## Sébastien Rodrigue

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4965216/publications.pdf

Version: 2024-02-01

46 papers 3,431 citations

218677 26 h-index 214800 47 g-index

50 all docs 50 docs citations

50 times ranked

4583 citing authors

#	Article	IF	Citations
1	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . Science, 2014, 344, 416-420.	12.6	506
2	Patterns and Implications of Gene Gain and Loss in the Evolution of Prochlorococcus. PLoS Genetics, 2007, 3, e231.	3.5	469
3	Whole Genome Amplification and De novo Assembly of Single Bacterial Cells. PLoS ONE, 2009, 4, e6864.	2.5	225
4	$\ddot{\text{l}}\textsc{f}$ Factors and Global Gene Regulation in Mycobacterium tuberculosis. Journal of Bacteriology, 2004, 186, 895-902.	2,2	199
5	The $\ddot{l}f$ factors of Mycobacterium tuberculosis. FEMS Microbiology Reviews, 2006, 30, 926-941.	8.6	191
6	Unlocking Short Read Sequencing for Metagenomics. PLoS ONE, 2010, 5, e11840.	2.5	157
7	Complete Genome Sequence of Escherichia coli BW25113. Genome Announcements, 2014, 2, .	0.8	148
8	Polyphosphate kinase is involved in stressâ€induced <i>mprABâ€sigEâ€rel</i> signalling in mycobacteria. Molecular Microbiology, 2007, 65, 261-276.	2.5	128
9	The Master Activator of IncA/C Conjugative Plasmids Stimulates Genomic Islands and Multidrug Resistance Dissemination. PLoS Genetics, 2014, 10, e1004714.	3.5	106
10	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. ISME Journal, 2013, 7, 184-198.	9.8	105
11	Novel Mycobacterium tuberculosis anti-Ïf factor antagonists control ÏfF activity by distinct mechanisms. Molecular Microbiology, 2002, 45, 1527-1540.	2.5	94
12	Translatome analysis of an NB-LRR immune response identifies important contributors to plant immunity in Arabidopsis. Journal of Experimental Botany, 2017, 68, 2333-2344.	4.8	88
13	Identification of Mycobacterial $\ddot{l}f$ Factor Binding Sites by Chromatin Immunoprecipitation Assays. Journal of Bacteriology, 2007, 189, 1505-1513.	2.2	87
14	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
15	The histone variant H2A.Z is an important regulator of enhancer activity. Nucleic Acids Research, 2015, 43, gkv825.	14.5	80
16	Posttranslational Regulation of Mycobacterium tuberculosis Extracytoplasmic-Function Sigma Factor IfL and Roles in Virulence and in Global Regulation of Gene Expression. Infection and Immunity, 2006, 74, 2457-2461.	2.2	72
17	Evidence of Complex Transcriptional, Translational, and Posttranslational Regulation of the Extracytoplasmic Function Sigma Factor $\parallel f \parallel $	2.2	61
18	Impact of donor–recipient phylogenetic distance on bacterial genome transplantation. Nucleic Acids Research, 2016, 44, 8501-8511.	14.5	60

