

SÃ©bastien Rodrigue

List of Publications by Year in descending order

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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	The Type IV Pilus of Plasmid TP114 Displays Adhesins Conferring Conjugation Specificity and Is Important for DNA Transfer in the Mouse Gut Microbiota. <i>Microbiology Spectrum</i> , 2022, 10, e0230321.	3.0	5
2	Crucial role of <i>Salmonella</i> genomic island 1 master activator in the parasitism of IncC plasmids. <i>Nucleic Acids Research</i> , 2021, 49, 7807-7824.	14.5	9
3	Molecular Mechanisms Influencing Bacterial Conjugation in the Intestinal Microbiota. <i>Frontiers in Microbiology</i> , 2021, 12, 673260.	3.5	30
4	Genome-scale metabolic modeling reveals key features of a minimal gene set. <i>Molecular Systems Biology</i> , 2021, 17, e10099.	7.2	15
5	High-efficiency delivery of CRISPR-Cas9 by engineered probiotics enables precise microbiome editing. <i>Molecular Systems Biology</i> , 2021, 17, e10335.	7.2	47
6	An engineered <i>Mycoplasma pneumoniae</i> to fight <i>Staphylococcus aureus</i> . <i>Molecular Systems Biology</i> , 2021, 17, e10574.	7.2	2
7	Relative virulence of <i>Staphylococcus aureus</i> bovine mastitis strains representing the main Canadian spa types and clonal complexes as determined using in vitro and in vivo mastitis models. <i>Journal of Dairy Science</i> , 2021, 104, 11904-11921.	3.4	8
8	Highly efficient gene transfer in the mouse gut microbiota is enabled by the IncI2 conjugative plasmid TP114. <i>Communications Biology</i> , 2020, 3, 523.	4.4	41
9	Bactericidal Activity of the Bacterial ATP Synthase Inhibitor Tomatidine and the Combination of Tomatidine and Aminoglycoside Against Persistent and Virulent Forms of <i>Staphylococcus aureus</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 805.	3.5	13
10	Integrative characterization of the near-minimal bacterium <i>Mesoplasma florum</i> . <i>Molecular Systems Biology</i> , 2020, 16, e9844.	7.2	12
11	The Use of In Silico Genome-Scale Models for the Rational Design of Minimal Cells. , 2020, , 141-175.		0
12	Assembly of large mobilizable genetic cargo by double recombinase operated insertion of DNA (DROID). <i>Plasmid</i> , 2019, 104, 102419.	1.4	5
13	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
14	Minimal cells, maximal knowledge. <i>ELife</i> , 2019, 8, .	6.0	26
15	Cloning and Transplantation of the <i>Mesoplasma florum</i> Genome. <i>ACS Synthetic Biology</i> , 2018, 7, 209-217.	3.8	40
16	Inferring the Minimal Genome of <i>Mesoplasma florum</i> by Comparative Genomics and Transposon Mutagenesis. <i>MSystems</i> , 2018, 3, .	3.8	15
17	Development of <i>oriC</i> -Based Plasmids for <i>Mesoplasma florum</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	13
18	Translatome analysis of an NB-LRR immune response identifies important contributors to plant immunity in <i>Arabidopsis</i> . <i>Journal of Experimental Botany</i> , 2017, 68, 2333-2344.	4.8	88

