

# Maxime Galan

## 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.

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	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> , <b>2022</b> , 2, 100082		0
100	Isolation and Genetic Characterization of Puumala Orthohantavirus Strains from France. <i>Pathogens</i> , <b>2021</b> , 10,	4.5	1
99	Unraveling the dietary diversity of Neotropical top predators using scat DNA metabarcoding: A case study on the elusive Giant Otter. <i>Environmental DNA</i> , <b>2021</b> , 3, 889-900	7.6	0
98	Pathogen-mediated selection favours the maintenance of innate immunity gene polymorphism in a widespread wild ungulate. <i>Journal of Evolutionary Biology</i> , <b>2021</b> , 34, 1156-1166	2.3	2
97	eDNA metabarcoding reveals a core and secondary diets of the greater horseshoe bat with strong spatio-temporal plasticity. <i>Environmental DNA</i> , <b>2021</b> , 3, 277-296	7.6	3
96	DNA Metabarcoding as a Tool for Disentangling Food Webs in Agroecosystems. <i>Insects</i> , <b>2020</b> , 11,	2.8	9
95	Genetic epidemiology of the Alpine ibex reservoir of persistent and virulent brucellosis outbreak. <i>Scientific Reports</i> , <b>2020</b> , 10, 4400	4.9	3
94	Birds and bats contribute to natural regulation of the millet head miner in tree-crop agroforestry systems. <i>Crop Protection</i> , <b>2020</b> , 132, 105127	2.7	7
93	In silico and empirical evaluation of twelve metabarcoding primer sets for insectivorous diet analyses. <i>Ecology and Evolution</i> , <b>2020</b> , 10, 6310-6332	2.8	7
92	Spatio-temporal trends in richness and persistence of bacterial communities in decline-phase water vole populations. <i>Scientific Reports</i> , <b>2020</b> , 10, 9506	4.9	4
91	Differential immune gene expression associated with contemporary range expansion in two invasive rodents in Senegal. <i>Scientific Reports</i> , <b>2020</b> , 10, 18257	4.9	0
90	Disentangling the effect of host genetics and gut microbiota on resistance to an intestinal parasite. <i>International Journal for Parasitology</i> , <b>2019</b> , 49, 873-883	4.3	3
89	Deciphering host-parasitoid interactions and parasitism rates of crop pests using DNA metabarcoding. <i>Scientific Reports</i> , <b>2019</b> , 9, 3646	4.9	20
88	Both candidate gene and neutral genetic diversity correlate with parasite resistance in female Mediterranean mouflon. <i>BMC Ecology</i> , <b>2019</b> , 19, 12	2.7	8
87	rpoB, a promising marker for analyzing the diversity of bacterial communities by amplicon sequencing. <i>BMC Microbiology</i> , <b>2019</b> , 19, 171	4.5	28
86	Metabarcoding for the parallel identification of several hundred predators and their prey: Application to bat species diet analysis. <i>Molecular Ecology Resources</i> , <b>2018</b> , 18, 474-489	8.4	72
85	Between-population differences in the genetic and maternal components of body mass in roe deer. <i>BMC Evolutionary Biology</i> , <b>2018</b> , 18, 39	3	7

