Carlos G Schrago

List of Publications by Year
in descending order

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89
papers

3,367
citations

236912
25
h-index

155644
55
g-index

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all docs

91
docs citations

91
times ranked

6664
citing authors

#	Article	IF	Citations
1	Detection and sequencing of Zika virus from amniotic fluid of fetuses with microcephaly in Brazil: a case study. Lancet Infectious Diseases, The, 2016, 16, 653-660.	9.1	981
2	The Role of bZIP Transcription Factors in Green Plant Evolution: Adaptive Features Emerging from Four Founder Genes. PLoS ONE, 2008, 3, e2944.	2.5	251
3	Timing the Origin of New World Monkeys. Molecular Biology and Evolution, 2003, 20, 1620-1625.	8.9	145
4	Evolution of the B3 DNA Binding Superfamily: New Insights into REM Family Gene Diversification. PLoS ONE, 2009, 4, e5791.	2.5	128
5	Multilocus phylogeny and statistical biogeography clarify the evolutionary history of major lineages of turtles. Molecular Phylogenetics and Evolution, 2017, 113, 59-66.	2.7	120
6	The evolution of South American endemic canids: a history of rapid diversification and morphological parallelism. Journal of Evolutionary Biology, 2010, 23, 311-322.	1.7	91
7	On the time scale of new world primate diversification. American Journal of Physical Anthropology, 2007, 132, 344-354.	2.1	89
8	Boronated tartrolon antibiotic produced by symbiotic cellulose-degrading bacteria in shipworm gills. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E295-304.	7.1	89
9	Geological Changes of the Americas and their Influence on the Diversification of the Neotropical Kissing Bugs (Hemiptera: Reduviidae: Triatominae). PLoS Neglected Tropical Diseases, 2016, 10, e0004527.	3.0	72
10	Comparative evolutionary epidemiology of dengue virus serotypes. Infection, Genetics and Evolution, 2012, 12, 309-314.	2.3	69
11	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. BMC Research Notes, 2013, 6, 160.	1.4	57
12	Expanded phylogenetic analyses of the class Heterotrichea (Ciliophora, Postciliodesmatophora) using five molecular markers and morphological data. Molecular Phylogenetics and Evolution, 2016, 95, 229-246.	2.7	56
13	Profile of small interfering RNAs from cotton plants infected with the polerovirus Cotton leafroll dwarf virus. BMC Molecular Biology, 2011, 12, 40.	3.0	55
14	Comparative evaluation of maximum parsimony and Bayesian phylogenetic reconstruction using empirical morphological data. Journal of Evolutionary Biology, 2018, 31, 1477-1484.	1.7	47
15	Global alteration of microRNAs and transposon-derived small RNAs in cotton (Gossypium hirsutum) during Cotton leafroll dwarf polerovirus (CLRDV) infection. Plant Molecular Biology, 2012, 80, 443-460.	3.9	46
16	Phylogenetic nomenclature and evolution of mannose-binding lectin (MBL2) haplotypes. BMC Genetics, 2010, 11, 38.	2.7	42
17	Long-Read Single Molecule Sequencing to Resolve Tandem Gene Copies: The <i>Mst77Y</i> Region on the <i>Drosophila melanogaster</i> Y Chromosome. G3: Genes, Genomes, Genetics, 2015, 5, 1145-1150.	1.8	40
18	Functional Copies of the <i>Mst77F</i> Gene on the Y Chromosome of <i>Drosophila melanogaster</i>. Genetics, 2010, 184, 295-307.	2.9	38

