Pablo Andres Orozco-terWengel

List of Publications by Year in descending order

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76 papers

3,724 citations

172207 29 h-index 56 g-index

84 all docs

84 docs citations

84 times ranked 6078 citing authors

#	Article	IF	Citations
1	PoPoolation: A Toolbox for Population Genetic Analysis of Next Generation Sequencing Data from Pooled Individuals. PLoS ONE, 2011, 6, e15925.	1.1	556
2	SNeP: a tool to estimate trends in recent effective population size trajectories using genome-wide SNP data. Frontiers in Genetics, 2015, 6, 109.	1.1	354
3	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	5.8	220
4	Adaptation of <i>Drosophila</i> to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. Molecular Ecology, 2012, 21, 4931-4941.	2.0	194
5	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	1.8	192
6	Ancient and modern DNA reveal dynamics of domestication and cross-continental dispersal of the dromedary. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6707-6712.	3.3	141
7	Massive Habitat-Specific Genomic Response in D. melanogaster Populations during Experimental Evolution in Hot and Cold Environments. Molecular Biology and Evolution, 2014, 31, 364-375.	3.5	138
8	Long-term sky islands generate highly divergent lineages of a narrowly distributed stream salamander (Pachyhynobius shangchengensis) in mid-latitude mountains of East Asia. BMC Evolutionary Biology, 2019, 19, 1.	3.2	117
9	High performance computation of landscape genomic models including local indicators of spatial association. Molecular Ecology Resources, 2017, 17, 1072-1089.	2.2	112
10	Genomic signatures of adaptive introgression from European mouflon into domestic sheep. Scientific Reports, 2017, 7, 7623.	1.6	92
11	Phylogeography, genetic structure and population divergence time of cheetahs in Africa and Asia: evidence for long-term geographic isolates. Molecular Ecology, 2011, 20, 706-724.	2.0	81
12	Domestication of cattle: Two or three events?. Evolutionary Applications, 2019, 12, 123-136.	1.5	80
13	More grist for the mill? Species delimitation in the genomic era and its implications for conservation. Conservation Genetics, 2019, 20, 101-113.	0.8	7 3
14	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. Molecular Biology and Evolution, 2016, 33, 2670-2681.	3.5	69
15	Contrasting effects of acute and chronic stress on the transcriptome, epigenome, and immune response of Atlantic salmon. Epigenetics, 2018, 13, 1191-1207.	1.3	67
16	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. Frontiers in Genetics, 2015, 6, 314.	1.1	64
17	Microsatellite Analysis of the Spectacled Bear (Tremarctos ornatus) Across its Range Distribution. Genes and Genetic Systems, 2005, 80, 57-69.	0.2	62
18	Radically different phylogeographies and patterns of genetic variation in two European brown frogs, genus Rana. Molecular Phylogenetics and Evolution, 2013, 68, 657-670.	1.2	56

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19	Hybridization masks speciation in the evolutionary history of the Galápagos marine iguana. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150425.	1.2	52
20	Developmental Stability: A Major Role for Cyclin G in Drosophila melanogaster. PLoS Genetics, 2011, 7, e1002314.	1.5	50
21	High mitochondrial differentiation levels between wild and domestic Bactrian camels: a basis for rapid detection of maternal hybridization. Animal Genetics, 2010, 41, 315-318.	0.6	45
22	Revisiting demographic processes in cattle with genome-wide population genetic analysis. Frontiers in Genetics, 2015, 6, 191.	1.1	45
23	Transcriptomic response to parasite infection in Nile tilapia (Oreochromis niloticus) depends on rearing density. BMC Genomics, 2018, 19, 723.	1.2	44
24	Dietary specialization drives multiple independent losses and gains in the bitter taste gene repertoire of Laurasiatherian Mammals. Frontiers in Zoology, 2016, 13, 28.	0.9	43
25	Demography and rapid local adaptation shape Creole cattle genome diversity in the tropics. Evolutionary Applications, 2019, 12, 105-122.	1.5	41
26	Multiple hybridization events between <i>Drosophila simulans</i> and <i>Drosophila mauritiana</i> are supported by mtDNA introgression. Molecular Ecology, 2010, 19, 4695-4707.	2.0	37
27	Genealogical lineage sorting leads to significant, but incorrect Bayesian multilocus inference of population structure. Molecular Ecology, 2011, 20, 1108-1121.	2.0	33
28	Dynamics and genetics of a disease-driven species decline to near extinction: lessons for conservation. Scientific Reports, 2016, 6, 30772.	1.6	33
29	Money spider dietary choice in pre―and postâ€harvest cereal crops using metabarcoding. Ecological Entomology, 2021, 46, 249-261.	1.1	32
30	Genetic Variation in Coat Colour Genes MC1R and ASIP Provides Insights Into Domestication and Management of South American Camelids. Frontiers in Genetics, 2018, 9, 487.	1.1	31
31	Ancient DNA reveals the lost domestication history of South American camelids in Northern Chile and across the Andes. ELife, 2021, 10 , .	2.8	31
32	Refugia in Patagonian fjords and the eastern Andes during the Last Glacial Maximum revealed by huemul (<i><scp>H</scp>ippocamelus bisulcus</i>) phylogeographical patterns and genetic diversity. Journal of Biogeography, 2013, 40, 2285-2298.	1.4	28
33	The devil is in the details: the effect of population structure on demographic inference. Heredity, 2016, 116, 349-350.	1.2	28
34	Population genomics of wild Chinese rhesus macaques reveals a dynamic demographic history and local adaptation, with implications for biomedical research. GigaScience, 2018, 7, .	3.3	27
35	Comparing genetic diversity and demographic history in co-distributed wild South American camelids. Heredity, 2018, 121, 387-400.	1.2	27
36	Nuclear DNA recapitulates the cryptic mitochondrial lineages of <i>Lumbricus rubellus </i> and suggests the existence of cryptic species in an ecotoxological soil sentinel. Biological Journal of the Linnean Society, 2013, 110, 780-795.	0.7	25

