evolution of DNA Topoisomerase III Beta (TOP3B) in Metazoa. Journal of Molecular Evolution, 2021, 89, 384-395.	1.8	5
12	General considerations for online teaching practices in bioinformatics in the time of COVID â€19. Biochemistry and Molecular Biology Education, 2021, 49, 683-684.	1.2	1
13	ProteinEvolverABC: coestimation of recombination and substitution rates in protein sequences by approximate Bayesian computation. Bioinformatics, 2021, 38, 58-64.	4.1	3
14	Analysis of selection in protein-coding sequences accounting for common biases. Briefings in Bioinformatics, 2021, 22, .	6.5	20
15	The influence of heterogeneous codon frequencies along sequences on the estimation of molecular adaptation. Bioinformatics, 2020, 36, 430-436.	4.1	2
16	ProtASR2: Ancestral reconstruction of protein sequences accounting for folding stability. Methods in Ecology and Evolution, 2020, 11, 248-257.	5.2	17
17	Genome-Wide Scan for Five Brain Oscillatory Phenotypes Identifies a New QTL Associated with Theta EEG Band. Brain Sciences, 2020, 10, 870.	2.3	1
18	Characterization of rare ABCC8 variants identified in Spanish pulmonary arterial hypertension patients. Scientific Reports, 2020, 10, 15135.	3.3	19

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19	Protein Evolution in the Flaviviruses. Journal of Molecular Evolution, 2020, 88, 473-476.	1.8	8
20	The Early Peopling of the Philippines based on mtDNA. Scientific Reports, 2020, 10, 4901.	3.3	15
21	High-throughput sequencing (HTS) for the analysis of viral populations. Infection, Genetics and Evolution, 2020, 80, 104208.	2.3	35
22	Influence of Paleolithic range contraction, admixture and longâ€distance dispersal on genetic gradients of modern humans in Asia. Molecular Ecology, 2020, 29, 2150-2159.	3.9	4
23	Applications of the Coalescent for the Evolutionary Analysis of Genetic Data. , 2019, , 746-758.		2
24	Gradual Distance Dispersal Shapes the Genetic Structure in an Alpine Grasshopper. Genes, 2019, 10, 590.	2.4	4
25	Spatially explicit analysis reveals complex human genetic gradients in the Iberian Peninsula. Scientific Reports, 2019, 9, 7825.	3.3	5
26	Survey of Crimean-Congo Hemorrhagic Fever Enzootic Focus, Spain, 2011–2015. Emerging Infectious Diseases, 2019, 25, 1177-1184.	4.3	42
27	SPLATCHE3: simulation of serial genetic data under spatially explicit evolutionary scenarios including long-distance dispersal. Bioinformatics, 2019, 35, 4480-4483.	4.1	41
28	The Molecular Clock in the Evolution of Protein Structures. Systematic Biology, 2019, 68, 987-1002.	5.6	14
29	Analyzing the functional divergence of Slo1 and Slo3 channel subfamilies. Molecular Phylogenetics and Evolution, 2019, 133, 33-41.	2.7	7
30	The Influence of Protein Stability on Sequence Evolution: Applications to Phylogenetic Inference. Methods in Molecular Biology, 2019, 1851, 215-231.	0.9	9
31	Substitution Rates Predicted by Stability-Constrained Models of Protein Evolution Are Not Consistent with Empirical Data. Molecular Biology and Evolution, 2018, 35, 743-755.	8.9	24
32	Mutation and recombination in pathogen evolution: Relevance, methods and controversies. Infection, Genetics and Evolution, 2018, 63, 295-306.	2.3	32
33	Microbial sequence typing in the genomic era. Infection, Genetics and Evolution, 2018, 63, 346-359.	2.3	50
34	Epiphytic fungal community in <i>Vitis vinifera</i> of the Portuguese wine regions. Letters in Applied Microbiology, 2018, 66, 93-102.	2.2	21
35	Contrasting evolutionary patterns in populations of demersal sharks throughout the western Mediterranean. Marine Biology, 2018, 165, 1.	1.5	14
36	Selecting among Alternative Scenarios of Human Evolution by Simulated Genetic Gradients. Genes, 2018, 9, 506.	2.4	4

