

Sergio L Pereira

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

2,633
citations

24
h-index

46
g-index

46
ext. papers

3,133
ext. citations

5.9
avg, IF

4.62
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 44 | Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014 , 506, 445-50 | 50.4 | 434 |
| 43 | Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. <i>Nature Neuroscience</i> , 2017 , 20, 602-611 | 25.5 | 427 |
| 42 | A mitogenomic timescale for birds detects variable phylogenetic rates of molecular evolution and refutes the standard molecular clock. <i>Molecular Biology and Evolution</i> , 2006 , 23, 1731-40 | 8.3 | 206 |
| 41 | Phylogenetic relationships and divergence times of Charadriiformes genera: multigene evidence for the Cretaceous origin of at least 14 clades of shorebirds. <i>Biology Letters</i> , 2007 , 3, 205-9 | 3.6 | 143 |
| 40 | Phylogenetics, biogeography and classification of, and character evolution in, gamebirds (Aves: Galliformes): effects of character exclusion, data partitioning and missing data. <i>Cladistics</i> , 2006 , 22, 495-532 | 3.5 | 132 |
| 39 | Multiple gene evidence for expansion of extant penguins out of Antarctica due to global cooling. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006 , 273, 11-7 | 4.4 | 102 |
| 38 | A Comprehensive Workflow for Read Depth-Based Identification of Copy-Number Variation from Whole-Genome Sequence Data. <i>American Journal of Human Genetics</i> , 2018 , 102, 142-155 | 11 | 97 |
| 37 | Mitochondrial and nuclear DNA sequences support a Cretaceous origin of Columbiformes and a dispersal-driven radiation in the Paleocene. <i>Systematic Biology</i> , 2007 , 56, 656-72 | 8.4 | 91 |
| 36 | A molecular timescale for galliform birds accounting for uncertainty in time estimates and heterogeneity of rates of DNA substitutions across lineages and sites. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 38, 499-509 | 4.1 | 89 |
| 35 | Phylogenetic relationships and historical biogeography of neotropical parrots (Psittaciformes: Psittacidae: Arini) inferred from mitochondrial and nuclear DNA sequences. <i>Systematic Biology</i> , 2006 , 55, 454-70 | 8.4 | 85 |
| 34 | Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. <i>Nature Communications</i> , 2015 , 6, 8718 | 17.4 | 74 |
| 33 | Fatal combined immunodeficiency associated with heterozygous mutation in STAT1. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 807-17 | 11.5 | 68 |
| 32 | Combined nuclear and mitochondrial DNA sequences resolve generic relationships within the Cracidae (Galliformes, Aves). <i>Systematic Biology</i> , 2002 , 51, 946-58 | 8.4 | 68 |
| 31 | Spell Checking Nature: Versatility of CRISPR/Cas9 for Developing Treatments for Inherited Disorders. <i>American Journal of Human Genetics</i> , 2016 , 98, 90-101 | 11 | 67 |
| 30 | Low number of mitochondrial pseudogenes in the chicken (<i>Gallus gallus</i>) nuclear genome: implications for molecular inference of population history and phylogenetics. <i>BMC Evolutionary Biology</i> , 2004 , 4, 17 | 3 | 67 |
| 29 | Mitochondrial genome organization and vertebrate phylogenetics. <i>Genetics and Molecular Biology</i> , 2000 , 23, 745-752 | 2 | 67 |
| 28 | VICARIANT SPECIATION OF CURASSOWS (AVES, CRACIDAE): A HYPOTHESIS BASED ON MITOCHONDRIAL DNA PHYLOGENY. <i>Auk</i> , 2004 , 121, 682 | 2.1 | 51 |