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19	Four National Maps of Broad Forest Type Provide Inconsistent Answers to the Question of What Burns in Canada. <i>Remote Sensing</i> , 2016, 8, 539.	4.0	5
20	Impact of donorâ€™recipient phylogenetic distance on bacterial genome transplantation. <i>Nucleic Acids Research</i> , 2016, 44, 8501-8511.	14.5	60
21	A Small-Volume, Low-Cost, and Versatile Continuous Culture Device. <i>PLoS ONE</i> , 2015, 10, e0133384.	2.5	25
22	Unraveling the regulatory network of IncA/C plasmid mobilization: When genomic islands hijack conjugative elements. <i>Mobile Genetic Elements</i> , 2015, 5, 34-38.	1.8	17
23	Transfer activation of SXT/R391 integrative and conjugative elements: unraveling the SetCD regulon. <i>Nucleic Acids Research</i> , 2015, 43, 2045-2056.	14.5	48
24	Selection and Validation of Spacer Sequences for CRISPR-Cas9 Genome Editing and Transcription Regulation in Bacteria. <i>Methods in Molecular Biology</i> , 2015, 1334, 233-244.	0.9	0
25	Precise Identification of Genome-Wide Transcription Start Sites in Bacteria by 5â€™-Rapid Amplification of cDNA Ends (5â€™-RACE). <i>Methods in Molecular Biology</i> , 2015, 1334, 143-159.	0.9	6
26	Precise Identification of DNA-Binding Proteins Genomic Location by Exonuclease Coupled Chromatin Immunoprecipitation (ChIP-exo). <i>Methods in Molecular Biology</i> , 2015, 1334, 173-193.	0.9	5
27	The histone variant H2A.Z is an important regulator of enhancer activity. <i>Nucleic Acids Research</i> , 2015, 43, gkv825.	14.5	80
28	Development of pVCR941X from <i>Vibrio cholerae</i> , a prototype for studying multidrug resistant IncA/C conjugative plasmids. <i>Frontiers in Microbiology</i> , 2014, 5, 44.	3.5	51
29	The Master Activator of IncA/C Conjugative Plasmids Stimulates Genomic Islands and Multidrug Resistance Dissemination. <i>PLoS Genetics</i> , 2014, 10, e1004714.	3.5	106
30	Complete Genome Sequence of <i>Escherichia coli</i> BW25113. <i>Genome Announcements</i> , 2014, 2, .	0.8	148
31	Single-Cell Genomics Reveals Hundreds of Coexisting Subpopulations in Wild <i>Prochlorococcus</i> . <i>Science</i> , 2014, 344, 416-420.	12.6	506
32	Biochemical and molecular characterization of a thermostable chitosanase produced by the strain <i>Paenibacillus</i> sp. 1794 newly isolated from compost. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 5801-5813.	3.6	41
33	Complete Genome Sequence of the <i>Mesoplasma florum</i> W37 Strain. <i>Genome Announcements</i> , 2013, 1, .	0.8	7
34	Ecology of uncultured <i>Prochlorococcus</i> clades revealed through single-cell genomics and biogeographic analysis. <i>ISME Journal</i> , 2013, 7, 184-198.	9.8	105
35	Comparative Analysis of Mobilizable Genomic Islands. <i>Journal of Bacteriology</i> , 2013, 195, 606-614.	2.2	37
36	Unlocking Short Read Sequencing for Metagenomics. <i>PLoS ONE</i> , 2010, 5, e11840.	2.5	157

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37	Whole Genome Amplification and De novo Assembly of Single Bacterial Cells. PLoS ONE, 2009, 4, e6864.	2.5	225
38	Evidence of Complex Transcriptional, Translational, and Posttranslational Regulation of the Extracytoplasmic Function Sigma Factor σ^E in Mycobacterium tuberculosis. Journal of Bacteriology, 2008, 190, 5963-5971.	2.2	61
39	Identification of Mycobacterial σ Factor Binding Sites by Chromatin Immunoprecipitation Assays. Journal of Bacteriology, 2007, 189, 1505-1513.	2.2	87
40	Patterns and Implications of Gene Gain and Loss in the Evolution of Prochlorococcus. PLoS Genetics, 2007, 3, e231.	3.5	469
41	Polyphosphate kinase is involved in stress-induced <i>mprAB</i> signalling in mycobacteria. Molecular Microbiology, 2007, 65, 261-276.	2.5	128
42	A recombinant Mycobacterium tuberculosis in vitro transcription system. FEMS Microbiology Letters, 2006, 255, 140-147.	1.8	38
43	The σ factors of Mycobacterium tuberculosis. FEMS Microbiology Reviews, 2006, 30, 926-941.	8.6	191
44	Posttranslational Regulation of Mycobacterium tuberculosis Extracytoplasmic-Function Sigma Factor σ^L and Roles in Virulence and in Global Regulation of Gene Expression. Infection and Immunity, 2006, 74, 2457-2461.	2.2	72
45	σ Factors and Global Gene Regulation in Mycobacterium tuberculosis. Journal of Bacteriology, 2004, 186, 895-902.	2.2	199
46	Novel Mycobacterium tuberculosis anti- σ factor antagonists control σ^E activity by distinct mechanisms. Molecular Microbiology, 2002, 45, 1527-1540.	2.5	94