

Laurent A F Frantz

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

4,901
citations

172457

29
h-index

161849

54
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57
all docs

57
docs citations

57
times ranked

6040
citing authors

#	ARTICLE	IF	CITATIONS
1	Population genomic, olfactory, dietary, and gut microbiota analyses demonstrate the unique evolutionary trajectory of feral pigs. <i>Molecular Ecology</i> , 2022, 31, 220-237.	3.9	16
2	Natural and human-driven selection of a single non-coding body size variant in ancient and modern canids. <i>Current Biology</i> , 2022, 32, 889-897.e9.	3.9	23
3	The biocultural origins and dispersal of domestic chickens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	28
4	Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.	27.8	48
5	Uncovering the enigmatic evolution of bears in greater depth: The hybrid origin of the Asiatic black bear. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	13
6	Genomes of Pleistocene Siberian Wolves Uncover Multiple Extinct Wolf Lineages. <i>Current Biology</i> , 2021, 31, 198-206.e8.	3.9	26
7	Dog domestication and the dual dispersal of people and dogs into the Americas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	112
8	Dire wolves were the last of an ancient New World canid lineage. <i>Nature</i> , 2021, 591, 87-91.	27.8	43
9	Pleistocene origins, western ghost lineages, and the emerging phylogeographic history of the red wolf and coyote. <i>Molecular Ecology</i> , 2021, 30, 4292-4304.	3.9	11
10	Reconsidering domestication from a process archaeology perspective. <i>World Archaeology</i> , 2021, 53, 56-77.	1.1	36
11	Modern Siberian dog ancestry was shaped by several thousand years of Eurasian-wide trade and human dispersal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
12	Kouprey (<i>Bos sauveli</i>) genomes unveil polytomic origin of wild Asian Bos. <i>IScience</i> , 2021, 24, 103226.	4.1	8
13	Ancient DNA suggests modern wolves trace their origin to a Late Pleistocene expansion from Beringia. <i>Molecular Ecology</i> , 2020, 29, 1596-1610.	3.9	70
14	Origins and genetic legacy of prehistoric dogs. <i>Science</i> , 2020, 370, 557-564.	12.6	152
15	A mitochondrial genetic divergence proxy predicts the reproductive compatibility of mammalian hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200690.	2.6	14
16	Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 449-460.	16.3	119
17	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020, 30, 693-701.	12.0	144
18	Arctic-adapted dogs emerged at the Pleistocene-Holocene transition. <i>Science</i> , 2020, 368, 1495-1499.	12.6	60

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19	Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17231-17238.	7.1	101
20	Microbial differences between dental plaque and historic dental calculus are related to oral biofilm maturation stage. Microbiome, 2019, 7, 102.	11.1	97
21	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. Nature Communications, 2019, 10, 1992.	12.8	38
22	Specialized sledge dogs accompanied Inuit dispersal across the North American Arctic. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20191929.	2.6	38
23	Synchronous diversification of Sulawesi's iconic artiodactyls driven by recent geological events. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172566.	2.6	17
24	Rabbits and the Specious Origins of Domestication. Trends in Ecology and Evolution, 2018, 33, 149-152.	8.7	28
25	Paleogenomics of Animal Domestication. Population Genomics, 2018, , 225-272.	0.5	14
26	Dogs accompanied humans during the Neolithic expansion into Europe. Biology Letters, 2018, 14, 20180286.	2.3	39
27	ABLE: blockwise site frequency spectra for inferring complex population histories and recombination. Genome Biology, 2018, 19, 145.	8.8	16
28	The evolutionary history of dogs in the Americas. Science, 2018, 361, 81-85.	12.6	140
29	Selection of Appropriate Metagenome Taxonomic Classifiers for Ancient Microbiome Research. MSystems, 2018, 3, .	3.8	35
30	The dental calculus metabolome in modern and historic samples. Metabolomics, 2017, 13, 134.	3.0	44
31	Analysis of the genetic variation in mitochondrial DNA, Y-chromosome sequences, and MC1R sheds light on the ancestry of Nigerian indigenous pigs. Genetics Selection Evolution, 2017, 49, 52.	3.0	8
32	Reconstructing Asian faunal introductions to eastern Africa from multi-proxy biomolecular and archaeological datasets. PLoS ONE, 2017, 12, e0182565.	2.5	53
33	A novel <i>MC1R</i> allele for black coat colour reveals the Polynesian ancestry and hybridization patterns of Hawaiian feral pigs. Royal Society Open Science, 2016, 3, 160304.	2.4	19
34	Genomic and archaeological evidence suggest a dual origin of domestic dogs. Science, 2016, 352, 1228-1231.	12.6	366
35	The Evolution of Suidae. Annual Review of Animal Biosciences, 2016, 4, 61-85.	7.4	85
36	Copy number variation in the speciation of pigs: a possible prominent role for olfactory receptors. BMC Genomics, 2015, 16, 330.	2.8	85

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37	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20152019.	2.6	25
38	Evolution of Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 188-189.	21.4	10
39	Evidence of long-term gene flow and selection during domestication from analyses of Eurasian wild and domestic pig genomes. <i>Nature Genetics</i> , 2015, 47, 1141-1148.	21.4	263
40	Inferring Bottlenecks from Genome-Wide Samples of Short Sequence Blocks. <i>Genetics</i> , 2015, 201, 1157-1169.	2.9	40
41	The genetics of indirect ecological effects of plant parasites and aphid herbivores. <i>Frontiers in Genetics</i> , 2014, 5, 72.	2.3	2
42	Host-plant genotypic diversity and community genetic interactions mediate aphid spatial distribution. <i>Ecology and Evolution</i> , 2014, 4, 121-131.	1.9	12
43	Testing models of speciation from genome sequences: divergence and asymmetric admixture in <i>S. islandicus</i> , <i>S. olearius</i> , <i>S. astasiensis</i> , <i>S. ussuriensis</i> during the Pliocene climatic fluctuations. <i>Molecular Ecology</i> , 2014, 23, 5566-5574.	3.9	32
44	Neandertal Admixture in Eurasia Confirmed by Maximum-Likelihood Analysis of Three Genomes. <i>Genetics</i> , 2014, 196, 1241-1251.	2.9	78
45	Untangling the hybrid nature of modern pig genomes: a mosaic derived from biogeographically distinct and highly divergent <i>Sus scrofa</i> populations. <i>Molecular Ecology</i> , 2014, 23, 4089-4102.	3.9	52
46	Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. <i>Nature Communications</i> , 2014, 5, 4392.	12.8	137
47	Hybrid origin of European commercial pigs examined by an in-depth haplotype analysis on chromosome 1. <i>Frontiers in Genetics</i> , 2014, 5, 442.	2.3	19
48	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. <i>BMC Genomics</i> , 2013, 14, 449.	2.8	118
49	Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and Geometric Morphometrics. <i>Molecular Biology and Evolution</i> , 2013, 30, 824-832.	8.9	196
50	Genome sequencing reveals fine scale diversification and reticulation history during speciation in <i>Sus</i> . <i>Genome Biology</i> , 2013, 14, R107.	9.6	137
51	Regions of Homozygosity in the Porcine Genome: Consequence of Demography and the Recombination Landscape. <i>PLoS Genetics</i> , 2012, 8, e1003100.	3.5	266
52	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	27.8	1,190
53	A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. <i>BMC Genomics</i> , 2012, 13, 586.	2.8	150