

Carlos G Schrago

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

3,367
citations

270111

25
h-index

175968

55
g-index

91
all docs

91
docs citations

91
times ranked

7363
citing authors

#	ARTICLE	IF	CITATIONS
1	The performance of outgroup-free rooting under evolutionary radiations. <i>Molecular Phylogenetics and Evolution</i> , 2022, 169, 107434.	1.2	3
2	Challenges in estimating virus divergence times in short epidemic timescales with special reference to the evolution of SARS-CoV-2 pandemic. <i>Genetics and Molecular Biology</i> , 2021, 44, e20200254.	0.6	2
3	Fast speciations and slow genes: uncovering the root of living canids. <i>Biological Journal of the Linnean Society</i> , 2020, 129, 492-504.	0.7	4
4	Molecular systematics reveals the origins of subsociality in tortoise beetles (Coleoptera, Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 Td (1.7	5
5	Employing statistical learning to derive species-level genetic diversity for mammalian species. <i>Mammal Review</i> , 2020, 50, 240-251.	2.2	10
6	Survey for positively selected coding regions in the genome of the hematophagous tsetse fly <i>Glossina morsitans</i> identifies candidate genes associated with feeding habits and embryonic development. <i>Genetics and Molecular Biology</i> , 2020, 43, e20180311.	0.6	1
7	The range of sampling times affects Zika virus evolutionary rates and divergence times. <i>Archives of Virology</i> , 2019, 164, 3027-3034.	0.9	3
8	The Estimated Pacemaker for Great Apes Supports the Hominoid Slowdown Hypothesis. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431985598.	0.6	3
9	Newly Discovered Occurrences and Gene Tree of the Extracellular Globins and Linker Chains from the Giant Hexagonal Bilayer Hemoglobin in Metazoans. <i>Genome Biology and Evolution</i> , 2019, 11, 597-612.	1.1	12
10	A multigene timescale and diversification dynamics of Ciliophora evolution. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106521.	1.2	37
11	Large ancestral effective population size explains the difficult phylogenetic placement of owl monkeys. <i>American Journal of Primatology</i> , 2019, 81, e22955.	0.8	18
12	Data partitioning and correction for ascertainment bias reduce the uncertainty of placental mammal divergence times inferred from the morphological clock. <i>Ecology and Evolution</i> , 2019, 9, 2255-2262.	0.8	11
13	Comparative evaluation of macroevolutionary regimes of Ruminantia and selected mammalian lineages. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 814-824.	0.7	1
14	Conservation analysis and decomposition of residue correlation networks in the phospholipase A2 superfamily (PLA2s): Insights into the structure-function relationships of snake venom toxins. <i>Toxicon</i> , 2018, 146, 50-60.	0.8	12
15	Impact of long-term chromosomal shuffling on the multispecies coalescent analysis of two anthropoid primate lineages. <i>Ecology and Evolution</i> , 2018, 8, 1206-1216.	0.8	2
16	Conservation phylogenetics and computational species delimitation of Neotropical primates. <i>Biological Conservation</i> , 2018, 217, 397-406.	1.9	11
17	Discovery of Novel Hemocyanin-Like Genes in Metazoans. <i>Biological Bulletin</i> , 2018, 235, 134-151.	0.7	19
18	Appropriate Assignment of Fossil Calibration Information Minimizes the Difference between Phylogenetic and Pedigree Mutation Rates in Humans. <i>Life</i> , 2018, 8, 49.	1.1	2