#	ARTICLE	IF	CITATIONS
19	A multigene timescale and diversification dynamics of Ciliophora evolution. Molecular Phylogenetics and Evolution, 2019, 139, 106521.	2.7	37
20	Epidemiologic and Evolutionary Trends of HIV-1 CRF31_BC-Related Strains in Southern Brazil. Journal of Acquired Immune Deficiency Syndromes (1999), 2007, 45, 328-333.	2.1	37
21	Combining fossil and molecular data to date the diversification of New World Primates. Journal of Evolutionary Biology, 2013, 26, 2438-2446.	1.7	35
22	On the origin of HIV-1 subtype C in South America. Aids, 2008, 22, 2001-2011.	2.2	33
23	The influence of taxon sampling on Bayesian divergence time inference under scenarios of rate heterogeneity among lineages. Journal of Theoretical Biology, 2015, 364, 31-39.	1.7	33
24	The Effective Population Sizes of the Anthropoid Ancestors of the Human-Chimpanzee Lineage Provide Insights on the Historical Biogeography of the Great Apes. Molecular Biology and Evolution, 2014, 31, 37-47.	8.9	32
25	Sigmodontine rodents diversified in South America prior to the complete rise of the Panamanian Isthmus. Journal of Zoological Systematics and Evolutionary Research, 2014, 52, 249-256.	1.4	31
26	Chronology of Deep Nodes in the Neotropical Primate Phylogeny: Insights from Mitochondrial Genomes. PLoS ONE, 2012, 7, e51699.	2.5	31
27	The precision of the hominid timescale estimated by relaxed clock methods. Journal of Evolutionary Biology, 2013, 26, 746-755.	1.7	29
28	Diversification of the Genus Anopheles and a Neotropical Clade from the Late Cretaceous. PLoS ONE, 2015, 10, e0134462.	2.5	29
29	Phylogenetic Status and Timescale for the Diversification of Steno and Sotalia Dolphins. PLoS ONE, 2011, 6, e28297.	2.5	29
30	CCR5 chemokine receptor gene evolution in New World monkeys (Platyrrhini, Primates): implication on resistance to lentiviruses. Infection, Genetics and Evolution, 2005, 5, 271-280.	2.3	24
31	Complete genome sequences of two new virus isolates associated with cotton blue disease resistance breaking in Brazil. Archives of Virology, 2015, 160, 1371-1374.	2.1	23
32	Evolution of TRIM5Î± B30.2 (SPRY) domain in New World primates. Infection, Genetics and Evolution, 2010, 10, 246-253.	2.3	22
33	Testing Synchrony in Historical Biogeography: The Case of New World Primates and Hystricognathi Rodents. Evolutionary Bioinformatics, 2012, 8, EBO.S9008.	1.2	19
34	Detection of different South American hantaviruses. Virus Research, 2015, 210, 106-113.	2.2	19
35	Discovery of Novel Hemocyanin-Like Genes in Metazoans. Biological Bulletin, 2018, 235, 134-151.	1.8	19
36	The Influence of Taxon Sampling and Tree Shape on Molecular Dating: An Empirical Example from Mammalian Mitochondrial Genomes. Bioinformatics and Biology Insights, 2012, 6, BBI.S9677.	2.0	18