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| 27 | A microcosting and cost-consequence analysis of clinical genomic testing strategies in autism spectrum disorder. <i>Genetics in Medicine</i> , 2017 , 19, 1268-1275 | 8.1 | 43 |
| 26 | DNA evidence for a Paleocene origin of the Alcidae (Aves: Charadriiformes) in the Pacific and multiple dispersals across northern oceans. <i>Molecular Phylogenetics and Evolution</i> , 2008 , 46, 430-45 | 4.1 | 41 |
| 25 | The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 56 participants. <i>Cmaj</i> , 2018 , 190, E126-E136 | 3.5 | 37 |
| 24 | The CF Canada-Sick Kids Program in individual CF therapy: A resource for the advancement of personalized medicine in CF. <i>Journal of Cystic Fibrosis</i> , 2019 , 18, 35-43 | 4.1 | 28 |
| 23 | Sex identification of parrots, toucans, and curassows by PCR: Perspectives for wild and captive population studies. <i>Zoo Biology</i> , 1998 , 17, 415-423 | 1.6 | 27 |
| 22 | Multiple Gene Evidence for Parallel Evolution and Retention of Ancestral Morphological States in the Shanks (Charadriiformes: Scolopacidae). <i>Condor</i> , 2005 , 107, 514 | 2.1 | 24 |
| 21 | Molecular architecture and rates of DNA substitutions of the mitochondrial control region of cracid birds. <i>Genome</i> , 2004 , 47, 535-45 | 2.4 | 24 |
| 20 | Molecular phylogenetics and biogeography of Neotropical piping guans (Aves: Galliformes): <i>Pipile Bonaparte, 1856</i> is synonym of <i>Aburria Reichenbach, 1853</i> . <i>Molecular Phylogenetics and Evolution</i> , 2005 , 35, 637-45 | 4.1 | 24 |
| 19 | Adult siblings with homozygous G6PC3 mutations expand our understanding of the severe congenital neutropenia type 4 (SCN4) phenotype. <i>BMC Medical Genetics</i> , 2012 , 13, 111 | 2.1 | 17 |
| 18 | The Cardiac Genome Clinic: implementing genome sequencing in pediatric heart disease. <i>Genetics in Medicine</i> , 2020 , 22, 1015-1024 | 8.1 | 15 |
| 17 | Genome and Transcriptome Assembly of the Canadian Beaver (<i>Citellus richardsoni</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 755-773 | 3.2 | 13 |
| 16 | Impact of DNA source on genetic variant detection from human whole-genome sequencing data. <i>Journal of Medical Genetics</i> , 2019 , 56, 809-817 | 5.8 | 12 |
| 15 | Whole-exome analysis of foetal autopsy tissue reveals a frameshift mutation in OBSL1, consistent with a diagnosis of 3-M Syndrome. <i>BMC Genomics</i> , 2015 , 16 Suppl 1, S12 | 4.5 | 9 |
| 14 | A homozygous mutation in the stem II domain of causes typical Roifman syndrome. <i>Npj Genomic Medicine</i> , 2017 , 2, 23 | 6.2 | 8 |
| 13 | Reintroduction of guans of the genus <i>Penelope</i> (Cracidae, Aves) in reforested areas in Brazil: assessment by DNA fingerprinting. <i>Biological Conservation</i> , 1999 , 87, 31-38 | 6.2 | 8 |
| 12 | The historical biogeography of <i>Pteroglossus aracarís</i> (Aves, Piciformes, Ramphastidae) based on Bayesian analysis of mitochondrial DNA sequences. <i>Genetics and Molecular Biology</i> , 2008 , 31, 964-973 | 2 | 7 |
| 11 | The enigmatic monotypic crab plover <i>Dromas ardeola</i> is closely related to pratincoles and coursers (Aves, Charadriiformes, Glareolidae). <i>Genetics and Molecular Biology</i> , 2010 , 33, 583-6 | 2 | 5 |
| 10 | Estimates of the genetic variability in a natural population of Bare-faced Curassow <i>Crax fasciolata</i> (Aves, Galliformes, Cracidae). <i>Bird Conservation International</i> , 2001 , 11, 301-308 | 1.7 | 5 |

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| 9 | Expanding the search for genetic biomarkers of Parkinson's disease into the living brain. <i>Neurobiology of Disease</i> , 2020 , 140, 104872 | 7.5 | 5 |
| 8 | The genetic diversity of Epstein-Barr virus in the setting of transplantation relative to non-transplant settings: A feasibility study. <i>Pediatric Transplantation</i> , 2016 , 20, 124-9 | 1.8 | 4 |
| 7 | Phylogenomics, Protein Family Evolution, and the Tree of Life: An Integrated Approach between Molecular Evolution and Computational Intelligence. <i>Studies in Computational Intelligence</i> , 2008 , 259-279 | 0.8 | 3 |
| 6 | Mitochondrial-DNA evidence shows the Australian Painted Snipe is a full species, <i>Rostratula australis</i> . <i>Emu</i> , 2007 , 107, 185-189 | 1.1 | 2 |
| 5 | A Distributed Whole Genome Sequencing Benchmark Study. <i>Frontiers in Genetics</i> , 2020 , 11, 612515 | 4.5 | 2 |
| 4 | Did increased taxon and character sampling really reveal novel intergeneric relationships in the Cracidae (Aves: Galliformes)? <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2009 , 47, 103-104 | 1.0 | 1 |
| 3 | Ant-Based Phylogenetic Reconstruction (ABPR): A new distance algorithm for phylogenetic estimation based on ant colony optimization. <i>Genetics and Molecular Biology</i> , 2008 , 31, 974-981 | 2 | 1 |
| 2 | Curassows and Related Birds. Second Edition. <i>Condor</i> , 2005 , 107, 479-480 | 2.1 | |
| 1 | Curassows and Related Birds. Second Edition. <i>Condor</i> , 2005 , 107, 479 | 2.1 | |