

Maxime Galan

List of Publications by Citations

Source: <https://exaly.com/author-pdf/948288/maxime-galan-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

101
papers

3,133
citations

32
h-index

53
g-index

113
ext. papers

3,664
ext. citations

4.2
avg, IF

4.77
L-index

#	Paper	IF	Citations
101	Landscape connectivity influences gene flow in a roe deer population inhabiting a fragmented landscape: an individual-based approach. <i>Molecular Ecology</i> , 2004 , 13, 2841-50	5.7	290
100	Genetic structure is influenced by landscape features: empirical evidence from a roe deer population. <i>Molecular Ecology</i> , 2006 , 15, 1669-79	5.7	215
99	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	4.5	153
98	Estimation of population allele frequencies from next-generation sequencing data: pool-versus individual-based genotyping. <i>Molecular Ecology</i> , 2013 , 22, 3766-79	5.7	147
97	Empirical assessment of RAD sequencing for interspecific phylogeny. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1272-4	8.3	108
96	Migration and recovery of the genetic diversity during the increasing density phase in cyclic vole populations. <i>Molecular Ecology</i> , 2006 , 15, 2665-76	5.7	84
95	Next-generation sequencing for rodent barcoding: species identification from fresh, degraded and environmental samples. <i>PLoS ONE</i> , 2012 , 7, e48374	3.7	75
94	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	8.4	72
93	Genetic structure of the cyclic fossorial water vole (<i>Arvicola terrestris</i>): landscape and demographic influences. <i>Molecular Ecology</i> , 2005 , 14, 2861-71	5.7	66
92	16S rRNA Amplicon Sequencing for Epidemiological Surveys of Bacteria in Wildlife. <i>MSystems</i> , 2016 , 1,	7.6	66
91	Mating system, sexual dimorphism, and the opportunity for sexual selection in a territorial ungulate. <i>Behavioral Ecology</i> , 2008 , 19, 309-316	2.3	62
90	Density-related changes in selection pattern for major histocompatibility complex genes in fluctuating populations of voles. <i>Molecular Ecology</i> , 2007 , 16, 5084-97	5.7	61
89	Cytonuclear discordance among Southeast Asian black rats (<i>Rattus rattus</i> complex). <i>Molecular Ecology</i> , 2013 , 22, 1019-34	5.7	59
88	Global parasite and <i>Rattus</i> rodent invasions: The consequences for rodent-borne diseases. <i>Integrative Zoology</i> , 2015 , 10, 409-23	1.9	59
87	Duplication, balancing selection and trans-species evolution explain the high levels of polymorphism of the DQA MHC class II gene in voles (<i>Arvicolinae</i>). <i>Immunogenetics</i> , 2006 , 58, 191-202	3.2	57
86	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, 1307-20	2.3	55
85	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	4	52

84	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, 403-17	3.8	52
83	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, 450-8	4.5	52
82	Invasion genetics of the introduced black rat (<i>Rattus rattus</i>) in Senegal, West Africa. <i>Molecular Ecology</i> , 2013 , 22, 286-300	5.7	51
81	Contrasted evolutionary histories of two Toll-like receptors (Tlr4 and Tlr7) in wild rodents (MURINAE). <i>BMC Evolutionary Biology</i> , 2013 , 13, 194	3	48
80	Landscape genetics highlights the role of bank vole metapopulation dynamics in the epidemiology of Puumala hantavirus. <i>Molecular Ecology</i> , 2011 , 20, 3569-83	5.7	46
79	Detection of <i>Orientia</i> sp. DNA in rodents from Asia, West Africa and Europe. <i>Parasites and Vectors</i> , 2015 , 8, 172	4	45
78	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003929	4.8	45
77	The Transplantation of β 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	0.9	45
76	ChickRH6: a chicken whole-genome radiation hybrid panel. <i>Genetics Selection Evolution</i> , 2002 , 34, 521-334.9		44
75	Molecular identification of four cryptic species of <i>Mastomys</i> (Rodentia, Murinae). <i>Biochemical Systematics and Ecology</i> , 2005 , 33, 681-689	1.4	44
74	The genetic similarity between pair members influences the frequency of extrapair paternity in alpine marmots. <i>Animal Behaviour</i> , 2008 , 76, 87-95	2.8	41
73	Assessment of a 16S rRNA amplicon Illumina sequencing procedure for studying the microbiome of a symbiont-rich aphid genus. <i>Molecular Ecology Resources</i> , 2016 , 16, 628-40	8.4	40
72	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, 341-8	4.4	39
71	Tnf- β 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, 1208-15	4.5	35
70	Host-parasite network structure is associated with community-level immunogenetic diversity. <i>Nature Communications</i> , 2014 , 5, 5172	17.4	34
69	Phylogeography of a Sahelian rodent species <i>Mastomys huberti</i> : a Plio-Pleistocene story of emergence and colonization of humid habitats. <i>Molecular Ecology</i> , 2008 , 17, 1036-53	5.7	32
68	Kinship, dispersal and hantavirus transmission in bank and common voles. <i>Archives of Virology</i> , 2008 , 153, 435-44	2.6	32
67	Recent discoveries of new hantaviruses widen their range and question their origins. <i>Annals of the New York Academy of Sciences</i> , 2008 , 1149, 84-9	6.5	32