84	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> , <b>2018</b> , 121, 199-207	3.8	15
83	Bank vole immunoheterogeneity may limit Nephropatia Epidemica emergence in a French non-endemic region. <i>Parasitology</i> , <b>2018</b> , 145, 393-407	2.7	6
82	Deciphering the demographic history of allochronic differentiation in the pine processionary moth <i>Thaumetopoea pityocampa</i> . <i>Molecular Ecology</i> , <b>2018</b> , 27, 264-278	5.7	17
81	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> , <b>2018</b> , 91, 36-51	1.9	16
80	Preliminary insights into the genetics of bank vole tolerance to Puumala hantavirus in Sweden. <i>Ecology and Evolution</i> , <b>2018</b> , 8, 11273-11292	2.8	4
79	Evaluating metabarcoding to analyse diet composition of species foraging in anthropogenic landscapes using Ion Torrent and Illumina sequencing. <i>Scientific Reports</i> , <b>2018</b> , 8, 17091	4.9	20
78	Early life infection and host senescence. <i>Experimental Gerontology</i> , <b>2018</b> , 114, 19-26	4.5	3
77	The Transplantation of B PUFA-Altered Gut Microbiota of fat-1 Mice to Wild-Type Littermates Prevents Obesity and Associated Metabolic Disorders. <i>Diabetes</i> , <b>2018</b> , 67, 1512-1523	0.9	45
76	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> , <b>2017</b> , 49, 318-329	4.5	25
75	Novel insights into the diet of the Pyrenean desman ( <i>Galemys pyrenaicus</i> ) using next-generation sequencing molecular analyses. <i>Journal of Mammalogy</i> , <b>2017</b> ,	1.8	9
74	Identifying environmental drivers of spatial genetic structure of the European pine marten ( <i>Martes martes</i> ). <i>Landscape Ecology</i> , <b>2017</b> , 32, 2261-2279	4.3	3
73	Consequences of organ choice in describing bacterial pathogen assemblages in a rodent population. <i>Epidemiology and Infection</i> , <b>2017</b> , 145, 3070-3075	4.3	4
72	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> , <b>2017</b> , 235, 67-72	6.4	9
71	Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities. <i>Scientific Reports</i> , <b>2017</b> , 7, 14995	4.9	13
70	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> , <b>2017</b> , 31, 785-801	1.8	4
69	Assessment of a 16S rRNA amplicon Illumina sequencing procedure for studying the microbiome of a symbiont-rich aphid genus. <i>Molecular Ecology Resources</i> , <b>2016</b> , 16, 628-40	8.4	40
68	Immune gene variability influences roe deer natal dispersal. <i>Oikos</i> , <b>2016</b> , 125, 1790-1801	4	4
67	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> , <b>2016</b> , 29, 438-54	2.3	11

66	16S rRNA Amplicon Sequencing for Epidemiological Surveys of Bacteria in Wildlife. <i>MSystems</i> , <b>2016</b> , 1,	7.6	66
65	Reduced microsatellite heterozygosity does not affect natal dispersal in three contrasting roe deer populations. <i>Oecologia</i> , <b>2015</b> , 177, 631-643	2.9	5
64	Detection of <i>Orientia</i> sp. DNA in rodents from Asia, West Africa and Europe. <i>Parasites and Vectors</i> , <b>2015</b> , 8, 172	4	45
63	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> , <b>2015</b> , 80, 505-509	1.6	28
62	Global parasite and <i>Rattus</i> rodent invasions: The consequences for rodent-borne diseases. <i>Integrative Zoology</i> , <b>2015</b> , 10, 409-23	1.9	59
61	Immunogenetic heterogeneity in a widespread ungulate: the European roe deer ( <i>Capreolus capreolus</i> ). <i>Molecular Ecology</i> , <b>2015</b> , 24, 3873-87	5.7	29
60	No evidence for ape <i>Plasmodium</i> infections in humans in Gabon. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126933	3.7	22
59	A Comparison between Transcriptome Sequencing and 16S Metagenomics for Detection of Bacterial Pathogens in Wildlife. <i>PLoS Neglected Tropical Diseases</i> , <b>2015</b> , 9, e0003929	4.8	45
58	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> , <b>2015</b> , 9, e0004097	4.8	20
57	Empirical assessment of RAD sequencing for interspecific phylogeny. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1272-4	8.3	108
56	Landscape features and helminth co-infection shape bank vole immunoheterogeneity, with consequences for Puumala virus epidemiology. <i>Heredity</i> , <b>2014</b> , 112, 274-81	3.6	14
55	Host-parasite network structure is associated with community-level immunogenetic diversity. <i>Nature Communications</i> , <b>2014</b> , 5, 5172	17.4	34
54	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> , <b>2014</b> , 7, 233	4	52
53	Species or local environment, what determines the infection of rodents by <i>Toxoplasma gondii</i> ?. <i>Parasitology</i> , <b>2014</b> , 141, 259-68	2.7	29
52	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> , <b>2014</b> , 76, 139-145	1.6	4
51	Contrasted evolutionary histories of two Toll-like receptors (Tlr4 and Tlr7) in wild rodents (MURINAE). <i>BMC Evolutionary Biology</i> , <b>2013</b> , 13, 194	3	48
50	Cytosuclear discordance among Southeast Asian black rats ( <i>Rattus rattus</i> complex). <i>Molecular Ecology</i> , <b>2013</b> , 22, 1019-34	5.7	59
49	Invasion genetics of the introduced black rat ( <i>Rattus rattus</i> ) in Senegal, West Africa. <i>Molecular Ecology</i> , <b>2013</b> , 22, 286-300	5.7	51

