## George C C Dicenzo

List of Publications by Year in descending order

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331670 345221 1,577 47 21 36 citations h-index g-index papers 65 65 65 1521 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The Divided Bacterial Genome: Structure, Function, and Evolution. Microbiology and Molecular Biology Reviews, 2017, 81, .	6.6	190
2	Taxonomy of Rhizobiaceae revisited: proposal of a new framework for genus delimitation. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	1.7	125
3	Examination of Prokaryotic Multipartite Genome Evolution through Experimental Genome Reduction. PLoS Genetics, 2014, 10, e1004742.	3.5	89
4	Metabolic modelling reveals the specialization of secondary replicons for niche adaptation in Sinorhizobium meliloti. Nature Communications, 2016, 7, 12219.	12.8	85
5	Multidisciplinary approaches for studying rhizobium–legume symbioses. Canadian Journal of Microbiology, 2019, 65, 1-33.	1.7	77
6	Harnessing Rhizobia to Improve Heavy-Metal Phytoremediation by Legumes. Genes, 2018, 9, 542.	2.4	72
7	Trade, Diplomacy, and Warfare: The Quest for Elite Rhizobia Inoculant Strains. Frontiers in Microbiology, 2017, 8, 2207.	3.5	67
8	Genome-scale metabolic reconstruction of the symbiosis between a leguminous plant and a nitrogen-fixing bacterium. Nature Communications, 2020, 11, 2574.	12.8	56
9	Preparation and characterization of gold nanoparticles prepared with aqueous extracts of Lamiaceae plants and the effect of follow-up treatment with atmospheric pressure glow microdischarge.  Arabian Journal of Chemistry, 2019, 12, 4118-4130.	4.9	54
10	Robustness encoded across essential and accessory replicons of the ecologically versatile bacterium Sinorhizobium meliloti. PLoS Genetics, 2018, 14, e1007357.	3.5	49
11	Cell Growth Inhibition upon Deletion of Four Toxin-Antitoxin Loci from the Megaplasmids of Sinorhizobium meliloti. Journal of Bacteriology, 2014, 196, 811-824.	2.2	42
12	The tRNA <sup>arg</sup> Gene and <i>engA</i> Are Essential Genes on the 1.7-Mb pSymB Megaplasmid of Sinorhizobium meliloti and Were Translocated Together from the Chromosome in an Ancestral Strain. Journal of Bacteriology, 2013, 195, 202-212.	2.2	40
13	Genetic redundancy is prevalent within the 6.7ÂMb Sinorhizobium meliloti genome. Molecular Genetics and Genomics, 2015, 290, 1345-1356.	2.1	40
14	PhoU Allows Rapid Adaptation to High Phosphate Concentrations by Modulating PstSCAB Transport Rate in Sinorhizobium meliloti. Journal of Bacteriology, 2017, 199, .	2.2	39
15	Genomic resources for identification of the minimal <scp><scp>N<sub>2</sub></scp></scp> â€fixing symbiotic genome. Environmental Microbiology, 2016, 18, 2534-2547.	3.8	36
16	Chromids Aid Genome Expansion and Functional Diversification in the Family <i>Burkholderiaceae</i> Molecular Biology and Evolution, 2019, 36, 562-574.	8.9	34
17	Deciphering the Symbiotic Plant Microbiome: Translating the Most Recent Discoveries on Rhizobia for the Improvement of Agricultural Practices in Metal-Contaminated and High Saline Lands. Agronomy, 2019, 9, 529.	3.0	32
18	Symbiotic and Nonsymbiotic Members of the Genus <i>Ensifer</i> (syn. <i>Sinorhizobium</i> ) Are Separated into Two Clades Based on Comparative Genomics and High-Throughput Phenotyping. Genome Biology and Evolution, 2020, 12, 2521-2534.	2,5	30

