## Sergio L Pereira

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. Nature Neuroscience, 2017, 20, 602-611.	7.1	691
2	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. Nature, 2014, 506, 445-450.	13.7	521
3	A Mitogenomic Timescale for Birds Detects Variable Phylogenetic Rates of Molecular Evolution and Refutes the Standard Molecular Clock. Molecular Biology and Evolution, 2006, 23, 1731-1740.	3.5	222
4	Phylogenetic relationships and divergence times of Charadriiformes genera: multigene evidence for the Cretaceous origin of at least 14 clades of shorebirds. Biology Letters, 2007, 3, 205-210.	1.0	173
5	A Comprehensive Workflow for Read Depth-Based Identification of Copy-Number Variation from Whole-Genome Sequence Data. American Journal of Human Genetics, 2018, 102, 142-155.	2.6	156
6	Phylogenetics, biogeography and classification of, and character evolution in, gamebirds (Aves:) Tj ETQq0 0 0 rgBT 495-532.	/Overlock 1.5	2 10 Tf 50 5 144
7	Multiple gene evidence for expansion of extant penguins out of Antarctica due to global cooling. Proceedings of the Royal Society B: Biological Sciences, 2006, 273, 11-17.	1.2	118
8	Mitochondrial and Nuclear DNA Sequences Support a Cretaceous Origin of Columbiformes and a Dispersal-Driven Radiation in the Paleogene. Systematic Biology, 2007, 56, 656-672.	2.7	110
9	Phylogenetic Relationships and Historical Biogeography of Neotropical Parrots (Psittaciformes:) Tj ETQq1 1 0.7845 55, 454-470.	814 rgBT /( 2.7	Overlock 10 108
10	Compound heterozygous mutations in the noncoding RNU4ATAC cause Roifman Syndrome by disrupting minor intron splicing. Nature Communications, 2015, 6, 8718.	5.8	104
11	A molecular timescale for galliform birds accounting for uncertainty in time estimates and heterogeneity of rates of DNA substitutions across lineages and sites. Molecular Phylogenetics and Evolution, 2006, 38, 499-509.	1.2	103
12	Mitochondrial genome organization and vertebrate phylogenetics. Genetics and Molecular Biology, 2000, 23, 745-752.	0.6	89
13	Spell Checking Nature: Versatility of CRISPR/Cas9 for Developing Treatments for Inherited Disorders. American Journal of Human Genetics, 2016, 98, 90-101.	2.6	86
14	Fatal combined immunodeficiency associated with heterozygous mutation in STAT1. Journal of Allergy and Clinical Immunology, 2014, 133, 807-817.	1.5	81
15	Low number of mitochondrial pseudogenes in the chicken (Gallus gallus) nuclear genome: implications for molecular inference of population history and phylogenetics. BMC Evolutionary Biology, 2004, 4, 17.	3.2	78
16	Combined Nuclear and Mitochondrial DNA Sequences Resolve Generic Relationships within the Cracidae (Galliformes, Aves). Systematic Biology, 2002, 51, 946-958.	2.7	75
17	A microcosting and cost–consequence analysis of clinical genomic testing strategies in autism spectrum disorder. Genetics in Medicine, 2017, 19, 1268-1275.	1.1	62
18	VICARIANT SPECIATION OF CURASSOWS (AVES, CRACIDAE): A HYPOTHESIS BASED ON MITOCHONDRIAL DNA PHYLOGENY. Auk, 2004, 121, 682.	0.7	58

