

Maxime Galan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/948288/publications.pdf>

Version: 2024-02-01

94
papers

4,033
citations

109264

35
h-index

138417

58
g-index

113
all docs

113
docs citations

113
times ranked

5717
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape connectivity influences gene flow in a roe deer population inhabiting a fragmented landscape: an individual-based approach. <i>Molecular Ecology</i> , 2004, 13, 2841-2850.	2.0	318
2	Genetic structure is influenced by landscape features: empirical evidence from a roe deer population. <i>Molecular Ecology</i> , 2006, 15, 1669-1679.	2.0	238
3	Estimation of population allele frequencies from next-generation sequencing data: pool versus individual-based genotyping. <i>Molecular Ecology</i> , 2013, 22, 3766-3779.	2.0	195
4	A 454 multiplex sequencing method for rapid and reliable genotyping of highly polymorphic genes in large-scale studies. <i>BMC Genomics</i> , 2010, 11, 296.	1.2	166
5	Empirical Assessment of RAD Sequencing for Interspecific Phylogeny. <i>Molecular Biology and Evolution</i> , 2014, 31, 1272-1274.	3.5	124
6	Metabarcoding for the parallel identification of several hundred predators and their prey: Application to bat species diet analysis. <i>Molecular Ecology Resources</i> , 2018, 18, 474-489.	2.2	118
7	16S rRNA Amplicon Sequencing for Epidemiological Surveys of Bacteria in Wildlife. <i>MSystems</i> , 2016, 1, .	1.7	106
8	Next-Generation Sequencing for Rodent Barcoding: Species Identification from Fresh, Degraded and Environmental Samples. <i>PLoS ONE</i> , 2012, 7, e48374.	1.1	94
9	Migration and recovery of the genetic diversity during the increasing density phase in cyclic vole populations. <i>Molecular Ecology</i> , 2006, 15, 2665-2676.	2.0	90
10	Global parasite and <i>Rattus</i> rodent invasions: The consequences for rodent-borne diseases. <i>Integrative Zoology</i> , 2015, 10, 409-423.	1.3	78
11	Genetic structure of the cyclic fossorial water vole (<i>Arvicola terrestris</i>): landscape and demographic influences. <i>Molecular Ecology</i> , 2005, 14, 2861-2871.	2.0	75
12	Mating system, sexual dimorphism, and the opportunity for sexual selection in a territorial ungulate. <i>Behavioral Ecology</i> , 2008, 19, 309-316.	1.0	71
13	Landscape genetics highlights the role of bank vole metapopulation dynamics in the epidemiology of Puumala hantavirus. <i>Molecular Ecology</i> , 2011, 20, no-no.	2.0	71
14	Cytonuclear discordance among Southeast Asian black rats (<i>Rattus rattus</i> complex). <i>Molecular Ecology</i> , 2013, 22, 1019-1034.	2.0	71
15	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. <i>BMC Microbiology</i> , 2019, 19, 171.	1.3	71
16	Genetic characterization of the human relapsing fever spirochete <i>Borrelia miyamotoi</i> in vectors and animal reservoirs of Lyme disease spirochetes in France. <i>Parasites and Vectors</i> , 2014, 7, 233.	1.0	68
17	Invasion genetics of the introduced black rat (<i>Rattus rattus</i>) in Senegal, West Africa. <i>Molecular Ecology</i> , 2013, 22, 286-300.	2.0	67
18	The Transplantation of 3 PUFA-Altered Gut Microbiota of fat-1 Mice to Wild-Type Littermates Prevents Obesity and Associated Metabolic Disorders. <i>Diabetes</i> , 2018, 67, 1512-1523.	0.3	65

