

# Damien F Meyer

## List of Publications by Year in descending order

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Version: 2024-02-01

35  
papers

1,666  
citations

361413

20  
h-index

377865

34  
g-index

40  
all docs

40  
docs citations

40  
times ranked

1943  
citing authors

#	ARTICLE	IF	CITATIONS
1	KaruBioNet: a network and discussion group for a better collaboration and structuring of bioinformatics in Guadeloupe (French West Indies). <i>Bioinformatics Advances</i> , 2022, 2, .	2.4	7
2	The super repertoire of type IV effectors in the pangenome of <i>Ehrlichia</i> spp. provides insights into host-specificity and pathogenesis. <i>PLoS Computational Biology</i> , 2021, 17, e1008788.	3.2	7
3	Critical Evaluation of Cross-Sectoral Collaborations to Inform the Implementation of the “One Health” Approach in Guadeloupe. <i>Frontiers in Public Health</i> , 2021, 9, 652079.	2.7	1
4	Searching algorithm for Type IV effector proteins (S4TE) 2.0: Improved tools for Type IV effector prediction, analysis and comparison in proteobacteria. <i>PLoS Computational Biology</i> , 2019, 15, e1006847.	3.2	33
5	Comparative Transcriptome Profiling of Virulent and Attenuated <i>Ehrlichia ruminantium</i> Strains Highlighted Strong Regulation of map1- and Metabolism Related Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 153.	3.9	9
6	Comparative Genomics of the Zoonotic Pathogen <i>Ehrlichia chaffeensis</i> Reveals Candidate Type IV Effectors and Putative Host Cell Targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 6, 204.	3.9	5
7	Iron Starvation Conditions Upregulate <i>Ehrlichia ruminantium</i> Type IV Secretion System, tr1 Transcription Factor and map1 Genes Family through the Master Regulatory Protein ErxR. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 535.	3.9	16
8	Interactions “ <i>Candidatus Liberibacter solanacearum</i> ”- <i>Bactericera cockerelli</i> : Haplotype Effect on Vector Fitness and Gene Expression Analyses. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 62.	3.9	47
9	Economic Game Theory to Model the Attenuation of Virulence of an Obligate Intracellular Bacterium. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 86.	3.9	14
10	Recombination Is a Major Driving Force of Genetic Diversity in the Anaplasmataceae <i>Ehrlichia ruminantium</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 111.	3.9	21
11	<i>Ehrlichia</i> 's molecular tricks to manipulate their host cells. <i>Microbes and Infection</i> , 2016, 18, 172-179.	1.9	30
12	Proteomic Profiling of the Outer Membrane Fraction of the Obligate Intracellular Bacterial Pathogen <i>Ehrlichia ruminantium</i> . <i>PLoS ONE</i> , 2015, 10, e0116758.	2.5	21
13	Identification and Characterization of <i>Anaplasma phagocytophilum</i> Proteins Involved in Infection of the Tick Vector, <i>Ixodes scapularis</i> . <i>PLoS ONE</i> , 2015, 10, e0137237.	2.5	31
14	Understanding Anaplasmataceae pathogenesis using “Omics” approaches. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 86.	3.9	30
15	Searching algorithm for type IV secretion system effectors 1.0: a tool for predicting type IV effectors and exploring their genomic context. <i>Nucleic Acids Research</i> , 2013, 41, 9218-9229.	14.5	50
16	Omics approaches to study the <i>Rickettsia Ehrlichia ruminantium</i> : towards improved knowledge on Heartwater disease. , 2013, , 112-115.		0
17	A new typing technique for the Rickettsiales <i>Ehrlichia ruminantium</i> : Multiple-locus variable number tandem repeat analysis. <i>Journal of Microbiological Methods</i> , 2012, 88, 205-211.	1.6	15
18	Tick-borne diseases in cattle: Applications of proteomics to develop new generation vaccines. <i>Journal of Proteomics</i> , 2012, 75, 4232-4250.	2.4	71

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19	Global gene expression profiling of <i>Ehrlichia ruminantium</i> at different stages of development. FEMS Immunology and Medical Microbiology, 2012, 64, 66-73.	2.7	28
20	Proteomic analyses of <i>Ehrlichia ruminantium</i> highlight differential expression of MAP1-family proteins. Veterinary Microbiology, 2012, 156, 305-314.	1.9	19
21	Tick-borne diseases in cattle: applications of proteomics and the development of new generation vaccines. , 2012, , 46-49.		0
22	Two New Complete Genome Sequences Offer Insight into Host and Tissue Specificity of Plant Pathogenic <i>Xanthomonas</i> spp. Journal of Bacteriology, 2011, 193, 5450-5464.	2.2	189
23	Mining the genetic diversity of <i>Ehrlichia ruminantium</i> using map genes family. Veterinary Parasitology, 2010, 167, 187-195.	1.8	23
24	Analysis of <i>Amblyomma</i> surveillance data in the Caribbean: Lessons for future control programmes. Veterinary Parasitology, 2010, 167, 327-335.	1.8	14
25	Identification of a genetic lineage within <i>Xanthomonas arboricola</i> pv. <i>juglandis</i> as the causal agent of vertical oozing canker of Persian (English) walnut in France. Plant Pathology, 2010, 59, 1014-1022.	2.4	40
26	Efficiency of inactivated vaccines against heartwater in Burkina Faso: Impact of <i>Ehrlichia ruminantium</i> genetic diversity. Vaccine, 2010, 28, 4573-4580.	3.8	25
27	Innovative approach for transcriptomic analysis of obligate intracellular pathogen: selective capture of transcribed sequences of <i>Ehrlichia ruminantium</i> . BMC Molecular Biology, 2009, 10, 111.	3.0	20
28	MLST scheme of <i>Ehrlichia ruminantium</i> : Genomic stasis and recombination in strains from Burkina-Faso. Infection, Genetics and Evolution, 2009, 9, 1320-1328.	2.3	24
29	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 204.	2.8	327
30	Genome sequence and rapid evolution of the rice pathogen <i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A. BMC Genomics, 2008, 9, 534.	2.8	33
31	The Type III Secretion System of <i>Xanthomonas fuscans</i> subsp. <i>fuscans</i> Is Involved in the Phyllosphere Colonization Process and in Transmission to Seeds of Susceptible Beans. Applied and Environmental Microbiology, 2008, 74, 2669-2678.	3.1	55
32	Plant Carbohydrate Scavenging through TonB-Dependent Receptors: A Feature Shared by Phytopathogenic and Aquatic Bacteria. PLoS ONE, 2007, 2, e224.	2.5	289
33	PopF1 and PopF2, Two Proteins Secreted by the Type III Protein Secretion System of <i>Ralstonia solanacearum</i> , Are Translocators Belonging to the HrpF/NopX Family. Journal of Bacteriology, 2006, 188, 4903-4917.	2.2	43
34	Optimization of pathogenicity assays to study the <i>Arabidopsis thaliana</i> <i>Xanthomonas campestris</i> pv. <i>campestris</i> pathosystem. Molecular Plant Pathology, 2005, 6, 327-333.	4.2	66
35	Host plant-dependent phenotypic reversion of <i>Ralstonia solanacearum</i> from non-pathogenic to pathogenic forms via alterations in the <i>phcA</i> gene. Molecular Microbiology, 2003, 49, 991-1003.	2.5	59