#	Article	IF	CITATIONS
19	Development of pVCR94Î"X from Vibrio cholerae, a prototype for studying multidrug resistant IncA/C conjugative plasmids. Frontiers in Microbiology, 2014, 5, 44.	3.5	51
20	Transfer activation of SXT/R391 integrative and conjugative elements: unraveling the SetCD regulon. Nucleic Acids Research, 2015, 43, 2045-2056.	14.5	48
21	Highâ€efficiency delivery of CRISPRâ€Cas9 by engineered probiotics enables precise microbiome editing. Molecular Systems Biology, 2021, 17, e10335.	7.2	47
22	Biochemical and molecular characterization of a thermostable chitosanase produced by the strain Paenibacillus sp. 1794 newly isolated from compost. Applied Microbiology and Biotechnology, 2013, 97, 5801-5813.	3.6	41
23	Highly efficient gene transfer in the mouse gut microbiota is enabled by the Incl2 conjugative plasmid TP114. Communications Biology, 2020, 3, 523.	4.4	41
24	Cloning and Transplantation of the <i>Mesoplasma florum</i> Genome. ACS Synthetic Biology, 2018, 7, 209-217.	3.8	40
25	A recombinantMycobacterium tuberculosis in vitrotranscription system. FEMS Microbiology Letters, 2006, 255, 140-147.	1.8	38
26	Comparative Analysis of Mobilizable Genomic Islands. Journal of Bacteriology, 2013, 195, 606-614.	2.2	37
27	Molecular Mechanisms Influencing Bacterial Conjugation in the Intestinal Microbiota. Frontiers in Microbiology, 2021, 12, 673260.	3.5	30
28	Minimal cells, maximal knowledge. ELife, 2019, 8, .	6.0	26
29	A Small-Volume, Low-Cost, and Versatile Continuous Culture Device. PLoS ONE, 2015, 10, e0133384.	2.5	25
30	Unraveling the regulatory network of IncA/C plasmid mobilization: When genomic islands hijack conjugative elements. Mobile Genetic Elements, 2015, 5, 34-38.	1.8	17
31	Inferring the Minimal Genome of $\langle i \rangle$ Mesoplasma florum $\langle i \rangle$ by Comparative Genomics and Transposon Mutagenesis. MSystems, 2018, 3, .	3.8	15
32	Genomeâ€scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	7.2	15
33	Development of <i>oriC</i> -Based Plasmids for Mesoplasma florum. Applied and Environmental Microbiology, 2017, 83, .	3.1	13
34	Bactericidal Activity of the Bacterial ATP Synthase Inhibitor Tomatidine and the Combination of Tomatidine and Aminoglycoside Against Persistent and Virulent Forms of Staphylococcus aureus. Frontiers in Microbiology, 2020, 11, 805.	3.5	13
35	Integrative characterization of the nearâ€minimal bacterium <i>Mesoplasma florum</i> . Molecular Systems Biology, 2020, 16, e9844.	7.2	12
36	Crucial role of $\langle i \rangle$ Salmonella $\langle  i \rangle$ genomic island 1 master activator in the parasitism of IncC plasmids. Nucleic Acids Research, 2021, 49, 7807-7824.	14.5	9

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37	Relative virulence of Staphylococcus aureus bovine mastitis strains representing the main Canadian spa types and clonal complexes as determined using in vitro and in vivo mastitis models. Journal of Dairy Science, 2021, 104, 11904-11921.	3.4	8
38	Complete Genome Sequence of the Mesoplasma florum W37 Strain. Genome Announcements, 2013, $1$ , .	0.8	7
39	Precise Identification of Genome-Wide Transcription Start Sites in Bacteria by 5′-Rapid Amplification of cDNA Ends (5′-RACE). Methods in Molecular Biology, 2015, 1334, 143-159.	0.9	6
40	Precise Identification of DNA-Binding Proteins Genomic Location by Exonuclease Coupled Chromatin Immunoprecipitation (ChIP-exo). Methods in Molecular Biology, 2015, 1334, 173-193.	0.9	5
41	Four National Maps of Broad Forest Type Provide Inconsistent Answers to the Question of What Burns in Canada. Remote Sensing, 2016, 8, 539.	4.0	5
42	Assembly of large mobilizable genetic cargo by double recombinase operated insertion of DNA (DROID). Plasmid, 2019, 104, 102419.	1.4	5
43	The Type IV Pilus of Plasmid TP114 Displays Adhesins Conferring Conjugation Specificity and Is Important for DNA Transfer in the Mouse Gut Microbiota. Microbiology Spectrum, 2022, 10, e0230321.	3.0	5
44	An engineered Mycoplasma pneumoniae to fight Staphylococcus aureus. Molecular Systems Biology, 2021, 17, e10574.	7.2	2
45	Selection and Validation of Spacer Sequences for CRISPR-Cas9 Genome Editing and Transcription Regulation in Bacteria. Methods in Molecular Biology, 2015, 1334, 233-244.	0.9	O
46	The Use of In Silico Genome-Scale Models for the Rational Design of Minimal Cells. , 2020, , 141-175.		0