#	Article	IF	Citations
19	Cold acclimation and prospects for cold-resilient crops. Plant Stress, 2021, 2, 100028.	5.5	29
20	Genomic and Biotechnological Characterization of the Heavy-Metal Resistant, Arsenic-Oxidizing Bacterium Ensifer sp. M14. Genes, 2018, 9, 379.	2.4	25
21	Heterologous Complementation Reveals a Specialized Activity for BacA in the <i>Medicago</i> ŝê" <i>Sinorhizobium meliloti</i> Symbiosis. Molecular Plant-Microbe Interactions, 2017, 30, 312-324.	2.6	24
22	Succinate Transport Is Not Essential for Symbiotic Nitrogen Fixation by Sinorhizobium meliloti or Rhizobium leguminosarum. Applied and Environmental Microbiology, 2018, 84, .	3.1	24
23	Creation and Characterization of a Genomically Hybrid Strain in the Nitrogen-Fixing Symbiotic Bacterium <i>Sinorhizobium meliloti</i> i>. ACS Synthetic Biology, 2018, 7, 2365-2378.	3.8	24
24	Proline auxotrophy in Sinorhizobium meliloti results in a plant-specific symbiotic phenotype. Microbiology (United Kingdom), 2015, 161, 2341-2351.	1.8	24
25	Rhizobium indicum sp. nov., isolated from root nodules of pea (Pisum sativum) cultivated in the Indian trans-Himalayas. Systematic and Applied Microbiology, 2020, 43, 126127.	2.8	21
26	< scp>  -Hydroxyproline and $<$ scp>d -Proline Catabolism in Sinorhizobium meliloti. Journal of Bacteriology, 2016, 198, 1171-1181.	2.2	20
27	<i>Proteobacteria</i> Contain Diverse flg22 Epitopes That Elicit Varying Immune Responses in <i>Arabidopsis thaliana</i> Molecular Plant-Microbe Interactions, 2021, 34, 504-510.	2.6	19
28	Effects of synthetic large-scale genome reduction on metabolism and metabolic preferences in a nutritionally complex environment. Metabolomics, 2016, 12, 1.	3.0	18
29	The genomes of rhizobia. Advances in Botanical Research, 2020, , 213-249.	1.1	17
30	Minimal gene set from <i>Sinorhizobium</i> ( <i>Ensifer</i> ) <i>meliloti</i> pSymA required for efficient symbiosis with <i>Medicago</i> Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	16
31	A Key Regulator of the Glycolytic and Gluconeogenic Central Metabolic Pathways in <i>Sinorhizobium meliloti</i> . Genetics, 2017, 207, 961-974.	2.9	15
32	Pulse-Modulated Radio-Frequency Alternating-Current-Driven Atmospheric-Pressure Glow Discharge for Continuous-Flow Synthesis of Silver Nanoparticles and Evaluation of Their Cytotoxicity toward Human Melanoma Cells. Nanomaterials, 2018, 8, 398.	4.1	15
33	Tn-Core: A Toolbox for Integrating Tn-seq Gene Essentiality Data and Constraint-Based Metabolic Modeling. ACS Synthetic Biology, 2019, 8, 158-169.	3.8	15
34	A putative 3â€hydroxyisobutyrylâ€CoA hydrolase is required for efficient symbiotic nitrogen fixation in <i>Sinorhizobium meliloti</i> and <i>Sinorhizobium fredii</i> NGR234. Environmental Microbiology, 2017, 19, 218-236.	3.8	14
35	Inter-replicon Gene Flow Contributes to Transcriptional Integration in the <i>Sinorhizobium meliloti</i> Multipartite Genome. G3: Genes, Genomes, Genetics, 2018, 8, 1711-1720.	1.8	14
36	Loss of malic enzymes leads to metabolic imbalance and altered levels of trehalose and putrescine in the bacterium Sinorhizobium meliloti. BMC Microbiology, 2016, 16, 163.	3.3	10

#	Article	IF	CITATIONS
37	DNA Methylation in <i>Ensifer</i> Species during Free-Living Growth and during Nitrogen-Fixing Symbiosis with <i>Medicago</i> spp MSystems, 2022, 7, e0109221.	3.8	7
38	Pervasive RNA Regulation of Metabolism Enhances the Root Colonization Ability of Nitrogen-Fixing Symbiotic $\hat{l}_{\pm}$ -Rhizobia. MBio, 2022, 13, e0357621.	4.1	7
39	Cold Acclimation in Brachypodium Is Accompanied by Changes in Above-Ground Bacterial and Fungal Communities. Plants, 2021, 10, 2824.	3.5	7
40	The <i>Brachypodium distachyon</i> cold-acclimated plasma membrane proteome is primed for stress resistance. G3: Genes, Genomes, Genetics, 2021, $11$ , .	1.8	6
41	Fermented juices as reducing and capping agents for the biosynthesis of size-defined spherical gold nanoparticles. Journal of Saudi Chemical Society, 2018, 22, 767-776.	5.2	5
42	Techniques for Large-Scale Bacterial Genome Manipulation and Characterization of the Mutants with Respect to In Silico Metabolic Reconstructions. Methods in Molecular Biology, 2018, 1716, 291-314.	0.9	4
43	Reference nodule transcriptomes for <scp><i>Melilotus officinalis</i></scp> and <scp><i>Medicago sativa</i></scp> cv. Algonquin. Plant Direct, 2022, 6, .	1.9	4
44	Brachypodium Antifreeze Protein Gene Products Inhibit Ice Recrystallisation, Attenuate Ice Nucleation, and Reduce Immune Response. Plants, 2022, 11, 1475.	3.5	3
45	Size-defined synthesis of magnetic nanorods by Salvia hispanica essential oil with electromagnetic excitation properties useful in microwave imagining. Journal of Magnetism and Magnetic Materials, 2019, 480, 87-96.	2.3	2
46	Genomic Diversity and Evolution of Rhizobia., 2019,, 37-46.		2
47	Tn-Core: Functionally Interpreting Transposon-Sequencing Data with Metabolic Network Analysis. Methods in Molecular Biology, 2021, 2189, 199-215.	0.9	1