

Sebastian E Ramos-Onsins

List of Publications by Year in descending order

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52
papers

8,698
citations

257357

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46
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56
all docs

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docs citations

56
times ranked

12443
citing authors

#	ARTICLE	IF	CITATIONS
1	Polygenic adaptation of rosette growth in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2021, 17, e1008748.	1.5	22
2	Genomic Diversity and Evolution of Quasispecies in Newcastle Disease Virus Infections. <i>Viruses</i> , 2020, 12, 1305.	1.5	7
3	The Identification of Runs of Homozygosity Gives a Focus on the Genetic Diversity and Adaptation of the "Charolais de Cuba" Cattle. <i>Animals</i> , 2020, 10, 2233.	1.0	0
4	Porcine Y-chromosome variation is consistent with the occurrence of paternal gene flow from non-Asian to Asian populations. <i>Heredity</i> , 2018, 120, 63-76.	1.2	14
5	The Site Frequency/Dosage Spectrum of Autopolyploid Populations. <i>Frontiers in Genetics</i> , 2018, 9, 480.	1.1	8
6	The neutral frequency spectrum of linked sites. <i>Theoretical Population Biology</i> , 2018, 123, 70-79.	0.5	11
7	Genetic diversity and selection signatures of the beef "Charolais de Cuba"™ breed. <i>Scientific Reports</i> , 2018, 8, 11005.	1.6	9
8	The Evolutionary Consequences of Transposon-Related Pericentromer Expansion in Melon. <i>Genome Biology and Evolution</i> , 2018, 10, 1584-1595.	1.1	20
9	DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. <i>Molecular Biology and Evolution</i> , 2017, 34, 3299-3302.	3.5	4,056
10	Decomposing the Site Frequency Spectrum: The Impact of Tree Topology on Neutrality Tests. <i>Genetics</i> , 2017, 207, 229-240.	1.2	32
11	Optimized Next-Generation Sequencing Genotype-Haplotype Calling for Genome Variability Analysis. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431772388.	0.6	1
12	Improving Bioinformatics Analysis of Large Sequence Datasets Parallelizing Tools for Population Genomics. <i>Lecture Notes in Computer Science</i> , 2017, , 457-467.	1.0	0
13	Identification of protein-damaging mutations in 10 swine taste receptors and 191 appetite-reward genes. <i>BMC Genomics</i> , 2016, 17, 685.	1.2	5
14	Approaching Long Genomic Regions and Large Recombination Rates with msParSm as an Alternative to MaCS. <i>Evolutionary Bioinformatics</i> , 2016, 12, EBO.S40268.	0.6	0
15	On genetic differentiation between domestic pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 190-192.	9.4	4
16	Use of targeted SNP selection for an improved anchoring of the melon (<i>Cucumis melo</i> L.) scaffold genome assembly. <i>BMC Genomics</i> , 2015, 16, 4.	1.2	67
17	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. <i>Molecular Biology and Evolution</i> , 2015, 32, 2760-2774.	3.5	80
18	A generalized Watterson estimator for next-generation sequencing: From trios to autopolyploids. <i>Theoretical Population Biology</i> , 2015, 100, 79-87.	0.5	4

