

Xavier Bailly

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,221
citations

361413

20
h-index

414414

32
g-index

34
all docs

34
docs citations

34
times ranked

1919
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Bacterial genospecies that are not ecologically coherent: population genomics of <i>Rhizobium leguminosarum</i> . <i>Open Biology</i> , 2015, 5, 140133. | 3.6 | 160 |
| 2 | Nitrogen-fixing nodules from rose wood legume trees (<i>Dalbergia</i> spp.) endemic to Madagascar host seven different genera belonging to α - and β -Proteobacteria. <i>Molecular Ecology</i> , 2005, 14, 4135-4146. | 3.9 | 108 |
| 3 | Horizontal Gene Transfer and Homologous Recombination Drive the Evolution of the Nitrogen-Fixing Symbionts of <i>Medicago</i> Species. <i>Journal of Bacteriology</i> , 2007, 189, 5223-5236. | 2.2 | 80 |
| 4 | Recombination and selection shape the molecular diversity pattern of nitrogen-fixing <i>Sinorhizobium</i> sp. associated to <i>Medicago</i> . <i>Molecular Ecology</i> , 2006, 15, 2719-2734. | 3.9 | 77 |
| 5 | Nitrogen-fixing sinorhizobia with <i>Medicago laciniata</i> constitute a novel biovar (bv. <i>medicaginis</i>) of <i>S. meliloti</i> . <i>Systematic and Applied Microbiology</i> , 2006, 29, 526-538. | 2.8 | 65 |
| 6 | Metacommunity and phylogenetic structure determine wildlife and zoonotic infectious disease patterns in time and space. <i>Ecology and Evolution</i> , 2015, 5, 865-873. | 1.9 | 64 |
| 7 | Does the impact of biodiversity differ between emerging and endemic pathogens? The need to separate the concepts of hazard and risk. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160129. | 4.0 | 58 |
| 8 | Mapping human risk of infection with <i>Borrelia burgdorferi sensu lato</i> , the agent of Lyme borreliosis, in a periurban forest in France. <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 644-652. | 2.7 | 52 |
| 9 | Analysis of microsatellite variation in the spider mite pest <i>Tetranychus turkestanii</i> (Acari: Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5 factors). <i>Biological Journal of the Linnean Society</i> , 2004, 82, 69-78. | 1.6 | 50 |
| 10 | Nickel Resistance Determinants in <i>Bradyrhizobium</i> Strains from Nodules of the Endemic New Caledonia Legume <i>Serianthes calycina</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 8018-8022. | 3.1 | 49 |
| 11 | Circulation of <i>Coxiella burnetii</i> in a Naturally Infected Flock of Dairy Sheep: Shedding Dynamics, Environmental Contamination, and Genotype Diversity. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7253-7260. | 3.1 | 46 |
| 12 | Population genomics of <i>Sinorhizobium medicae</i> based on low-coverage sequencing of sympatric isolates. <i>ISME Journal</i> , 2011, 5, 1722-1734. | 9.8 | 41 |
| 13 | Research perspectives on animal health in the era of artificial intelligence. <i>Veterinary Research</i> , 2021, 52, 40. | 3.0 | 34 |
| 14 | A new multiple-locus variable-number tandem repeat analysis reveals different clusters for <i>Anaplasma phagocytophilum</i> circulating in domestic and wild ruminants. <i>Parasites and Vectors</i> , 2014, 7, 439. | 2.5 | 32 |
| 15 | Phylogenetics of the <i>Spiroplasma ixodetis</i> endosymbiont reveals past transfers between ticks and other arthropods. <i>Ticks and Tick-borne Diseases</i> , 2019, 10, 575-584. | 2.7 | 28 |
| 16 | Single Genotype of <i>Anaplasma phagocytophilum</i> Identified from Ticks, Camargue, France. <i>Emerging Infectious Diseases</i> , 2013, 19, 825-7. | 4.3 | 26 |
| 17 | Multilocus sequence analysis of <i>Anaplasma phagocytophilum</i> reveals three distinct lineages with different host ranges in clinically ill French cattle. <i>Veterinary Research</i> , 2014, 45, 114. | 3.0 | 26 |
| 18 | High-Throughput Sequence Typing Reveals Genetic Differentiation and Host Specialization among Populations of the <i>Borrelia burgdorferi</i> Species Complex that Infect Rodents. <i>PLoS ONE</i> , 2014, 9, e88581. | 2.5 | 26 |

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| 19 | Comparative Population Genomics of the <i>Borrelia burgdorferi</i> Species Complex Reveals High Degree of Genetic Isolation among Species and Underscores Benefits and Constraints to Studying Intra-Specific Epidemiological Processes. <i>PLoS ONE</i> , 2014, 9, e94384. | 2.5 | 25 |
| 20 | Interdisciplinarity and Infectious Diseases: An Ebola Case Study. <i>PLoS Pathogens</i> , 2015, 11, e1004992. | 4.7 | 25 |
| 21 | Rarity of microbial species: In search of reliable associations. <i>PLoS ONE</i> , 2019, 14, e0200458. | 2.5 | 20 |
| 22 | Molecular epidemiology of <i>Coxiella burnetii</i> in French livestock reveals the existence of three main genotype clusters and suggests species-specific associations as well as regional stability. <i>Infection, Genetics and Evolution</i> , 2017, 48, 142-149. | 2.3 | 19 |
| 23 | Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a β^2 -Helical Passenger. <i>Frontiers in Microbiology</i> , 2017, 8, 2607. | 3.5 | 17 |
| 24 | Differential homotypic and heterotypic interactions of antigen 43 (Ag43) variants in autotransporter-mediated bacterial autoaggregation. <i>Scientific Reports</i> , 2019, 9, 11100. | 3.3 | 16 |
| 25 | Host specificity, pathogen exposure, and superinfections impact the distribution of <i>Anaplasma phagocytophilum</i> genotypes in ticks, roe deer, and livestock in a fragmented agricultural landscape. <i>Infection, Genetics and Evolution</i> , 2017, 55, 31-44. | 2.3 | 15 |
| 26 | Contribution of nitric oxide synthase from coagulase-negative staphylococci to the development of red myoglobin derivatives. <i>International Journal of Food Microbiology</i> , 2018, 266, 310-316. | 4.7 | 15 |
| 27 | Multiple independent transmission cycles of a tick-borne pathogen within a local host community. <i>Scientific Reports</i> , 2016, 6, 31273. | 3.3 | 11 |
| 28 | New analysis for consistency among markers in the study of genetic diversity: development and application to the description of bacterial diversity. <i>BMC Evolutionary Biology</i> , 2007, 7, 156. | 3.2 | 10 |
| 29 | Development of a lab-made microarray for analyzing the genetic diversity of nitrogen fixing symbionts <i>Sinorhizobium meliloti</i> and <i>Sinorhizobium medicae</i> . <i>Journal of Microbiological Methods</i> , 2006, 67, 114-124. | 1.6 | 7 |
| 30 | Distribution of <i>Medicago</i> Species and Their Microsymbionts in a Saline Region of Algeria. <i>Arid Land Research and Management</i> , 2006, 20, 219-231. | 1.6 | 5 |
| 31 | Hidden Markov phylogenetic models offer an interesting perspective to identify "high risk lineages" of environmental pathogens. <i>Infection, Genetics and Evolution</i> , 2017, 55, 45-47. | 2.3 | 3 |
| 32 | Characterization of internal ribosome entry sites according to secondary structure analysis to classify border disease virus strains. <i>Journal of Virological Methods</i> , 2020, 275, 113704. | 2.1 | 1 |