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37	Locusâ€dependent selection in cropâ€wild hybrids of lettuce under field conditions and its implication for GM crop development. Evolutionary Applications, 2011, 4, 648-659.	1.5	23
38	Software solutions for the livestock genomics SNP array revolution. Animal Genetics, 2015, 46, 343-353.	0.6	22
39	Simple Rules for an Efficient Use of Geographic Information Systems in Molecular Ecology. Frontiers in Ecology and Evolution, 2017, 5, .	1.1	21
40	Genomic selection strategies for breeding adaptation and production in dairy cattle under climate change. Heredity, 2019, 123, 307-317.	1.2	21
41	Mitochondrial introgressive hybridization following a demographic expansion in the tomato frogs of <scp>M</scp> adagascar, genus <scp><i>D</i></scp> <i>yscophus</i> . Molecular Ecology, 2013, 22, 6074-6090.	2.0	18
42	Comparative transcriptomics reveal conserved impacts of rearing density on immune response of two important aquaculture species. Fish and Shellfish Immunology, 2020, 104, 192-201.	1.6	18
43	Authors' Reply to Letter to the Editor: Continued improvement to genetic diversity indicator for CBD. Conservation Genetics, 2021, 22, 533-536.	0.8	18
44	Living on a volcano's edge: genetic isolation of an extremophile terrestrial metazoan. Heredity, 2014, 112, 132-142.	1.2	16
45	Rapid identification and interpretation of gene–environment associations using the new R.SamBada landscape genomics pipeline. Molecular Ecology Resources, 2019, 19, 1355-1365.	2.2	16
46	No signs of inbreeding despite long-term isolation and habitat fragmentation in the critically endangered Montseny brook newt (Calotriton arnoldi). Heredity, 2017, 118, 424-435.	1.2	14
47	MEDI: Macronutrient Extraction and Determination from invertebrates, a rapid, cheap and streamlined protocol. Methods in Ecology and Evolution, 2021, 12, 593-601.	2.2	14
48	Phylogeography and phylogenetic relationships of Malagasy tree and ground boas. Biological Journal of the Linnean Society, 2008, 95, 640-652.	0.7	13
49	Mitochondrial Introgression, Color Pattern Variation, and Severe Demographic Bottlenecks in Three Species of Malagasy Poison Frogs, Genus Mantella. Genes, 2019, 10, 317.	1.0	12
50	PoPoolation DB: a user-friendly web-based database for the retrieval of natural polymorphisms in Drosophila. BMC Genetics, 2011, 12, 27.	2.7	11
51	Detection of selection signatures in the genome of a farmed population of anadromous rainbow trout (Oncorhynchus mykiss). Genomics, 2021, 113, 3395-3404.	1.3	11
52	Maintenance of Genetic Diversity in an Introduced Island Population of Guanacos after Seven Decades and Two Severe Demographic Bottlenecks: Implications for Camelid Conservation. PLoS ONE, 2014, 9, e91714.	1.1	11
53	Genetic identification of units for conservation in tomato frogs, genus Dyscophus. Conservation Genetics, 2006, 7, 473-482.	0.8	10
54	Mixed signals from hybrid genomes. Molecular Ecology, 2014, 23, 3941-3943.	2.0	10

