

Violette Da Cunha

List of Publications by Year in descending order

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Version: 2024-02-01

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papers

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citations

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33
all docs

33
docs citations

33
times ranked

1830
citing authors

#	ARTICLE	IF	CITATIONS
1	The expanding Asgard Archaea and their elusive relationships with Eukarya. , 2022, 1, 3-12.		7
2	Are bacteria claustrophobic? The problem of micrometric spatial confinement for the culturing of micro-organisms. RSC Advances, 2021, 11, 12500-12506.	3.6	3
3	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
4	Archaeal tyrosine recombinases. FEMS Microbiology Reviews, 2021, 45, .	8.6	5
5	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
6	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
7	NAD ⁺ pool depletion as a signal for the Rex regulon involved in Streptococcus agalactiae virulence. PLoS Pathogens, 2021, 17, e1009791.	4.7	6
8	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
9	G-Quadruplexes in the Archaea Domain. Biomolecules, 2020, 10, 1349.	4.0	31
10	Pervasive Suicidal Integrases in Deep-Sea Archaea. Molecular Biology and Evolution, 2020, 37, 1727-1743.	8.9	1
11	WASPS: web-assisted symbolic plasmid synteny server. Bioinformatics, 2019, 36, 1629-1631.	4.1	3
12	The global distribution and evolutionary history of the pT26 archaeal plasmid family. Environmental Microbiology, 2019, 21, 4685-4705.	3.8	4
13	The Tree of Life. Grand Challenges in Biology and Biotechnology, 2018, , 55-99.	2.4	8
14	Asgard archaea do not close the debate about the universal tree of life topology. PLoS Genetics, 2018, 14, e1007215.	3.5	80
15	Plasmid vesicles mimicking virions. Nature Microbiology, 2017, 2, 1340-1341.	13.3	9
16	Lokiarchaea are close relatives of Euryarchaeota, not bridging the gap between prokaryotes and eukaryotes. PLoS Genetics, 2017, 13, e1006810.	3.5	136
17	Arguments Reinforcing the Three-Domain View of Diversified Cellular Life. Archaea, 2016, 2016, 1-11.	2.3	25
18	Comparative genomics reveals conserved positioning of essential genomic clusters in highly rearranged Thermococcales chromosomes. Biochimie, 2015, 118, 313-321.	2.6	15

#	ARTICLE	IF	CITATIONS
19	Single nucleotide resolution RNA-seq uncovers new regulatory mechanisms in the opportunistic pathogen <i>Streptococcus agalactiae</i> . <i>BMC Genomics</i> , 2015, 16, 419.	2.8	53
20	<i>Streptococcus agalactiae</i> clones infecting humans were selected and fixed through the extensive use of tetracycline. <i>Nature Communications</i> , 2014, 5, 4544.	12.8	208
21	<i>Neutrophil</i> nuclease <i>NeuA</i> (<i>Gbs</i> 0661), an extracellular nuclease of <i>Streptococcus agalactiae</i> , attacks the neutrophil extracellular traps and is needed for full virulence. <i>Molecular Microbiology</i> , 2013, 89, 518-531.	2.5	89
22	Reductive evolution in <i>Streptococcus agalactiae</i> and the emergence of a host adapted lineage. <i>BMC Genomics</i> , 2013, 14, 252.	2.8	81
23	Modular Evolution of <i>Tn</i> <i>GBS</i> s, a New Family of Integrative and Conjugative Elements Associating Insertion Sequence Transposition, Plasmid Replication, and Conjugation for Their Spreading. <i>Journal of Bacteriology</i> , 2013, 195, 1979-1990.	2.2	54
24	The Abi-domain Protein Abx1 Interacts with the CovS Histidine Kinase to Control Virulence Gene Expression in Group B <i>Streptococcus</i> . <i>PLoS Pathogens</i> , 2013, 9, e1003179.	4.7	47
25	Rga, a RofA-Like Regulator, Is the Major Transcriptional Activator of the PI-2a Pilus in <i>Streptococcus agalactiae</i> . <i>Microbial Drug Resistance</i> , 2012, 18, 286-297.	2.0	15
26	The highly dynamic CRISPR1 system of <i>Streptococcus agalactiae</i> controls the diversity of its mobilome. <i>Molecular Microbiology</i> , 2012, 85, 1057-1071.	2.5	153
27	Genome Sequence of <i>Streptococcus gallolyticus</i> : Insights into Its Adaptation to the Bovine Rumen and Its Ability To Cause Endocarditis. <i>Journal of Bacteriology</i> , 2010, 192, 2266-2276.	2.2	120
28	Atypical association of DDE transposition with conjugation specifies a new family of mobile elements. <i>Molecular Microbiology</i> , 2009, 71, 948-959.	2.5	45