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19	Evaluating DNA evidence in a genetically complex population. <i>Forensic Science International: Genetics</i> , 2018, 36, 141-147.	1.6	5
20	Comparative evaluation of maximum parsimony and Bayesian phylogenetic reconstruction using empirical morphological data. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1477-1484.	0.8	47
21	Incomplete lineage sorting impacts the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed: An analysis based on Cetacea. <i>Ecology and Evolution</i> , 2018, 8, 6965-6971.	0.8	5
22	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. <i>Journal of Evolutionary Biology</i> , 2018, 31, 1623-1631.	0.8	7
23	Co-circulation of Araraquara and Juquitiba Hantavirus in Brazilian Cerrado. <i>Microbial Ecology</i> , 2018, 75, 783-789.	1.4	8
24	New bunya-like viruses: Highlighting their relations. <i>Infection, Genetics and Evolution</i> , 2017, 49, 164-173.	1.0	13
25	Multilocus phylogeny and statistical biogeography clarify the evolutionary history of major lineages of turtles. <i>Molecular Phylogenetics and Evolution</i> , 2017, 113, 59-66.	1.2	120
26	Evolutionary analysis of Chironius snakes unveils cryptic diversity and provides clues to diversification in the Neotropics. <i>Molecular Phylogenetics and Evolution</i> , 2017, 116, 108-119.	1.2	12
27	Discovery and evolution of novel hemerythrin genes in annelid worms. <i>BMC Evolutionary Biology</i> , 2017, 17, 85.	3.2	12
28	Broad Phylogenetic Occurrence of the Oxygen-Binding Hemerythrins in Bilaterians. <i>Genome Biology and Evolution</i> , 2017, 9, 2580-2591.	1.1	9
29	Performance of Hidden Markov Models in Recovering the Standard Classification of Glycoside Hydrolases. <i>Evolutionary Bioinformatics</i> , 2017, 13, 117693431770340.	0.6	7
30	Arrival and diversification of mabuyine skinks (Squamata: Scincidae) in the Neotropics based on a fossil-calibrated timetree. <i>PeerJ</i> , 2017, 5, e3194.	0.9	10
31	Geological Changes of the Americas and their Influence on the Diversification of the Neotropical Kissing Bugs (Hemiptera: Reduviidae: Triatominae). <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004527.	1.3	72
32	Detection and sequencing of Zika virus from amniotic fluid of fetuses with microcephaly in Brazil: a case study. <i>Lancet Infectious Diseases</i> , The, 2016, 16, 653-660.	4.6	981
33	Expanded phylogenetic analyses of the class Heterotrichea (Ciliophora, Postciliodesmatophora) using five molecular markers and morphological data. <i>Molecular Phylogenetics and Evolution</i> , 2016, 95, 229-246.	1.2	56
34	Evolution of <i>Philodendron</i> (Araceae) species in Neotropical biomes. <i>PeerJ</i> , 2016, 4, e1744.	0.9	17
35	Redescription and Phylogenetic Position of <i>Condylostoma arenarium</i> Spiegel, 1926 (Ciliophora,) Tj ETQq1 1 0,784314,rgBT /O	0.8	8
36	Diversification of the Genus <i>Anopheles</i> and a Neotropical Clade from the Late Cretaceous. <i>PLoS ONE</i> , 2015, 10, e0134462.	1.1	29