66	Candidatus Neoehrlichia mikurensis in bank voles, France. <i>Emerging Infectious Diseases</i> , 2012 , 18, 2063-510.2	30
65	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	30
64	Species or local environment, what determines the infection of rodents by <i>Toxoplasma gondii</i> ?. <i>Parasitology</i> , 2014 , 141, 259-68	2.7 29
63	Immunogenetic heterogeneity in a widespread ungulate: the European roe deer (<i>Capreolus capreolus</i>). <i>Molecular Ecology</i> , 2015 , 24, 3873-87	5.7 29
62	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	1.6 28
61	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. <i>BMC Microbiology</i> , 2019 , 19, 171	4.5 28
60	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	27
59	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	4.5 25
58	No evidence for ape <i>Plasmodium</i> infections in humans in Gabon. <i>PLoS ONE</i> , 2015 , 10, e0126933	3.7 22
57	No difference between the sexes in fine-scale spatial genetic structure of roe deer. <i>PLoS ONE</i> , 2010 , 5, e14436	3.7 22
56	SESAME (SEquence Sorter & AMPlicon Explorer): genotyping based on high-throughput multiplex amplicon sequencing. <i>Bioinformatics</i> , 2011 , 27, 277-8	7.2 21
55	Polymorphic microsatellite loci and PCR multiplexing in the common vole, <i>Microtus arvalis</i> . <i>Molecular Ecology Notes</i> , 2007 , 7, 830-832	21
54	Deciphering host-parasitoid interactions and parasitism rates of crop pests using DNA metabarcoding. <i>Scientific Reports</i> , 2019 , 9, 3646	4.9 20
53	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	4.8 20
52	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	4.9 20
51	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . <i>Molecular Ecology</i> , 2018 , 27, 264-278	5.7 17
50	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, 2507-12	16
49	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	1.9 16

48	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	3.8	15
47	Linking demography and host dispersal to <i>Trichuris arvicolae</i> distribution in a cyclic vole species. <i>International Journal for Parasitology</i> , 2007 , 37, 813-24	4.3	15
46	Landscape features and helminth co-infection shape bank vole immunoheterogeneity, with consequences for Puumala virus epidemiology. <i>Heredity</i> , 2014 , 112, 274-81	3.6	14
45	Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities. <i>Scientific Reports</i> , 2017 , 7, 14995	4.9	13
44	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		13
43	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	1.9	12
42	A multiplex panel of dinucleotide microsatellite markers for the water vole, <i>Arvicola terrestris</i> . <i>Molecular Ecology Notes</i> , 2004 , 4, 620-622		12
41	Discongruence of Mhc and cytochrome b phylogeographical patterns in <i>Myodes glareolus</i> (Rodentia: Cricetidae). <i>Biological Journal of the Linnean Society</i> , 2012 , 105, 881-899	1.9	11
40	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, 279-90	4.8	11
39	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, 438-54	2.3	11
38	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 ,	1.8	9
37	DNA Metabarcoding as a Tool for Disentangling Food Webs in Agroecosystems. <i>Insects</i> , 2020 , 11,	2.8	9
36	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	6.4	9
35	Both candidate gene and neutral genetic diversity correlate with parasite resistance in female Mediterranean mouflon. <i>BMC Ecology</i> , 2019 , 19, 12	2.7	8
34	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		8
33	Birds and bats contribute to natural regulation of the millet head miner in tree-crop agroforestry systems. <i>Crop Protection</i> , 2020 , 132, 105127	2.7	7
32	In silico and empirical evaluation of twelve metabarcoding primer sets for insectivorous diet analyses. <i>Ecology and Evolution</i> , 2020 , 10, 6310-6332	2.8	7
31	Between-population differences in the genetic and maternal components of body mass in roe deer. <i>BMC Evolutionary Biology</i> , 2018 , 18, 39	3	7