#	ARTICLE	IF	CITATIONS
19	Duplication, balancing selection and trans-species evolution explain the high levels of polymorphism of the DQA MHC class II gene in voles (Arvicolinae). <i>Immunogenetics</i> , 2006, 58, 191-202.	1.2	64
20	Density-related changes in selection pattern for major histocompatibility complex genes in fluctuating populations of voles. <i>Molecular Ecology</i> , 2007, 16, 5084-5097.	2.0	64
21	Association between the DQA MHC class II gene and Puumala virus infection in <i>Myodes glareolus</i> , the bank vole. <i>Infection, Genetics and Evolution</i> , 2008, 8, 450-458.	1.0	64
22	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003929.	1.3	62
23	Assessment of a 16S rRNA amplicon Illumina sequencing procedure for studying the microbiome of a symbiotic aphid genus. <i>Molecular Ecology Resources</i> , 2016, 16, 628-640.	2.2	60
24	Multiple parasites mediate balancing selection at two MHC class II genes in the fossorial water vole: insights from multivariate analyses and population genetics. <i>Journal of Evolutionary Biology</i> , 2008, 21, 1307-1320.	0.8	58
25	Contrasted evolutionary histories of two Toll-like receptors (Tlr4 and Tlr7) in wild rodents (MURINAE). <i>BMC Evolutionary Biology</i> , 2013, 13, 194.	3.2	58
26	HETEROZYGOSITY-FITNESS CORRELATIONS REVEALED BY NEUTRAL AND CANDIDATE GENE MARKERS IN ROE DEER FROM A LONG-TERM STUDY. <i>Evolution; International Journal of Organic Evolution</i> , 2009, 63, 403-417.	1.1	56
27	ChickRH6: a chicken whole-genome radiation hybrid panel. <i>Genetics Selection Evolution</i> , 2002, 34, 521-33.	1.2	54
28	Detection of <i>Orientia</i> sp. DNA in rodents from Asia, West Africa and Europe. <i>Parasites and Vectors</i> , 2015, 8, 172.	1.0	54
29	Molecular identification of four cryptic species of <i>Mastomys</i> (Rodentia, Murinae). <i>Biochemical Systematics and Ecology</i> , 2005, 33, 681-689.	0.6	53
30	Tnf- α expression and promoter sequences reflect the balance of tolerance/resistance to Puumala hantavirus infection in European bank vole populations. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1208-1217.	1.0	51
31	Host-parasite network structure is associated with community-level immunogenetic diversity. <i>Nature Communications</i> , 2014, 5, 5172.	5.8	49
32	Dispersal is not female biased in a resource-defence mating ungulate, the European roe deer. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 341-348.	1.2	47
33	Deciphering host-parasitoid interactions and parasitism rates of crop pests using DNA metabarcoding. <i>Scientific Reports</i> , 2019, 9, 3646.	1.6	47
34	The genetic similarity between pair members influences the frequency of extrapair paternity in alpine marmots. <i>Animal Behaviour</i> , 2008, 76, 87-95.	0.8	45
35	A new method to identify the endangered Pyrenean desman (<i>Galemys pyrenaicus</i>) and to study its diet, using next generation sequencing from faeces. <i>Mammalian Biology</i> , 2015, 80, 505-509.	0.8	40
36	Kinship, dispersal and hantavirus transmission in bank and common voles. <i>Archives of Virology</i> , 2008, 153, 435-444.	0.9	39

#	ARTICLE	IF	CITATIONS
37	Immunogenetic heterogeneity in a widespread ungulate: the European roe deer (<i>Capreolus</i>)	2.0	38
38	Phylogeography of a Sahelian rodent species <i>Mastomys huberti</i> : a Pliocene-Pleistocene story of emergence and colonization of humid habitats. <i>Molecular Ecology</i> , 2008, 17, 1036-1053.	2.0	37
39	Species or local environment, what determines the infection of rodents by <i>Toxoplasma gondii</i> ?. <i>Parasitology</i> , 2014, 141, 259-268.	0.7	37
40	Microevolution of bank voles (<i>Myodes glareolus</i>) at neutral and immune-related genes during multiannual dynamic cycles: Consequences for Puumala hantavirus epidemiology. <i>Infection, Genetics and Evolution</i> , 2017, 49, 318-329.	1.0	37
41	<i>Candidatus</i> <i>Neoehrlichia mikurensis</i> in Bank Voles, France. <i>Emerging Infectious Diseases</i> , 2012, 18, 2063-2065.	2.0	35
42	Analysis of major histocompatibility complex class II gene in water voles using capillary electrophoresis-single stranded conformation polymorphism. <i>Molecular Ecology Notes</i> , 2005, 5, 173-176.	1.7	34
43	Recent Discoveries of New Hantaviruses Widen Their Range and Question Their Origins. <i>Annals of the New York Academy of Sciences</i> , 2008, 1149, 84-89.	1.8	34
44	No Difference between the Sexes in Fine-Scale Spatial Genetic Structure of Roe Deer. <i>PLoS ONE</i> , 2010, 5, e14436.	1.1	30
45	Urban Market Gardening and Rodent-Borne Pathogenic <i>Leptospira</i> in Arid Zones: A Case Study in Niamey, Niger. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0004097.	1.3	29
46	Evaluating metabarcoding to analyse diet composition of species foraging in anthropogenic landscapes using Ion Torrent and Illumina sequencing. <i>Scientific Reports</i> , 2018, 8, 17091.	1.6	29
47	Cross-amplification tests of ungulate primers in roe deer (<i>Capreolus capreolus</i>) to develop a multiplex panel of 12 microsatellite loci. <i>Molecular Ecology Notes</i> , 2003, 3, 142-146.	1.7	28
48	Landscape features and helminth co-infection shape bank vole immunoheterogeneity, with consequences for Puumala virus epidemiology. <i>Heredity</i> , 2014, 112, 274-281.	1.2	28
49	In silico and empirical evaluation of twelve metabarcoding primer sets for insectivorous diet analyses. <i>Ecology and Evolution</i> , 2020, 10, 6310-6332.	0.8	28
50	No Evidence for Ape <i>Plasmodium</i> Infections in Humans in Gabon. <i>PLoS ONE</i> , 2015, 10, e0126933.	1.1	27
51	Associations between MHC genes and Puumala virus infection in <i>Myodes glareolus</i> are detected in wild populations, but not from experimental infection data. <i>Journal of General Virology</i> , 2010, 91, 2507-2512.	1.3	24
52	Polymorphic microsatellite loci and PCR multiplexing in the common vole, <i>Microtus arvalis</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 830-832.	1.7	23
53	SESAME (SEquence Sorter & Amplicon Explorer): genotyping based on high-throughput multiplex amplicon sequencing. <i>Bioinformatics</i> , 2011, 27, 277-278.	1.8	22
54	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . <i>Molecular Ecology</i> , 2018, 27, 264-278.	2.0	22