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37	Complete genome sequences of two new virus isolates associated with cotton blue disease resistance breaking in Brazil. <i>Archives of Virology</i> , 2015, 160, 1371-1374.	0.9	23
38	Long-Read Single Molecule Sequencing to Resolve Tandem Gene Copies: The <i>Mst77Y</i> Region on the <i>Drosophila melanogaster</i> Y Chromosome. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1145-1150.	0.8	40
39	Detection of different South American hantaviruses. <i>Virus Research</i> , 2015, 210, 106-113.	1.1	19
40	Characterization and comparative analysis of a simian foamy virus complete genome isolated from Brazilian capuchin monkeys. <i>Virus Research</i> , 2015, 208, 1-6.	1.1	8
41	The influence of taxon sampling on Bayesian divergence time inference under scenarios of rate heterogeneity among lineages. <i>Journal of Theoretical Biology</i> , 2015, 364, 31-39.	0.8	33
42	Performance of genomic data sets on the estimation of the divergence time of New World and Old World anthropoids. <i>Genetics and Molecular Research</i> , 2014, 13, 1425-1437.	0.3	0
43	Characterization of Juititba Virus in <i>Oligoryzomys fornesi</i> from Brazilian Cerrado. <i>Viruses</i> , 2014, 6, 1473-1482.	1.5	15
44	Analysis of Adaptive Evolution in Lyssavirus Genomes Reveals Pervasive Diversifying Selection during Species Diversification. <i>Viruses</i> , 2014, 6, 4465-4478.	1.5	4
45	Multispecies Coalescent Analysis of the Early Diversification of Neotropical Primates: Phylogenetic Inference under Strong Gene Trees/Species Tree Conflict. <i>Genome Biology and Evolution</i> , 2014, 6, 3105-3114.	1.1	15
46	Sigmodontine rodents diversified in South America prior to the complete rise of the Panamanian Isthmus. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2014, 52, 249-256.	0.6	31
47	The Effective Population Sizes of the Anthropoid Ancestors of the Human-Chimpanzee Lineage Provide Insights on the Historical Biogeography of the Great Apes. <i>Molecular Biology and Evolution</i> , 2014, 31, 37-47.	3.5	32
48	Estimation of the ancestral effective population sizes of African great apes under different selection regimes. <i>Genetica</i> , 2014, 142, 273-280.	0.5	6
49	The limiting distribution of the effective population size of the ancestor of humans and chimpanzees. <i>Journal of Theoretical Biology</i> , 2014, 357, 55-61.	0.8	5
50	Morphology and Phylogenetic Position of an Unusual <i>Stentor polymorphus</i> (Ciliophora: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 22	0.8	8
51	Assignment of Calibration Information to Deeper Phylogenetic Nodes is More Effective in Obtaining Precise and Accurate Divergence Time Estimates. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13908.	0.6	18
52	Floral Evolution of <i>Philodendron</i> Subgenus <i>Meconostigma</i> (Araceae). <i>PLoS ONE</i> , 2014, 9, e89701.	1.1	10
53	Phylogenetic analysis of the S segment from Juititba hantavirus: Identification of two distinct lineages in <i>Oligoryzomys nigripes</i> . <i>Infection, Genetics and Evolution</i> , 2013, 18, 262-268.	1.0	17
54	Combining fossil and molecular data to date the diversification of New World Primates. <i>Journal of Evolutionary Biology</i> , 2013, 26, 2438-2446.	0.8	35

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55	The precision of the hominid timescale estimated by relaxed clock methods. <i>Journal of Evolutionary Biology</i> , 2013, 26, 746-755.	0.8	29
56	Positive selection along the evolution of primate mitogenomes. <i>Mitochondrion</i> , 2013, 13, 846-851.	1.6	11
57	Phylogeny and chronology of the major lineages of New World hystricognath rodents: insights on the biogeography of the Eocene/Oligocene arrival of mammals in South America. <i>BMC Research Notes</i> , 2013, 6, 160.	0.6	57
58	Boronated tartrolon antibiotic produced by symbiotic cellulose-degrading bacteria in shipworm gills. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E295-304.	3.3	89
59	Conventional Simulation of Biological Sequences Leads to a Biased Assessment of Multi-Loci Phylogenetic Analysis. <i>Evolutionary Bioinformatics</i> , 2013, 9, EBO.S12483.	0.6	3
60	The Influence of Taxon Sampling and Tree Shape on Molecular Dating: An Empirical Example from Mammalian Mitochondrial Genomes. <i>Bioinformatics and Biology Insights</i> , 2012, 6, BBI.S9677.	1.0	18
61	Impact of the Partitioning Scheme on Divergence Times Inferred from Mammalian Genomic Data Sets. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9627.	0.6	7
62	Testing Synchrony in Historical Biogeography: The Case of New World Primates and Hystricognathi Rodents. <i>Evolutionary Bioinformatics</i> , 2012, 8, EBO.S9008.	0.6	19
63	Global alteration of microRNAs and transposon-derived small RNAs in cotton (<i>Gossypium hirsutum</i>) during Cotton leafroll dwarf polerovirus (CLRDV) infection. <i>Plant Molecular Biology</i> , 2012, 80, 443-460.	2.0	46
64	Detection of the first incidence of <i>Akodon paranaensis</i> naturally infected with the Jabora virus strain (Hantavirus) in Brazil. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2012, 107, 424-428.	0.8	14
65	Incorrect handling of calibration information in divergence time inference: an example from volcanic islands. <i>Ecology and Evolution</i> , 2012, 2, 493-500.	0.8	10
66	Comparative evolutionary epidemiology of dengue virus serotypes. <i>Infection, Genetics and Evolution</i> , 2012, 12, 309-314.	1.0	69
67	Molecular evolution of α 4 integrin binding site to lentiviral envelope proteins in new world primates. <i>Infection, Genetics and Evolution</i> , 2012, 12, 1501-1507.	1.0	14
68	Chronology of Deep Nodes in the Neotropical Primate Phylogeny: Insights from Mitochondrial Genomes. <i>PLoS ONE</i> , 2012, 7, e51699.	1.1	31
69	The Use of Bioinformatics for Studying HIV Evolutionary and Epidemiological History in South America. <i>AIDS Research and Treatment</i> , 2011, 2011, 1-13.	0.3	12
70	Profile of small interfering RNAs from cotton plants infected with the polerovirus Cotton leafroll dwarf virus. <i>BMC Molecular Biology</i> , 2011, 12, 40.	3.0	55
71	Molecular characterization of BK polyomavirus subtypes in renal transplant recipients in Brazil. <i>Journal of Medical Virology</i> , 2011, 83, 1401-1405.	2.5	16
72	Phylogenetic Status and Timescale for the Diversification of <i>Steno</i> and <i>Sotalia</i> Dolphins. <i>PLoS ONE</i> , 2011, 6, e28297.	1.1	29