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37	Assignment of Calibration Information to Deeper Phylogenetic Nodes is More Effective in Obtaining Precise and Accurate Divergence Time Estimates. Evolutionary Bioinformatics, 2014, 10, EBO.S13908.	1.2	18
38	Large ancestral effective population size explains the difficult phylogenetic placement of owl monkeys. American Journal of Primatology, 2019, 81, e22955.	1.7	18
39	Phylogenetic analysis of the S segment from Juquitiba hantavirus: Identification of two distinct lineages in Oligoryzomys nigripes. Infection, Genetics and Evolution, 2013, 18, 262-268.	2.3	17
40	Evolution of<i>Philodendron</i>(Araceae) species in Neotropical biomes. PeerJ, 2016, 4, e1744.	2.0	17
41	Molecular characterization of BK polyomavirus subtypes in renal transplant recipients in Brazil. Journal of Medical Virology, 2011, 83, 1401-1405.	5.0	16
42	MamMiBase: a mitochondrial genome database for mammalian phylogenetic studies. Bioinformatics, 2005, 21, 2566-2567.	4.1	15
43	Characterization of Juquitiba Virus in Oligoryzomys fornesi from Brazilian Cerrado. Viruses, 2014, 6, 1473-1482.	3.3	15
44	Multispecies Coalescent Analysis of the Early Diversification of Neotropical Primates: Phylogenetic Inference under Strong Gene Trees/Species Tree Conflict. Genome Biology and Evolution, 2014, 6, 3105-3114.	2.5	15
45	Detection of the first incidence of Akodon paranaensis naturally infected with the Jabora virus strain (Hantavirus) in Brazil. Memorias Do Instituto Oswaldo Cruz, 2012, 107, 424-428.	1.6	14
46	Molecular evolution of Î±4 integrin binding site to lentiviral envelope proteins in new world primates. Infection, Genetics and Evolution, 2012, 12, 1501-1507.	2.3	14
47	New bunya-like viruses: Highlighting their relations. Infection, Genetics and Evolution, 2017, 49, 164-173.	2.3	13
48	The Use of Bioinformatics for Studying HIV Evolutionary and Epidemiological History in South America. AIDS Research and Treatment, 2011, 2011, 1-13.	0.7	12
49	Evolutionary analysis of Chironius snakes unveils cryptic diversity and provides clues to diversification in the Neotropics. Molecular Phylogenetics and Evolution, 2017, 116, 108-119.	2.7	12
50	Discovery and evolution of novel hemerythrin genes in annelid worms. BMC Evolutionary Biology, 2017, 17, 85.	3.2	12
51	Conservation analysis and decomposition of residue correlation networks in the phospholipase A2 superfamily (PLA2s): Insights into the structure-function relationships of snake venom toxins. Toxicon, 2018, 146, 50-60.	1.6	12
52	Newly Discovered Occurrences and Gene Tree of the Extracellular Globins and Linker Chains from the Giant Hexagonal Bilayer Hemoglobin in Metazoans. Genome Biology and Evolution, 2019, 11, 597-612.	2.5	12
53	Positive selection along the evolution of primate mitogenomes. Mitochondrion, 2013, 13, 846-851.	3.4	11
54	Conservation phylogenetics and computational species delimitation of Neotropical primates. Biological Conservation, 2018, 217, 397-406.	4.1	11

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55	Data partitioning and correction for ascertainment bias reduce the uncertainty of placental mammal divergence times inferred from the morphological clock. Ecology and Evolution, 2019, 9, 2255-2262.	1.9	11
56	Differential Evolution of Human Immunodeficiency Virus Type 1 Protease and Reverse Transcriptase Genes Between HAART-Failing and Naive- Treated Individuals. Current HIV Research, 2009, 7, 601-605.	0.5	10
57	Incorrect handling of calibration information in divergence time inference: an example from volcanic islands. Ecology and Evolution, 2012, 2, 493-500.	1.9	10
58	Employing statistical learning to derive speciesâ€level genetic diversity for mammalian species. Mammal Review, 2020, 50, 240-251.	4.8	10
59	Floral Evolution of Philodendron Subgenus Meconostigma (Araceae). PLoS ONE, 2014, 9, e89701.	2.5	10
60	Arrival and diversification of mabuyine skinks (Squamata: Scincidae) in the Neotropics based on a fossil-calibrated timetree. PeerJ, 2017, 5, e3194.	2.0	10
61	Broad Phylogenetic Occurrence of the Oxygen-Binding Hemerythrins in Bilaterians. Genome Biology and Evolution, 2017, 9, 2580-2591.	2.5	9
62	Morphology and Phylogenetic Position of an Unusual <i>Stentor polymorphus</i> (Ciliophora:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46	1.7	8
63	Redescription and Phylogenetic Position of <i>Condylostoma arenarium</i> Spiegel, 1926 (Ciliophora,) Tj ETQq1 1 0.784314 rgBT /Ov	1.7	8
64	Characterization and comparative analysis of a simian foamy virus complete genome isolated from Brazilian capuchin monkeys. Virus Research, 2015, 208, 1-6.	2.2	8
65	Co-circulation of Araraquara and Juquitiba Hantavirus in Brazilian Cerrado. Microbial Ecology, 2018, 75, 783-789.	2.8	8
66	Impact of the Partitioning Scheme on Divergence Times Inferred from Mammalian Genomic Data Sets. Evolutionary Bioinformatics, 2012, 8, EBO.S9627.	1.2	7
67	Performance of Hidden Markov Models in Recovering the Standard Classification of Glycoside Hydrolases. Evolutionary Bioinformatics, 2017, 13, 117693431770340.	1.2	7
68	Multispecies coalescent analysis confirms standing phylogenetic instability in Hexapoda. Journal of Evolutionary Biology, 2018, 31, 1623-1631.	1.7	7
69	Positive Selection on HIV Accessory Proteins and the Analysis of Molecular Adaptation After Interspecies Transmission. Journal of Molecular Evolution, 2008, 66, 598-604.	1.8	6
70	The origin of South American HIV-1 subtype C: lack of evidence for a Mozambican ancestry. Aids, 2009, 23, 1926-1928.	2.2	6
71	Estimation of the ancestral effective population sizes of African great apes under different selection regimes. Genetica, 2014, 142, 273-280.	1.1	6
72	The limiting distribution of the effective population size of the ancestor of humans and chimpanzees. Journal of Theoretical Biology, 2014, 357, 55-61.	1.7	5