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55	Distribution and molecular phylogeny of biliary trematodes (Opisthorchiidae) infecting native Lutra lutra and alien Neovison vison across Europe. Parasitology International, 2016, 65, 163-170.	0.6	10
56	Phylogeography and Population Genetics of Vicugna vicugna: Evolution in the Arid Andean High Plateau. Frontiers in Genetics, 2019, 10, 445.	1.1	10
57	Lessons learnt on the analysis of large sequence data in animal genomics. Animal Genetics, 2018, 49, 147-158.	0.6	8
58	Landscape Genomics of a Widely Distributed Snake, Dolichophis caspius (Gmelin, 1789) across Eastern Europe and Western Asia. Genes, 2020, 11, 1218.	1.0	6
59	Unlocking the potential of a validated single nucleotide polymorphism array for genomic monitoring of trade in cheetahs (Acinonyx jubatus). Molecular Biology Reports, 2021, 48, 171-181.	1.0	6
60	Innate and Adaptive Immune Genes Associated with MERS-CoV Infection in Dromedaries. Cells, 2021, 10, 1291.	1.8	6
61	First extraction of eDNA from tree hole water to detect tree frogs: a simple field method piloted in Madagascar. Conservation Genetics Resources, 2022, 14, 99-107.	0.4	6
62	Assessment of nematodes in Punjab Urial (Ovis vignei punjabiensis) population in Kalabagh Game Reserve: development of a DNA barcode approach. European Journal of Wildlife Research, 2019, 65, 1.	0.7	5
63	Dispersal and genetic structure in a tropical small mammal, the Bornean tree shrew (Tupaia longipes), in a fragmented landscape along the Kinabatangan River, Sabah, Malaysia. BMC Genetics, 2020, 21, 43.	2.7	5
64	Isolation and characterization of six polymorphic microsatellite loci for the Malagasy spider tortoise, Pyxis arachnoides and cross-amplification in Pyxis planicauda. Amphibia - Reptilia, 2013, 34, 125-128.	0.1	4
65	Cross-amplification of nonspecific microsatellites markers: a useful tool to study endangered/vulnerable species of southern Andes deer. Genetics and Molecular Research, 2014, 13, 3193-3200.	0.3	3
66	Genetic diversity and parasite facilitated establishment of the invasive signal crayfish (<i>Pacifastacus) Tj ETQq0</i>	0 0 rgBT /	Overlock 10 ⁻
67	Local Ancestry to Identify Selection in Response to Trypanosome Infection in Baoul \tilde{A} © x Zebu Crossbred Cattle in Burkina Faso. Frontiers in Genetics, 2021, 12, 670390.	1.1	3
68	The critical role of natural forest as refugium for generalist species in oil palm-dominated landscapes. PLoS ONE, 2021, 16, e0257814.	1.1	2
69	Spatial dynamics of Chinese MuntjacÂrelated to past and future climate fluctuations. Environmental Epigenetics, 2021, 67, 361-370.	0.9	1
70	The effect of oil palmâ€dominated landscapes on the home range and distribution of a generalist species, the Asian water monitor. Ecology and Evolution, 2022, 12, e8531.	0.8	1
71	A population genetic analysis of the Critically Endangered Madagascar big-headed turtle, Erymnochelys madagascariensis across captive and wild populations. Scientific Reports, 2022, 12, .	1.6	1
72	An unexpected new red-bellied Stumpffia (Microhylidae) from forest fragments in central Madagascar highlights remaining cryptic diversity. ZooKeys, 0, 1104, 1-28.	0.5	1

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73	Modelling genetics within ecosystems. Nature, 2013, 495, 47-47.	13.7	0
74	The complete mitogenome of the Mountain chicken frog, Leptodactylus fallax. Mitochondrial DNA Part B: Resources, 2021, 6, 1372-1373.	0.2	0
75	The complete mitochondrial genome of rare and Critically Endangered Anilany helenae (Microhylidae) of Madagascar. Mitochondrial DNA Part B: Resources, 2022, 7, 153-155.	0.2	O
76	Diversidad genética y estructura poblacional del ovino JunÃn mediante el uso de microarreglos de alta densidad de marcadores polimórficos de nucleótido simple (SNP). Revista De Investigaciones Veterinarias Del Peru, 2022, 33, e21459.	0.0	0