#	ARTICLE	IF	CITATIONS
55	DNA Metabarcoding as a Tool for Disentangling Food Webs in Agroecosystems. <i>Insects</i> , 2020, 11, 294.	1.0	22
56	Deciphering the fine nucleotide diversity of full HLA class I and class II genes in a well-documented population from sub-Saharan Africa. <i>Hla</i> , 2018, 91, 36-51.	0.4	20
57	DNA sequencing to help identify crop pests and their natural enemies in agro-ecosystems: The case of the millet head miner <i>Heliocheilus albipunctella</i> (Lepidoptera: Noctuidae) in sub-Saharan Africa. <i>Biological Control</i> , 2018, 121, 199-207.	1.4	19
58	eDNA metabarcoding reveals a core and secondary diets of the greater horseshoe bat with strong spatio-temporal plasticity. <i>Environmental DNA</i> , 2021, 3, 277-296.	3.1	19
59	Multiple paternity occurs with low frequency in the territorial roe deer, <i>Capreolus capreolus</i> . <i>Biological Journal of the Linnean Society</i> , 2009, 97, 128-139.	0.7	18
60	Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities. <i>Scientific Reports</i> , 2017, 7, 14995.	1.6	18
61	Linking demography and host dispersal to <i>Trichuris arvicolae</i> distribution in a cyclic vole species. <i>International Journal for Parasitology</i> , 2007, 37, 813-824.	1.3	17
62	Birds and bats contribute to natural regulation of the millet head miner in tree-crop agroforestry systems. <i>Crop Protection</i> , 2020, 132, 105127.	1.0	17
63	Evidence of gene orthology and trans-species polymorphism, but not of parallel evolution, despite high levels of concerted evolution in the major histocompatibility complex of flamingo species. <i>Journal of Evolutionary Biology</i> , 2016, 29, 438-454.	0.8	16
64	Both candidate gene and neutral genetic diversity correlate with parasite resistance in female Mediterranean mouflon. <i>BMC Ecology</i> , 2019, 19, 12.	3.0	16
65	Negative relationships between cellular immune response, Mhc class II heterozygosity and secondary sexual trait in the montane water vole. <i>Evolutionary Applications</i> , 2010, 3, 279-290.	1.5	15
66	Novel insights into the diet of the Pyrenean desman (<i>Galemys pyrenaicus</i>) using next-generation sequencing molecular analyses. <i>Journal of Mammalogy</i> , 2017, , .	0.6	15
67	Experimental infections of wild bank voles (<i>Myodes glareolus</i>) from nephropatia epidemica endemic and non-endemic regions revealed slight differences in Puumala virological course and immunological responses. <i>Virus Research</i> , 2017, 235, 67-72.	1.1	14
68	Bank vole immunoheterogeneity may limit Nephropatia Epidemica emergence in a French non-endemic region. <i>Parasitology</i> , 2018, 145, 393-407.	0.7	14
69	A multiplex panel of microsatellite markers for widespread sub-Saharan rodents of the genus <i>Mastomys</i> . <i>Molecular Ecology Notes</i> , 2004, 4, 321-323.	1.7	13
70	Pathogen-mediated selection favours the maintenance of innate immunity gene polymorphism in a widespread wild ungulate. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1156-1166.	0.8	13
71	A multiplex panel of dinucleotide microsatellite markers for the water vole, <i>Arvicola terrestris</i> . <i>Molecular Ecology Notes</i> , 2004, 4, 620-622.	1.7	12
72	Genetic epidemiology of the Alpine ibex reservoir of persistent and virulent brucellosis outbreak. <i>Scientific Reports</i> , 2020, 10, 4400.	1.6	12

