Xavier Bailly

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Research perspectives on animal health in the era of artificial intelligence. Veterinary Research, 2021, 52, 40.	3.0	34
2	Characterization of internal ribosome entry sites according to secondary structure analysis to classify border disease virus strains. Journal of Virological Methods, 2020, 275, 113704.	2.1	1
3	Differential homotypic and heterotypic interactions of antigen 43 (Ag43) variants in autotransporter-mediated bacterial autoaggregation. Scientific Reports, 2019, 9, 11100.	3.3	16
4	Rarity of microbial species: In search of reliable associations. PLoS ONE, 2019, 14, e0200458.	2.5	20
5	Phylogenetics of the Spiroplasma ixodetis endosymbiont reveals past transfers between ticks and other arthropods. Ticks and Tick-borne Diseases, 2019, 10, 575-584.	2.7	28
6	Contribution of nitric oxide synthase from coagulase-negative staphylococci to the development of red myoglobin derivatives. International Journal of Food Microbiology, 2018, 266, 310-316.	4.7	15
7	Does the impact of biodiversity differ between emerging and endemic pathogens? The need to separate the concepts of hazard and risk. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160129.	4.0	58
8	Molecular epidemiology of Coxiella burnetii in French livestock reveals the existence of three main genotype clusters and suggests species-specific associations as well as regional stability. Infection, Genetics and Evolution, 2017, 48, 142-149.	2.3	19
9	Host specificity, pathogen exposure, and superinfections impact the distribution of Anaplasma phagocytophilum genotypes in ticks, roe deer, and livestock in a fragmented agricultural landscape. Infection, Genetics and Evolution, 2017, 55, 31-44.	2.3	15
10	Hidden Markov phylogenetic models offer an interesting perspective to identify "high risk lineages―of environmental pathogens. Infection, Genetics and Evolution, 2017, 55, 45-47.	2.3	3
11	Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a l²-Helical Passenger. Frontiers in Microbiology, 2017, 8, 2607.	3.5	17
12	Multiple independent transmission cycles of a tick-borne pathogen within a local host community. Scientific Reports, 2016, 6, 31273.	3.3	11
13	Mapping human risk of infection with Borrelia burgdorferi sensu lato, the agent of Lyme borreliosis, in a periurban forest in France. Ticks and Tick-borne Diseases, 2016, 7, 644-652.	2.7	52
14	Interdisciplinarity and Infectious Diseases: An Ebola Case Study. PLoS Pathogens, 2015, 11, e1004992.	4.7	25
15	Bacterial genospecies that are not ecologically coherent: population genomics of <i>Rhizobium leguminosarum</i> . Open Biology, 2015, 5, 140133.	3.6	160
16	Metacommunity and phylogenetic structure determine wildlife and zoonotic infectious disease patterns in time and space. Ecology and Evolution, 2015, 5, 865-873.	1.9	64
17	Circulation of Coxiella burnetii in a Naturally Infected Flock of Dairy Sheep: Shedding Dynamics, Environmental Contamination, and Genotype Diversity. Applied and Environmental Microbiology, 2015, 81, 7253-7260.	3.1	46
18	Comparative Population Genomics of the Borrelia burgdorferi Species Complex Reveals High Degree of Genetic Isolation among Species and Underscores Benefits and Constraints to Studying Intra-Specific Epidemiological Processes. PLoS ONE, 2014, 9, e94384.	2.5	25

XAVIER BAILLY

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19	Multilocus sequence analysis of Anaplasma phagocytophilum reveals three distinct lineages with different host ranges in clinically ill French cattle. Veterinary Research, 2014, 45, 114.	3.0	26
20	A new multiple-locus variable-number tandem repeat analysis reveals different clusters for Anaplasma phagocytophilum circulating in domestic and wild ruminants. Parasites and Vectors, 2014, 7, 439.	2.5	32
21	High-Throughput Sequence Typing Reveals Genetic Differentiation and Host Specialization among Populations of the Borrelia burgdorferi Species Complex that Infect Rodents. PLoS ONE, 2014, 9, e88581.	2.5	26
22	Single Genotype of <i>Anaplasma phagocytophilum</i> Identified from Ticks, Camargue, France. Emerging Infectious Diseases, 2013, 19, 825-7.	4.3	26
23	Population genomics of <i>Sinorhizobium medicae</i> based on low-coverage sequencing of sympatric isolates. ISME Journal, 2011, 5, 1722-1734.	9.8	41
24	Nickel Resistance Determinants in <i>Bradyrhizobium</i> Strains from Nodules of the Endemic New Caledonia Legume <i>Serianthes calycina</i> . Applied and Environmental Microbiology, 2007, 73, 8018-8022.	3.1	49
25	Horizontal Gene Transfer and Homologous Recombination Drive the Evolution of the Nitrogen-Fixing Symbionts of Medicago Species. Journal of Bacteriology, 2007, 189, 5223-5236.	2.2	80
26	New analysis for consistency among markers in the study of genetic diversity: development and application to the description of bacterial diversity. BMC Evolutionary Biology, 2007, 7, 156.	3.2	10
27	Distribution ofMedicagoSpecies and Their Microsymbionts in a Saline Region of Algeria. Arid Land Research and Management, 2006, 20, 219-231.	1.6	5
28	Recombination and selection shape the molecular diversity pattern of nitrogen-fixing Sinorhizobium sp. associated to Medicago. Molecular Ecology, 2006, 15, 2719-2734.	3.9	77
29	Development of a lab-made microarray for analyzing the genetic diversity of nitrogen fixing symbionts Sinorhizobium meliloti and Sinorhizobium medicae. Journal of Microbiological Methods, 2006, 67, 114-124.	1.6	7
30	Nitrogen-fixing sinorhizobia with Medicago laciniata constitute a novel biovar (bv. medicaginis) of S. meliloti. Systematic and Applied Microbiology, 2006, 29, 526-538.	2.8	65
31	Nitrogen-fixing nodules from rose wood legume trees (Dalbergia spp.) endemic to Madagascar host seven different genera belonging to α- and β-Proteobacteria. Molecular Ecology, 2005, 14, 4135-4146.	3.9	108
32	Analysis of microsatellite variation in the spider mite pest Tetranychus turkestani (Acari:) Tj ETQq0 0 0 rgBT /Ove	rlock 10 Tf	50 227 Td (

factors. Biological Journal of the Linnean Society, 2004, 82, 69-78.