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37	Consequences of diverse evolutionary processes on american genetic gradients of modern humans. Heredity, 2018, 121, 548-556.	2.6	8
38	Influence of mutation bias and hydrophobicity on the substitution rates and sequence entropies of protein evolution. PeerJ, 2018, 6, e5549.	2.0	12
39	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. Systematic Biology, 2017, 66, syw121.	5.6	29
40	Evaluating the Neolithic Expansion at Both Shores of the Mediterranean Sea. Molecular Biology and Evolution, 2017, 34, 3232-3242.	8.9	13
41	Heterogeneous recombination among Hepatitis B virus genotypes. Infection, Genetics and Evolution, 2017, 54, 486-490.	2.3	23
42	Multilocus Sequence Typing of Pathogens. , 2017, , 383-404.		12
43	Forensic genetics and genomics: Much more than just a human affair. PLoS Genetics, 2017, 13, e1006960.	3.5	71
44	Long-Distance Dispersal Shaped Patterns of Human Genetic Diversity in Eurasia. Molecular Biology and Evolution, 2016, 33, 946-958.	8.9	36
45	Influence of mutation and recombination on HIV-1 in vitro fitness recovery. Molecular Phylogenetics and Evolution, 2016, 94, 264-270.	2.7	31
46	Ecological connectivity shapes quasispecies structure of <scp>RNA</scp> viruses in an Antarctic lake. Molecular Ecology, 2015, 24, 4812-4825.	3.9	56
47	Trends in substitution models of molecular evolution. Frontiers in Genetics, 2015, 6, 319.	2.3	115
48	Genetic Consequences of Antiviral Therapy on HIV-1. Computational and Mathematical Methods in Medicine, 2015, 2015, 1-9.	1.3	13
49	Maximum-Likelihood Phylogenetic Inference with Selection on Protein Folding Stability. Molecular Biology and Evolution, 2015, 32, 2195-2207.	8.9	48
50	Recombination in viruses: Mechanisms, methods of study, and evolutionary consequences. Infection, Genetics and Evolution, 2015, 30, 296-307.	2.3	255
51	CodABC: A Computational Framework to Coestimate Recombination, Substitution, and Molecular Adaptation Rates by Approximate Bayesian Computation. Molecular Biology and Evolution, 2015, 32, 1109-1112.	8.9	20
52	Advances in Computer Simulation of Genome Evolution: Toward More Realistic Evolutionary Genomics Analysis by Approximate Bayesian Computation. Journal of Molecular Evolution, 2015, 80, 189-192.	1.8	18
53	Simulation of Genome-Wide Evolution under Heterogeneous Substitution Models and Complex Multispecies Coalescent Histories. Molecular Biology and Evolution, 2014, 31, 1295-1301.	8.9	39
54	Genetic consequences of habitat fragmentation during a range expansion. Heredity, 2014, 112, 291-299.	2.6	128

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55	Coestimation of recombination, substitution and molecular adaptation rates by approximate Bayesian computation. Heredity, 2014, 112, 255-264.	2.6	30
56	Spatial and Temporal Simulation of Human Evolution. Methods, Frameworks and Applications. Current Genomics, 2014, 15, 245-255.	1.6	16
57	Protein evolution along phylogenetic histories under structurally constrained substitution models. Bioinformatics, 2013, 29, 3020-3028.	4.1	48
58	Influence of Admixture and Paleolithic Range Contractions on Current European Diversity Gradients. Molecular Biology and Evolution, 2013, 30, 57-61.	8.9	48
59	Computer Programs and Methodologies for the Simulation of DNA Sequence Data with Recombination. Frontiers in Genetics, 2013, 4, 9.	2.3	15
60	The importance and application of the ancestral recombination graph. Frontiers in Genetics, 2013, 4, 206.	2.3	32
61	Consequences of Range Contractions and Range Shifts on Molecular Diversity. Molecular Biology and Evolution, 2012, 29, 207-218.	8.9	204
62	Simulation of coding sequence evolution. , 2012, , 126-132.		7
63	Simulation of Molecular Data under Diverse Evolutionary Scenarios. PLoS Computational Biology, 2012, 8, e1002495.	3.2	55
64	Phylodynamics of HIV-1 from a Phase III AIDS Vaccine Trial in Bangkok, Thailand. PLoS ONE, 2011, 6, e16902.	2.5	34
65	Characterization of phylogenetic networks with NetTest. BMC Bioinformatics, 2010, 11, 268.	2.6	11
66	Coalescent Simulation of Intracodon Recombination. Genetics, 2010, 184, 429-437.	2.9	72
67	The Effect of Recombination on the Reconstruction of Ancestral Sequences. Genetics, 2010, 184, 1133-1139.	2.9	72
68	Computational Design of Centralized HIV-1 Genes. Current HIV Research, 2010, 8, 613-621.	0.5	27
69	Prediction and analysis of binding affinities for chemically diverse HIVâ€1 PR inhibitors by the modified SAFE_p approach. Journal of Computational Chemistry, 2009, 30, 1229-1240.	3.3	7
70	Ethnic differences in the adaptation rate of HIV gp120 from a vaccine trial. Retrovirology, 2009, 6, 67.	2.0	26
71	Characterization of Reticulate Networks Based on the Coalescent with Recombination. Molecular Biology and Evolution, 2008, 25, 2517-2520.	8.9	22
72	Recodon: Coalescent simulation of coding DNA sequences with recombination, migration and demography. BMC Bioinformatics, 2007, 8, 458.	2.6	49