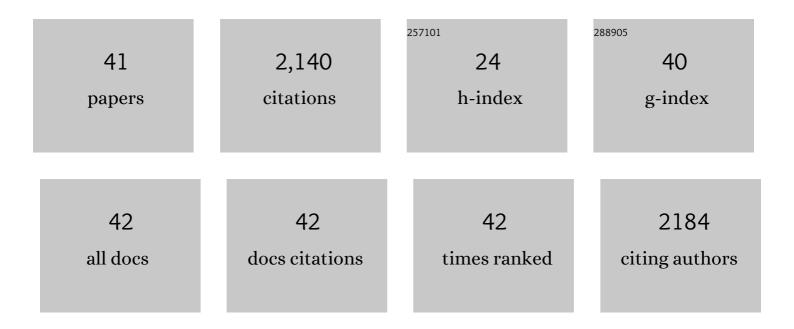
Sophie Payot

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	FirmiData: a set of 40 genomes of Firmicutes with a curated annotation of ICEs and IMEs. BMC Research Notes, 2022, 15, 157.	0.6	2
2	Structural and Biochemical Analysis of OrfG: The VirB8-like Component of the Conjugative Type IV Secretion System of ICESt3 From Streptococcus thermophilus. Frontiers in Molecular Biosciences, 2021, 8, 642606.	1.6	3
3	Update on the Mechanisms of Antibiotic Resistance and the Mobile Resistome in the Emerging Zoonotic Pathogen Streptococcus suis. Microorganisms, 2021, 9, 1765.	1.6	23
4	Chromosomal Conjugative and Mobilizable Elements in Streptococcus suis: Major Actors in the Spreading of Antimicrobial Resistance and Bacteriocin Synthesis Genes. Pathogens, 2020, 9, 22.	1.2	28
5	Abundance, Diversity and Role of ICEs and IMEs in the Adaptation of Streptococcus salivarius to the Environment. Genes, 2020, 11, 999.	1.0	10
6	Mobilization of IMEs Integrated in the oriT of ICEs Involves Their Own Relaxase Belonging to the Rep-Trans Family of Proteins. Genes, 2020, 11, 1004.	1.0	3
7	Characterization of a relaxase belonging to the MOBT family, a widespread family in Firmicutes mediating the transfer of ICEs. Mobile DNA, 2019, 10, 18.	1.3	17
8	Surface proteins involved in the adhesion of Streptococcus salivarius to human intestinal epithelial cells. Applied Microbiology and Biotechnology, 2018, 102, 2851-2865.	1.7	26
9	Impact of Cell Surface Molecules on Conjugative Transfer of the Integrative and Conjugative Element ICE <i>St3</i> of Streptococcus thermophilus. Applied and Environmental Microbiology, 2018, 84, .	1.4	17
10	Diversity of Integrative and Conjugative Elements of Streptococcus salivarius and Their Intra- and Interspecies Transfer. Applied and Environmental Microbiology, 2017, 83, .	1.4	22
11	A Climpse into the World of Integrative and Mobilizable Elements in Streptococci Reveals an Unexpected Diversity and Novel Families of Mobilization Proteins. Frontiers in Microbiology, 2017, 8, 443.	1.5	33
12	The Obscure World of Integrative and Mobilizable Elements, Highly Widespread Elements that Pirate Bacterial Conjugative Systems. Genes, 2017, 8, 337.	1.0	94
13	Antigen I/II encoded by integrative and conjugative elements of Streptococcus agalactiae and role in biofilm formation. Microbial Pathogenesis, 2015, 88, 1-9.	1.3	28
14	Resistance Genes and Genetic Elements Associated with Antibiotic Resistance in Clinical and Commensal Isolates of Streptococcus salivarius. Applied and Environmental Microbiology, 2015, 81, 4155-4163.	1.4	38
15	Analysis of Streptococcus agalactiae pan-genome for prevalence, diversity and functionality of integrative and conjugative or mobilizable elements integrated in the tRNALys CTT gene. Molecular Genetics and Genomics, 2015, 290, 1727-1740.	1.0	22
16	New Insights into the Classification and Integration Specificity of Streptococcus Integrative Conjugative Elements through Extensive Genome Exploration. Frontiers in Microbiology, 2015, 6, 1483.	1.5	64
17	Conjugative and mobilizable genomic islands in bacteria: evolution and diversity. FEMS Microbiology Reviews, 2014, 38, 720-760.	3.9	294
18	High Genetic Diversity among Strains of the Unindustrialized Lactic Acid Bacterium Carnobacterium maltaromaticum in Dairy Products as Revealed by Multilocus Sequence Typing. Applied and Environmental Microbiology, 2014, 80, 3920-3929.	1.4	19