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73	Evolution of TRIM5 ^Δ B30.2 (SPRY) domain in New World primates. <i>Infection, Genetics and Evolution</i> , 2010, 10, 246-253.	1.0	22
74	Phylogenetic nomenclature and evolution of mannose-binding lectin (MBL2) haplotypes. <i>BMC Genetics</i> , 2010, 11, 38.	2.7	42
75	The evolution of South American endemic canids: a history of rapid diversification and morphological parallelism. <i>Journal of Evolutionary Biology</i> , 2010, 23, 311-322.	0.8	91
76	Functional Copies of the <i>Mst77F</i> Gene on the Y Chromosome of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2010, 184, 295-307.	1.2	38
77	Differential Evolution of Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Genes Between HAART-Failing and Naive- Treated Individuals. <i>Current HIV Research</i> , 2009, 7, 601-605.	0.2	10
78	The origin of South American HIV-1 subtype C: lack of evidence for a Mozambican ancestry. <i>Aids</i> , 2009, 23, 1926-1928.	1.0	6
79	Evolution of the B3 DNA Binding Superfamily: New Insights into REM Family Gene Diversification. <i>PLoS ONE</i> , 2009, 4, e5791.	1.1	128
80	Positive Selection on HIV Accessory Proteins and the Analysis of Molecular Adaptation After Interspecies Transmission. <i>Journal of Molecular Evolution</i> , 2008, 66, 598-604.	0.8	6
81	On the origin of HIV-1 subtype C in South America. <i>Aids</i> , 2008, 22, 2001-2011.	1.0	33
82	The Role of bZIP Transcription Factors in Green Plant Evolution: Adaptive Features Emerging from Four Founder Genes. <i>PLoS ONE</i> , 2008, 3, e2944.	1.1	251
83	On the time scale of new world primate diversification. <i>American Journal of Physical Anthropology</i> , 2007, 132, 344-354.	2.1	89
84	Epidemiologic and Evolutionary Trends of HIV-1 CRF31_BC-Related Strains in Southern Brazil. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2007, 45, 328-333.	0.9	37
85	An empirical examination of the standard errors of maximum likelihood phylogenetic parameters under the molecular clock via bootstrapping. <i>Genetics and Molecular Research</i> , 2006, 5, 233-41.	0.3	3
86	CCR5 chemokine receptor gene evolution in New World monkeys (Platyrrhini, Primates): implication on resistance to lentiviruses. <i>Infection, Genetics and Evolution</i> , 2005, 5, 271-280.	1.0	24
87	MamMiBase: a mitochondrial genome database for mammalian phylogenetic studies. <i>Bioinformatics</i> , 2005, 21, 2566-2567.	1.8	15
88	Analysis of differential selective forces acting on the coat protein (P3) of the plant virus family Luteoviridae. <i>Genetics and Molecular Research</i> , 2005, 4, 790-802.	0.3	5
89	Timing the Origin of New World Monkeys. <i>Molecular Biology and Evolution</i> , 2003, 20, 1620-1625.	3.5	145