48	Estimation of population allele frequencies from next-generation sequencing data: pool-versus individual-based genotyping. <i>Molecular Ecology</i> , <b>2013</b> , 22, 3766-79	5.7	147
47	Apport de lâimmunogâtiqâe âa comprâension des interactions entre le campagnol roussâre <i>Myodes glareolus</i> et lâhantavirus Puumala. <i>Bulletin De LâAcademie Veterinaire De France</i> , <b>2013</b> , 166, 171-183	4	
46	Discongruence of Mhc and cytochrome b phylogeographical patterns in <i>Myodes glareolus</i> (Rodentia: Cricetidae). <i>Biological Journal of the Linnean Society</i> , <b>2012</b> , 105, 881-899	1.9	11
45	Next-generation sequencing for rodent barcoding: species identification from fresh, degraded and environmental samples. <i>PLoS ONE</i> , <b>2012</b> , 7, e48374	3.7	75
44	Candidatus <i>Neoehrlichia mikurensis</i> in bank voles, France. <i>Emerging Infectious Diseases</i> , <b>2012</b> , 18, 2063-510.2	30	
43	Landscape genetics highlights the role of bank vole metapopulation dynamics in the epidemiology of Puumala hantavirus. <i>Molecular Ecology</i> , <b>2011</b> , 20, 3569-83	5.7	46
42	SESAME (SEquence Sorter & AMPlicon Explorer): genotyping based on high-throughput multiplex amplicon sequencing. <i>Bioinformatics</i> , <b>2011</b> , 27, 277-8	7.2	21
41	No difference between the sexes in fine-scale spatial genetic structure of roe deer. <i>PLoS ONE</i> , <b>2010</b> , 5, e14436	3.7	22
40	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> , <b>2010</b> , 91, 2507-12	12.9	16
39	A 454 multiplex sequencing method for rapid and reliable genotyping of highly polymorphic genes in large-scale studies. <i>BMC Genomics</i> , <b>2010</b> , 11, 296	4.5	153
38	Negative relationships between cellular immune response, Mhc class II heterozygosity and secondary sexual trait in the montane water vole. <i>Evolutionary Applications</i> , <b>2010</b> , 3, 279-90	4.8	11
37	Tnf-â 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> , <b>2010</b> , 10, 1208-17	4.7	35
36	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> , <b>2009</b> , 167, 144-6	1.9	3
35	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> , <b>2009</b> , 63, 403-17	3.8	52
34	Multiple paternity occurs with low frequency in the territorial roe deer, <i>Capreolus capreolus</i> . <i>Biological Journal of the Linnean Society</i> , <b>2009</b> , 97, 128-139	1.9	12
33	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> , <b>2008</b> , 21, 1307-20	2.3	55
32	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> , <b>2008</b> , 17, 1036-53	5.7	32
31	The genetic similarity between pair members influences the frequency of extrapair paternity in alpine marmots. <i>Animal Behaviour</i> , <b>2008</b> , 76, 87-95	2.8	41

