

# 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	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
2	Plant Carbohydrate Scavenging through TonB-Dependent Receptors: A Feature Shared by Phytopathogenic and Aquatic Bacteria. PLoS ONE, 2007, 2, e224.	2.5	289
3	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
4	Tick-borne diseases in cattle: Applications of proteomics to develop new generation vaccines. Journal of Proteomics, 2012, 75, 4232-4250.	2.4	71
5	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
6	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
7	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
8	Searching algorithm for type IV secretion system effectors 1.0: a tool for predicting type IV effectors and exploring their genomic context. Nucleic Acids Research, 2013, 41, 9218-9229.	14.5	50
9	Interactions <i>Candidatus Liberibacter solanacearum</i> <i>Bactericera cockerelli</i> : Haplotype Effect on Vector Fitness and Gene Expression Analyses. Frontiers in Cellular and Infection Microbiology, 2016, 6, 62.	3.9	47
10	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
11	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
12	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
13	Searching algorithm for Type IV effector proteins (S4TE) 2.0: Improved tools for Type IV effector prediction, analysis and comparison in proteobacteria. PLoS Computational Biology, 2019, 15, e1006847.	3.2	33
14	Identification and Characterization of <i>Anaplasma phagocytophilum</i> Proteins Involved in Infection of the Tick Vector, <i>Ixodes scapularis</i> . PLoS ONE, 2015, 10, e0137237.	2.5	31
15	Understanding Anaplasmataceae pathogenesis using "Omics" approaches. Frontiers in Cellular and Infection Microbiology, 2014, 4, 86.	3.9	30
16	<i>Ehrlichia</i> 's molecular tricks to manipulate their host cells. Microbes and Infection, 2016, 18, 172-179.	1.9	30
17	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
18	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

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19	MLST scheme of Ehrlichia ruminantium: Genomic stasis and recombination in strains from Burkina-Faso. <i>Infection, Genetics and Evolution</i> , 2009, 9, 1320-1328.	2.3	24
20	Mining the genetic diversity of Ehrlichia ruminantium using map genes family. <i>Veterinary Parasitology</i> , 2010, 167, 187-195.	1.8	23
21	Proteomic Profiling of the Outer Membrane Fraction of the Obligate Intracellular Bacterial Pathogen Ehrlichia ruminantium. <i>PLoS ONE</i> , 2015, 10, e0116758.	2.5	21
22	Recombination Is a Major Driving Force of Genetic Diversity in the Anaplasmataceae Ehrlichia ruminantium. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 111.	3.9	21
23	Innovative approach for transcriptomic analysis of obligate intracellular pathogen: selective capture of transcribed sequences of Ehrlichia ruminantium. <i>BMC Molecular Biology</i> , 2009, 10, 111.	3.0	20
24	Proteomic analyses of Ehrlichia ruminantium highlight differential expression of MAP1-family proteins. <i>Veterinary Microbiology</i> , 2012, 156, 305-314.	1.9	19
25	Iron Starvation Conditions Upregulate Ehrlichia ruminantium 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
26	A new typing technique for the Rickettsiales Ehrlichia ruminantium: Multiple-locus variable number tandem repeat analysis. <i>Journal of Microbiological Methods</i> , 2012, 88, 205-211.	1.6	15
27	Analysis of Amblyomma surveillance data in the Caribbean: Lessons for future control programmes. <i>Veterinary Parasitology</i> , 2010, 167, 327-335.	1.8	14
28	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
29	Comparative Transcriptome Profiling of Virulent and Attenuated Ehrlichia ruminantium Strains Highlighted Strong Regulation of map1- and Metabolism Related Genes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 153.	3.9	9
30	The super repertoire of type IV effectors in the pangenome of Ehrlichia spp. provides insights into host-specificity and pathogenesis. <i>PLoS Computational Biology</i> , 2021, 17, e1008788.	3.2	7
31	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
32	Comparative Genomics of the Zoonotic Pathogen Ehrlichia chaffeensis Reveals Candidate Type IV Effectors and Putative Host Cell Targets. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 6, 204.	3.9	5
33	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
34	Tick-borne diseases in cattle: applications of proteomics and the development of new generation vaccines. , 2012, , 46-49.		0
35	Omics approaches to study the Rickettsia Ehrlichia ruminantium: towards improved knowledge on Heartwater disease. , 2013, , 112-115.		0