Sergio L Pereira

List of Publications by Year in Descending Order

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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 2,633 24 46 g-index

46 g-index

46 ext. papers ext. citations 5.9 avg, IF L-index

#	Paper	IF	Citations
44	The Cardiac Genome Clinic: implementing genome sequencing in pediatric heart disease. <i>Genetics in Medicine</i> , 2020 , 22, 1015-1024	8.1	15
43	A Distributed Whole Genome Sequencing Benchmark Study. Frontiers in Genetics, 2020, 11, 612515	4.5	2
42	Expanding the search for genetic biomarkers of Parkinson u disease into the living brain. Neurobiology of Disease, 2020 , 140, 104872	7.5	5
41	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
40	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
39	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
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	Genome and Transcriptome Assembly of the Canadian Beaver (). <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 755-773	3.2	13
36	Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder. <i>Nature Neuroscience</i> , 2017 , 20, 602-611	25.5	427
35	A homozygous mutation in the stem II domain of causes typical Roifman syndrome. <i>Npj Genomic Medicine</i> , 2017 , 2, 23	6.2	8
34	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
33	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
32	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
31	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
30	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
29	Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. <i>Nature</i> , 2014 , 506, 445-50	50.4	434
28	Fatal combined immunodeficiency associated with heterozygous mutation in STAT1. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 807-17	11.5	68

27	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
26	The enigmatic monotypic crab plover Dromas ardeola is closely related to pratincoles and coursers (Aves, Charadriiformes, Glareolidae). <i>Genetics and Molecular Biology</i> , 2010 , 33, 583-6	2	5
25	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	3-1:84	1
24	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
23	The historical biogeography of Pteroglossus aracaris (Aves, Piciformes, Ramphastidae) based on Bayesian analysis of mitochondrial DNA sequences. <i>Genetics and Molecular Biology</i> , 2008 , 31, 964-973	2	7
22	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
21	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 , 259-27	7 9 .8	3
20	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
19	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
18	Mitochondrial-DNA evidence shows the Australian Painted Snipe is a full species, Rostratula australis. <i>Emu</i> , 2007 , 107, 185-189	1.1	2
17	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
16	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
15	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
14	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	-332	132
13	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
12	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
11	Molecular phylogenetics and biogeography of Neotropical piping guans (Aves: Galliformes): Pipile Bonaparte, 1856 is synonym of Aburria Reichenbach, 1853. <i>Molecular Phylogenetics and Evolution</i> , 2005 , 35, 637-45	4.1	24
10	Curassows and Related Birds. Second Edition. <i>Condor</i> , 2005 , 107, 479-480	2.1	

9	Curassows and Related Birds. Second Edition. <i>Condor</i> , 2005 , 107, 479	2.1	
8	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
7	Low number of mitochondrial pseudogenes in the chicken (Gallus gallus) nuclear genome: implications for molecular inference of population history and phylogenetics. <i>BMC Evolutionary Biology</i> , 2004 , 4, 17	3	67
6	VICARIANT SPECIATION OF CURASSOWS (AVES, CRACIDAE): A HYPOTHESIS BASED ON MITOCHONDRIAL DNA PHYLOGENY. <i>Auk</i> , 2004 , 121, 682	2.1	51
5	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
4	Estimates of the genetic variability in a natural population of Bare-faced Curassow Crax fasciolata (Aves, Galliformes, Cracidae). <i>Bird Conservation International</i> , 2001 , 11, 301-308	1.7	5
3	Mitochondrial genome organization and vertebrate phylogenetics. <i>Genetics and Molecular Biology</i> , 2000 , 23, 745-752	2	67
2	Reintroduction of guans of the genus Penelope (Cracidae, Aves) in reforested areas in Brazil: assessment by DNA fingerprinting. <i>Biological Conservation</i> , 1999 , 87, 31-38	6.2	8
1	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