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#	Article	IF	CITATIONS
19	The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 56 participants. Cmaj, 2018, 190, E126-E136.	0.9	57
20	The Cardiac Genome Clinic: implementing genome sequencing in pediatric heart disease. Genetics in Medicine, 2020, 22, 1015-1024.	1.1	51
21	The CF Canada-Sick Kids Program in individual CF therapy: A resource for the advancement of personalized medicine in CF. Journal of Cystic Fibrosis, 2019, 18, 35-43.	0.3	50
22	DNA evidence for a Paleocene origin of the Alcidae (Aves: Charadriiformes) in the Pacific and multiple dispersals across northern oceans. Molecular Phylogenetics and Evolution, 2008, 46, 430-445.	1.2	47
23	Sex identification of parrots, toucans, and curassows by PCR: Perspectives for wild and captive population studies. Zoo Biology, 1998, 17, 415-423.	0.5	37
24	Impact of DNA source on genetic variant detection from human whole-genome sequencing data. Journal of Medical Genetics, 2019, 56, 809-817.	1.5	32
25	MULTIPLE GENE EVIDENCE FOR PARALLEL EVOLUTION AND RETENTION OF ANCESTRAL MORPHOLOGICAL STATES IN THE SHANKS (CHARADRIIFORMES: SCOLOPACIDAE). Condor, 2005, 107, 514.	0.7	29
26	Molecular phylogenetics and biogeography of Neotropical piping guans (Aves: Galliformes): Pipile Bonaparte, 1856 is synonym of Aburria Reichenbach, 1853. Molecular Phylogenetics and Evolution, 2005, 35, 637-645.	1.2	27
27	Molecular architecture and rates of DNA substitutions of the mitochondrial control region of cracid birds. Genome, 2004, 47, 535-545.	0.9	26
28	Adult siblings with homozygous G6PC3 mutations expand our understanding of the severe congenital neutropenia type 4 (SCN4) phenotype. BMC Medical Genetics, 2012, 13, 111.	2.1	19
29	<i>De Novo</i> Genome and Transcriptome Assembly of the Canadian Beaver ( <i>Castor canadensis</i> ). G3: Genes, Genomes, Genetics, 2017, 7, 755-773.	0.8	18
30	A homozygous mutation in the stem II domain of RNU4ATAC causes typical Roifman syndrome. Npj Genomic Medicine, 2017, 2, 23.	1.7	14
31	Reintroduction of guans of the genus Penelope (Cracidae, Aves) in reforested areas in Brazil: assessment by DNA fingerprinting. Biological Conservation, 1999, 87, 31-38.	1.9	13
32	Expanding the search for genetic biomarkers of Parkinson's disease into the living brain. Neurobiology of Disease, 2020, 140, 104872.	2.1	11
33	Whole-exome analysis of foetal autopsy tissue reveals a frameshift mutation in OBSL1, consistent with a diagnosis of 3-M Syndrome. BMC Genomics, 2015, 16, S12.	1.2	9
34	The historical biogeography of Pteroglossus aracaris (Aves, Piciformes, Ramphastidae) based on Bayesian analysis of mitochondrial DNA sequences. Genetics and Molecular Biology, 2008, 31, 964-973.	0.6	8
35	Trio genome sequencing for developmental delay and pediatric heart conditions: A comparative microcost analysis. Genetics in Medicine, 2022, 24, 1027-1036.	1.1	7
36	Estimates of the genetic variability in a natural population of Bare-faced Curassow Crax fasciolata (Aves, Galliformes, Cracidae). Bird Conservation International, 2001, 11, 301-308.	0.7	6

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37	The enigmatic monotypic crab plover Dromas ardeola is closely related to pratincoles and coursers (Aves, Charadriiformes, Glareolidae). Genetics and Molecular Biology, 2010, 33, 583-586.	0.6	6
38	A Distributed Whole Genome Sequencing Benchmark Study. Frontiers in Genetics, 2020, 11, 612515.	1.1	6
39	The genetic diversity of Epstein–Barr virus in the setting of transplantation relative to nonâ€ŧransplant settings: A feasibility study. Pediatric Transplantation, 2016, 20, 124-129.	0.5	5
40	Mitochondrial-DNA evidence shows the Australian Painted Snipe is a full species, Rostratula australis. Emu, 2007, 107, 185-189.	0.2	3
41	Phylogenomics, Protein Family Evolution, and the Tree of Life: An Integrated Approach between Molecular Evolution and Computational Intelligence. Studies in Computational Intelligence, 2008, , 259-279.	0.7	3
42	Ant-Based Phylogenetic Reconstruction (ABPR): A new distance algorithm for phylogenetic estimation based on ant colony optimization. Genetics and Molecular Biology, 2008, 31, 974-981.	0.6	2
43	Curassows and Related Birds. Second Edition. Condor, 2005, 107, 479.	0.7	1
44	Did increased taxon and character sampling really reveal novel intergeneric relationships in the Cracidae (Aves: Galliformes)?. Journal of Zoological Systematics and Evolutionary Research, 2009, 47, 103-104.	0.6	1
45	Curassows and Related Birds. Second Edition. Condor, 2005, 107, 479-480.	0.7	Ο