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19	Conjugative Transfer and cis-Mobilization of a Genomic Island by an Integrative and Conjugative Element of Streptococcus agalactiae. Journal of Bacteriology, 2013, 195, 1142-1151.	1.0	22
20	Characterization of Carnobacterium maltaromaticum LMA 28 for its positive technological role in soft cheese making. Food Microbiology, 2013, 36, 223-230.	2.1	22
21	Characterization of a New CAMP Factor Carried by an Integrative and Conjugative Element in Streptococcus agalactiae and Spreading in Streptococci. PLoS ONE, 2012, 7, e48918.	1.1	28
22	Diversity and Mobility of Integrative and Conjugative Elements in Bovine Isolates of <i>S</i> <i>treptococcus agalactiae</i> , <i>S. dysgalactiae</i> subsp. <i>dysgalactiae</i> , and <i>S. uberis</i> . Applied and Environmental Microbiology, 2010, 76, 7957-7965.	1.4	75
23	Integrative Conjugative Elements and Related Elements Are Major Contributors to the Genome Diversity of <i>Streptococcus agalactiae</i> . Journal of Bacteriology, 2008, 190, 6913-6917.	1.0	74
24	Regulation of the expression of the CmeABC efflux pump inCampylobacter jejuni: identification of a point mutation abolishing the binding of the CmeR repressor in anin vitro-selected multidrug-resistant mutant. FEMS Microbiology Letters, 2007, 267, 89-94.	0.7	30
25	Fitness of antimicrobial-resistant Campylobacter and Salmonella. Microbes and Infection, 2006, 8, 1972-1978.	1.0	78
26	Mechanisms of fluoroquinolone and macrolide resistance in Campylobacter spp Microbes and Infection, 2006, 8, 1967-1971.	1.0	176
27	High genetic variation in the multidrug transporter cmeB gene in Campylobacter jejuni and Campylobacter coli. Journal of Antimicrobial Chemotherapy, 2006, 58, 168-172.	1.3	23
28	Synergy between Efflux Pump CmeABC and Modifications in Ribosomal Proteins L4 and L22 in Conferring Macrolide Resistance in Campylobacter jejuni and Campylobacter coli. Antimicrobial Agents and Chemotherapy, 2006, 50, 3893-3896.	1.4	99
29	Involvement of the CmeABC efflux pump in the macrolide resistance of Campylobacter coli. Journal of Antimicrobial Chemotherapy, 2005, 56, 948-950.	1.3	70
30	Bile Salts Modulate Expression of the CmeABC Multidrug Efflux Pump in Campylobacter jejuni. Journal of Bacteriology, 2005, 187, 7417-7424.	1.0	167
31	Prevalence and antimicrobial resistance of Campylobacter coli isolated from fattening pigs in France. Veterinary Microbiology, 2004, 101, 91-99.	0.8	57
32	Relative contribution of target gene mutation and efflux to fluoroquinolone and erythromycin resistance, in French poultry and pig isolates of Campylobacter coli. International Journal of Antimicrobial Agents, 2004, 23, 468-472.	1.1	89
33	Selection and Characterization of Fluoroquinolone-Resistant Mutants ofCampylobacter jejuniUsing Enrofloxacin. Microbial Drug Resistance, 2002, 8, 335-343.	0.9	73
34	Relationships between cellobiose catabolism, enzyme levels, and metabolic intermediates inClostridium cellulolyticum grown in a synthetic medium. , 2000, 67, 327-335.		34
35	The analysis of microbial proteomes: Strategies and data exploitation. Electrophoresis, 2000, 21, 1178-1186.	1.3	29
36	Growth inhibition of Clostridium cellulolyticum by an inefficiently regulated carbon flow. Microbiology (United Kingdom), 1999, 145, 1831-1838.	0.7	43

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#	Article	IF	CITATIONS
37	Effect of dilution rate, cellobiose and ammonium availabilities on Clostridium cellulolyticum sporulation. Applied Microbiology and Biotechnology, 1999, 52, 670-674.	1.7	8
38	Induction of lactate production associated with a decrease in NADH cell content enables growth resumption of Clostridium cellulolyticum in batch cultures on cellobiose. Research in Microbiology, 1999, 150, 465-473.	1.0	17
39	Carbon and Electron Flow in <i>Clostridium cellulolyticum</i> Grown in Chemostat Culture on Synthetic Medium. Journal of Bacteriology, 1999, 181, 3262-3269.	1.0	86
40	The Extracellular Xylan Degradative System in <i>Clostridium cellulolyticum</i> Cultivated on Xylan: Evidence for Cell-Free Cellulosome Production. Journal of Bacteriology, 1999, 181, 4035-4040.	1.0	36
41	Metabolism of cellobiose by Clostridium cellulolyticum growing in continuous culture: evidence for decreased NADH reoxidation as a factor limiting growth. Microbiology (United Kingdom), 1998, 144, 375-384.	0.7	61