30	Mating system, sexual dimorphism, and the opportunity for sexual selection in a territorial ungulate. <i>Behavioral Ecology</i> , <b>2008</b> , 19, 309-316	2.3	62
29	Kinship, dispersal and hantavirus transmission in bank and common voles. <i>Archives of Virology</i> , <b>2008</b> , 153, 435-44	2.6	32
28	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> , <b>2008</b> , 8, 450-8	4.5	52
27	Recent discoveries of new hantaviruses widen their range and question their origins. <i>Annals of the New York Academy of Sciences</i> , <b>2008</b> , 1149, 84-9	6.5	32
26	Density-related changes in selection pattern for major histocompatibility complex genes in fluctuating populations of voles. <i>Molecular Ecology</i> , <b>2007</b> , 16, 5084-97	5.7	61
25	A set of 21 polymorphic microsatellites in Alpine chamois ( <i>Rupicapra rupicapra</i> ). <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 243-247		3
24	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> , <b>2007</b> , 7, 684-687		8
23	Polymorphic microsatellite loci and PCR multiplexing in the common vole, <i>Microtus arvalis</i> . <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 830-832		21
22	Linking demography and host dispersal to <i>Trichuris arvicolae</i> distribution in a cyclic vole species. <i>International Journal for Parasitology</i> , <b>2007</b> , 37, 813-24	4.3	15
21	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> , <b>2006</b> , 58, 191-202	3.2	57
20	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> , <b>2006</b> , 273, 341-8	4.4	39
19	Genetic structure is influenced by landscape features: empirical evidence from a roe deer population. <i>Molecular Ecology</i> , <b>2006</b> , 15, 1669-79	5.7	215
18	Migration and recovery of the genetic diversity during the increasing density phase in cyclic vole populations. <i>Molecular Ecology</i> , <b>2006</b> , 15, 2665-76	5.7	84
17	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> , <b>2006</b> , 32, 301-304 <sup>1</sup>		7
16	Analysis of major histocompatibility complex class II gene in water voles using capillary electrophoresis-single stranded conformation polymorphism. <i>Molecular Ecology Notes</i> , <b>2005</b> , 5, 173-176		30
15	Genetic structure of the cyclic fossorial water vole ( <i>Arvicola terrestris</i> ): landscape and demographic influences. <i>Molecular Ecology</i> , <b>2005</b> , 14, 2861-71	5.7	66
14	Molecular identification of four cryptic species of <i>Mastomys</i> (Rodentia, Murinae). <i>Biochemical Systematics and Ecology</i> , <b>2005</b> , 33, 681-689	1.4	44
13	Landscape connectivity influences gene flow in a roe deer population inhabiting a fragmented landscape: an individual-based approach. <i>Molecular Ecology</i> , <b>2004</b> , 13, 2841-50	5.7	290

12	A multiplex panel of microsatellite markers for widespread sub-Saharan rodents of the genus <i>Mastomys</i> . <i>Molecular Ecology Notes</i> , <b>2004</b> , 4, 321-323	13
11	A multiplex panel of dinucleotide microsatellite markers for the water vole, <i>Arvicola terrestris</i> . <i>Molecular Ecology Notes</i> , <b>2004</b> , 4, 620-622	12
10	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> , <b>2003</b> , 3, 142-146	27
9	ChickRH6: a chicken whole-genome radiation hybrid panel. <i>Genetics Selection Evolution</i> , <b>2002</b> , 34, 521-334.9	44
8	Evaluating metabarcoding to analyse diet composition of species foraging in anthropogenic landscapes using Ion Torrent and Illumina sequencing	2
7	Differential immune gene expression associated with contemporary range expansion of two invasive rodents in Senegal	1
6	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
5	Metabarcoding for the parallel identification of several hundred predators and their preys: application to bat species diet analysis	1
4	High throughput amplicon sequencing to assess within- and between-host genetic diversity in plant viruses	1
3	Pathogen community composition and co-infection patterns in a wild community of rodents	1
2	Antagonistic pathogen-mediated selection favours the maintenance of innate immune gene polymorphism in a widespread wild ungulate	3
1	In silico and empirical evaluation of twelve COI & 16S metabarcoding primer sets for insectivorous diet analyses	1