#	ARTICLE	IF	CITATIONS
73	Discongruence of Mhc and cytochrome b phylogeographical patterns in <i>Myodes glareolus</i> (Rodentia): Tj ETQq1 1 0,784314 rgBT /Overlock 10 Tf 5	0.7	1
74	Between-population differences in the genetic and maternal components of body mass in roe deer. <i>BMC Evolutionary Biology</i> , 2018, 18, 39.	3.2	10
75	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , 2018, 8, 11273-11292.	0.8	9
76	Efficiency of Fluorescent Multiplex Polymerase Chain Reactions (PCRs) for Rapid Genotyping of Harbour Porpoises (<i>Phocoena phocoena</i>) with 11 Microsatellite Loci. <i>Aquatic Mammals</i> , 2006, 32, 301-304.	0.4	9
77	New polymorphic microsatellite loci for rodents of the genus <i>Mastomys</i> using PCR multiplexing, and cross-species amplification in <i>Myomys</i> and <i>Praomys</i> . <i>Molecular Ecology Notes</i> , 2007, 7, 684-687.	1.7	8
78	Unraveling the dietary diversity of Neotropical top predators using scat DNA metabarcoding: A case study on the elusive Giant Otter. <i>Environmental DNA</i> , 2021, 3, 889-900.	3.1	8
79	Spatio-temporal trends in richness and persistence of bacterial communities in decline-phase water vole populations. <i>Scientific Reports</i> , 2020, 10, 9506.	1.6	7
80	Reduced microsatellite heterozygosity does not affect natal dispersal in three contrasting roe deer populations. <i>Oecologia</i> , 2015, 177, 631-643.	0.9	5
81	Immune gene variability influences roe deer natal dispersal. <i>Oikos</i> , 2016, 125, 1790-1801.	1.2	5
82	Identifying environmental drivers of spatial genetic structure of the European pine marten (<i>Martes</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.9	5
83	Consequences of organ choice in describing bacterial pathogen assemblages in a rodent population. <i>Epidemiology and Infection</i> , 2017, 145, 3070-3075.	1.0	5
84	Diet Analysis of <i>Leopoldamys Neilli</i> , a Cave-dwelling Rodent in Southeast Asia, Using Next-Generation Sequencing from Feces. <i>Journal of Cave and Karst Studies</i> , 2014, 76, 139-145.	0.3	5
85	Effects of parasite and historic driven selection on the diversity and structure of a MHC-II gene in a small mammal species (<i>Peromyscus leucopus</i>) undergoing range expansion. <i>Evolutionary Ecology</i> , 2017, 31, 785-801.	0.5	4
86	Disentangling the effect of host genetics and gut microbiota on resistance to an intestinal parasite. <i>International Journal for Parasitology</i> , 2019, 49, 873-883.	1.3	4
87	Increasing helminth infection burden depauperates the diversity of the gut microbiota and alters its composition in mice. <i>Current Research in Parasitology and Vector-borne Diseases</i> , 2022, 2, 100082.	0.7	4
88	A set of 21 polymorphic microsatellites in Alpine chamois (<i>Rupicapra rupicapra</i>). <i>Molecular Ecology Notes</i> , 2007, 7, 243-247.	1.7	3
89	Characterization and PCR multiplexing of polymorphic microsatellite loci in the whipworm <i>Trichuris arvicolae</i> , parasite of arvicoline rodents and their cross-species utilization in <i>T. muris</i> , parasite of murines. <i>Molecular and Biochemical Parasitology</i> , 2009, 167, 144-146.	0.5	3
90	Early life infection and host senescence. <i>Experimental Gerontology</i> , 2018, 114, 19-26.	1.2	3

#	ARTICLE	IF	CITATIONS
91	How Bank Vole-PUUV Interactions Influence the Eco-Evolutionary Processes Driving Nephropathia Epidemica Epidemiology—An Experimental and Genomic Approach. Pathogens, 2020, 9, 789.	1.2	2
92	Isolation and Genetic Characterization of Puumala Orthohantavirus Strains from France. Pathogens, 2021, 10, 349.	1.2	2
93	Differential immune gene expression associated with contemporary range expansion in two invasive rodents in Senegal. Scientific Reports, 2020, 10, 18257.	1.6	1
94	Large-scale geography survey provides insights into the colonization history of a major aphid pest on its cultivated apple host in Europe, North America and North Africa. , 0, 1, .		0