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73	Evaluating DNA evidence in a genetically complex population. Forensic Science International: Genetics, 2018, 36, 141-147.	3.1	5
74	Incomplete lineage sorting impacts the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed: An analysis based on Cetacea. Ecology and Evolution, 2018, 8, 6965-6971.	1.9	5
75	Molecular systematics reveals the origins of subsociality in tortoise beetles (Coleoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	3.9	5
76	Analysis of differential selective forces acting on the coat protein (P3) of the plant virus family Luteoviridae. Genetics and Molecular Research, 2005, 4, 790-802.	0.2	5
77	Analysis of Adaptive Evolution in Lyssavirus Genomes Reveals Pervasive Diversifying Selection during Species Diversification. Viruses, 2014, 6, 4465-4478.	3.3	4
78	Fast speciations and slow genes: uncovering the root of living canids. Biological Journal of the Linnean Society, 2020, 129, 492-504.	1.6	4
79	Conventional Simulation of Biological Sequences Leads to a Biased Assessment of Multi-Loci Phylogenetic Analysis. Evolutionary Bioinformatics, 2013, 9, EBO.S12483.	1.2	3
80	The range of sampling times affects Zika virus evolutionary rates and divergence times. Archives of Virology, 2019, 164, 3027-3034.	2.1	3
81	The Estimated Pacemaker for Great Apes Supports the Hominoid Slowdown Hypothesis. Evolutionary Bioinformatics, 2019, 15, 117693431985598.	1.2	3
82	The performance of outgroup-free rooting under evolutionary radiations. Molecular Phylogenetics and Evolution, 2022, 169, 107434.	2.7	3
83	An empirical examination of the standard errors of maximum likelihood phylogenetic parameters under the molecular clock via bootstrapping. Genetics and Molecular Research, 2006, 5, 233-41.	0.2	3
84	Impact of longâ€term chromosomal shuffling on the multispecies coalescent analysis of two anthropoid primate lineages. Ecology and Evolution, 2018, 8, 1206-1216.	1.9	2
85	Appropriate Assignment of Fossil Calibration Information Minimizes the Difference between Phylogenetic and Pedigree Mutation Rates in Humans. Life, 2018, 8, 49.	2.4	2
86	Challenges in estimating virus divergence times in short epidemic timescales with special reference to the evolution of SARS-CoV-2 pandemic. Genetics and Molecular Biology, 2021, 44, e20200254.	1.3	2
87	Comparative evaluation of macroevolutionary regimes of Ruminantia and selected mammalian lineages. Biological Journal of the Linnean Society, 2018, 123, 814-824.	1.6	1
88	Survey for positively selected coding regions in the genome of the hematophagous tsetse fly Glossina morsitans identifies candidate genes associated with feeding habits and embryonic development. Genetics and Molecular Biology, 2020, 43, e20180311.	1.3	1
89	Performance of genomic data sets on the estimation of the divergence time of New World and Old World anthropoids. Genetics and Molecular Research, 2014, 13, 1425-1437.	0.2	0