## Violette Da Cunha

List of Publications by Year in descending order

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VIOLETTE DA CUNHA

#	Article	IF	CITATIONS
1	Streptococcus agalactiae clones infecting humans were selected and fixed through the extensive use of tetracycline. Nature Communications, 2014, 5, 4544.	12.8	208
2	The highly dynamic CRISPR1 system of <i>Streptococcus agalactiae</i> controls the diversity of its mobilome. Molecular Microbiology, 2012, 85, 1057-1071.	2.5	153
3	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. PLoS Genetics, 2017, 13, e1006810.	3.5	136
4	Genome Sequence of <i>Streptococcus gallolyticus</i> : Insights into Its Adaptation to the Bovine Rumen and Its Ability To Cause Endocarditis. Journal of Bacteriology, 2010, 192, 2266-2276.	2.2	120
5	<scp>N</scp> uclease <scp>A</scp> ( <scp>Gbs</scp> 0661), an extracellular nuclease of <i><scp>S</scp>treptococcus agalactiae</i> , attacks the neutrophil extracellular traps and is needed for full virulence. Molecular Microbiology, 2013, 89, 518-531.	2.5	89
6	Reductive evolution in Streptococcus agalactiae and the emergence of a host adapted lineage. BMC Genomics, 2013, 14, 252.	2.8	81
7	Asgard archaea do not close the debate about the universal tree of life topology. PLoS Genetics, 2018, 14, e1007215.	3.5	80
8	Modular Evolution of Tn <i>GBS</i> s, a New Family of Integrative and Conjugative Elements Associating Insertion Sequence Transposition, Plasmid Replication, and Conjugation for Their Spreading. Journal of Bacteriology, 2013, 195, 1979-1990.	2.2	54
9	Single nucleotide resolution RNA-seq uncovers new regulatory mechanisms in the opportunistic pathogen Streptococcus agalactiae. BMC Genomics, 2015, 16, 419.	2.8	53
10	The Abi-domain Protein Abx1 Interacts with the CovS Histidine Kinase to Control Virulence Gene Expression in Group B Streptococcus. PLoS Pathogens, 2013, 9, e1003179.	4.7	47
11	Atypical association of DDE transposition with conjugation specifies a new family of mobile elements. Molecular Microbiology, 2009, 71, 948-959.	2.5	45
12	G-Quadruplexes in the Archaea Domain. Biomolecules, 2020, 10, 1349.	4.0	31
13	Arguments Reinforcing the Three-Domain View of Diversified Cellular Life. Archaea, 2016, 2016, 1-11.	2.3	25
14	Phylogeny of the Varidnaviria Morphogenesis Module: Congruence and Incongruence With the Tree of Life and Viral Taxonomy. Frontiers in Microbiology, 2021, 12, 704052.	3.5	18
15	Rga, a RofA-Like Regulator, Is the Major Transcriptional Activator of the PI-2a Pilus inStreptococcus agalactiae. Microbial Drug Resistance, 2012, 18, 286-297.	2.0	15
16	Comparative genomics reveals conserved positioning of essential genomic clusters in highly rearranged Thermococcales chromosomes. Biochimie, 2015, 118, 313-321.	2.6	15
17	Plasmid vesicles mimicking virions. Nature Microbiology, 2017, 2, 1340-1341.	13.3	9
18	The Tree of Life. Grand Challenges in Biology and Biotechnology, 2018, , 55-99.	2.4	8

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19	Exploring short k-mer profiles in cells and mobile elements from Archaea highlights the major influence of both the ecological niche and evolutionary history. BMC Genomics, 2021, 22, 186.	2.8	8
20	The expanding AsgardÂarchaea and their elusive relationships with Eukarya. , 2022, 1, 3-12.		7
21	NAD+ pool depletion as a signal for the Rex regulon involved in Streptococcus agalactiae virulence. PLoS Pathogens, 2021, 17, e1009791.	4.7	6
22	Archaeal tyrosine recombinases. FEMS Microbiology Reviews, 2021, 45, .	8.6	5
23	The global distribution and evolutionary history of the pT26â€⊋ archaeal plasmid family. Environmental Microbiology, 2019, 21, 4685-4705.	3.8	4
24	WASPS: web-assisted symbolic plasmid synteny server. Bioinformatics, 2019, 36, 1629-1631.	4.1	3
25	Are bacteria claustrophobic? The problem of micrometric spatial confinement for the culturing of micro-organisms. RSC Advances, 2021, 11, 12500-12506.	3.6	3
26	The hyperthermophilic archaeon Thermococcus kodakarensis is resistant to pervasive negative supercoiling activity of DNA gyrase. Nucleic Acids Research, 2021, 49, 12332-12347.	14.5	3
27	Pervasive Suicidal Integrases in Deep-Sea Archaea. Molecular Biology and Evolution, 2020, 37, 1727-1743.	8.9	1
28	BAGET 2.0: an updated web tool for the effortless retrieval of prokaryotic gene context and sequence. Bioinformatics, 2021, 37, 2750-2752.	4.1	1