30	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 ^{3,1}	7
29	Bank vole immunoheterogeneity may limit Nephropatia Epidemica emergence in a French non-endemic region. <i>Parasitology</i> , 2018 , 145, 393-407	2.7 6
28	Reduced microsatellite heterozygosity does not affect natal dispersal in three contrasting roe deer populations. <i>Oecologia</i> , 2015 , 177, 631-643	2.9 5
27	Immune gene variability influences roe deer natal dispersal. <i>Oikos</i> , 2016 , 125, 1790-1801	4 4
26	Consequences of organ choice in describing bacterial pathogen assemblages in a rodent population. <i>Epidemiology and Infection</i> , 2017 , 145, 3070-3075	4.3 4
25	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	1.8 4
24	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	1.6 4
23	Apport de lâimmunogâique à la compréhension des interactions entre le campagnol roussâtre <i>Myodes glareolus</i> et lâhantavirus Puumala. <i>Bulletin De LAcademie Veterinaire De France</i> , 2013 , 166, 171-183	4
22	Spatio-temporal trends in richness and persistence of bacterial communities in decline-phase water vole populations. <i>Scientific Reports</i> , 2020 , 10, 9506	4.9 4
21	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , 2018 , 8, 11273-11292	2.8 4
20	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	4.3 3
19	Genetic epidemiology of the Alpine ibex reservoir of persistent and virulent brucellosis outbreak. <i>Scientific Reports</i> , 2020 , 10, 4400	4.9 3
18	Identifying environmental drivers of spatial genetic structure of the European pine marten (<i>Martes martes</i>). <i>Landscape Ecology</i> , 2017 , 32, 2261-2279	4.3 3
17	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, 144-6	1.9 3
16	A set of 21 polymorphic microsatellites in Alpine chamois (<i>Rupicapra rupicapra</i>). <i>Molecular Ecology Notes</i> , 2007 , 7, 243-247	3
15	Antagonistic pathogen-mediated selection favours the maintenance of innate immune gene polymorphism in a widespread wild ungulate	3
14	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	7.6 3
13	Early life infection and host senescence. <i>Experimental Gerontology</i> , 2018 , 114, 19-26	4.5 3

12	Evaluating metabarcoding to analyse diet composition of species foraging in anthropogenic landscapes using Ion Torrent and Illumina sequencing		2
11	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	2.3	2
10	Differential immune gene expression associated with contemporary range expansion of two invasive rodents in Senegal		1
9	16S rRNA amplicon sequencing for epidemiological surveys of bacteria in wildlife: the importance of cleaning post-sequencing data before estimating positivity, prevalence and co-infection		1
8	Metabarcoding for the parallel identification of several hundred predators and their preys: application to bat species diet analysis		1
7	High throughput amplicon sequencing to assess within- and between-host genetic diversity in plant viruses		1
6	Pathogen community composition and co-infection patterns in a wild community of rodents		1
5	In silico and empirical evaluation of twelve COI & 16S metabarcoding primer sets for insectivorous diet analyses		1
4	Isolation and Genetic Characterization of Puumala Orthohantavirus Strains from France. <i>Pathogens</i> , 2021 , 10,	4.5	1
3	Differential immune gene expression associated with contemporary range expansion in two invasive rodents in Senegal. <i>Scientific Reports</i> , 2020 , 10, 18257	4.9	0
2	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	7.6	0
1	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