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19	A Deep Catalog of Autosomal Single Nucleotide Variation in the Pig. PLoS ONE, 2015, 10, e0118867.	1.1	22
20	PopGenome: An Efficient Swiss Army Knife for Population Genomic Analyses in R. Molecular Biology and Evolution, 2014, 31, 1929-1936.	3.5	871
21	Resequencing studies of nonmodel organisms using closely related reference genomes: optimal experimental designs and bioinformatics approaches for population genomics. Molecular Ecology, 2014, 23, 1764-1779.	2.0	45
22	Mining the pig genome to investigate the domestication process. Heredity, 2014, 113, 471-484.	1.2	30
23	msPar: A Parallel Coalescent Simulator. Lecture Notes in Computer Science, 2014, , 321-330.	1.0	2
24	Worldwide genetic relationships of pigs as inferred from X chromosome <scp>SNP</scp>s. Animal Genetics, 2013, 44, 130-138.	0.6	9
25	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. BMC Genomics, 2013, 14, 148.	1.2	45
26	Population genomics from pool sequencing. Molecular Ecology, 2013, 22, 5561-5576.	2.0	133
27	Evolution of recombination in eutherian mammals: insights into mechanisms that affect recombination rates and crossover interference. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20131945.	1.2	74
28	Neutrality Tests for Sequences with Missing Data. Genetics, 2012, 191, 1397-1401.	1.2	38
29	Genome-Wide Footprints of Pig Domestication and Selection Revealed through Massive Parallel Sequencing of Pooled DNA. PLoS ONE, 2011, 6, e14782.	1.1	135
30	Evolutionary study of a potential selection target region in the pig. Heredity, 2011, 106, 330-338.	1.2	15
31	Population history in <i>Arabidopsis halleri</i> using multilocus analysis. Molecular Ecology, 2010, 19, 3364-3379.	2.0	11
32	Optimal Neutrality Tests Based on the Frequency Spectrum. Genetics, 2010, 186, 353-365.	1.2	34
33	Assessing the Influence of Adjacent Gene Orientation on the Evolution of Gene Upstream Regions in <i>Arabidopsis thaliana</i> . Genetics, 2010, 185, 695-701.	1.2	4
34	Multilocus Patterns of Nucleotide Diversity, Population Structure and Linkage Disequilibrium in <i>Boechera stricta</i> , a Wild Relative of <i>Arabidopsis</i> . Genetics, 2009, 181, 1021-1033.	1.2	54
35	Multilocus analysis of variation using a large empirical data set: phenylpropanoid pathway genes in <i>Arabidopsis thaliana</i> . Molecular Ecology, 2008, 17, 1211-1223.	2.0	28
36	Statistical Power Analysis of Neutrality Tests Under Demographic Expansions, Contractions and Bottlenecks With Recombination. Genetics, 2008, 179, 555-567.	1.2	242

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37	Population genetic inference using a fixed number of segregating sites: a reassessment. <i>Genetical Research</i> , 2007, 89, 231-244.	0.3	9
38	Mlcoalsim: Multilocus Coalescent Simulations. <i>Evolutionary Bioinformatics</i> , 2007, 3, 117693430700300.	0.6	12
39	Mlcoalsim: multilocus coalescent simulations. <i>Evolutionary Bioinformatics</i> , 2007, 3, 41-4.	0.6	24
40	Highly structured nucleotide variation within and among <i>Arabidopsis lyrata</i> populations at the FAH1 and DFR gene regions. <i>Molecular Ecology</i> , 2006, 15, 2059-2068.	2.0	16
41	Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2006, 23, 1642-1642.	3.5	19
42	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.	3.5	3
43	Birth-and-Death Evolution of the Cecropin Multigene Family in <i>Drosophila</i> . <i>Journal of Molecular Evolution</i> , 2005, 60, 1-11.	0.8	31
44	A Multilocus Sequence Survey in <i>Arabidopsis thaliana</i> Reveals a Genome-Wide Departure From a Neutral Model of DNA Sequence Polymorphism. <i>Genetics</i> , 2005, 169, 1601-1615.	1.2	188
45	Multilocus Analysis of Variation and Speciation in the Closely Related Species <i>Arabidopsis halleri</i> and <i>A. lyrata</i> . <i>Genetics</i> , 2004, 166, 373-388.	1.2	124
46	Statistical Properties of New Neutrality Tests Against Population Growth. <i>Molecular Biology and Evolution</i> , 2002, 19, 2092-2100.	3.5	1,770
47	Primers for 22 candidate genes for ecological adaptations in Brassicaceae. <i>Molecular Ecology Notes</i> , 2002, 2, 258-262.	1.7	48
48	Worldwide DNA sequence variation in a 10-kilobase noncoding region on human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11354-11358.	3.3	175
49	Molecular and Chromosomal Phylogeny in the Obscura Group of <i>Drosophila</i> Inferred from Sequences of the <i>therp49</i> Gene Region. <i>Molecular Phylogenetics and Evolution</i> , 1998, 9, 33-41.	1.2	52
50	Molecular Evolution of the Cecropin Multigene Family in <i>Drosophila</i> : Functional Genes vs. Pseudogenes. <i>Genetics</i> , 1998, 150, 157-171.	1.2	79
51	A Genomic Perspective on Wild Boar Demography and Evolution. , 0, , 376-387.		3
52	Assessing a novel sequencing-based approach for population genomics in non-model species. , 0, , .		2