Gabriella Pessi

List of Publications by Year
in descending order

59 papers	5,288 citations	117625 34 h-index	133252 59 g-index
62 all docs	62 docs citations	62 times ranked	5884 citing authors

#	Article	IF	Citations
1	The genome sequence of <i>Bifidobacterium longum</i> reflects its adaptation to the human gastrointestinal tract. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14422-14427.	7.1	874
2	Explosive cell lysis as a mechanism for the biogenesis of bacterial membrane vesicles and biofilms. Nature Communications, 2016, 7, 11220.	12.8	487
3	The Global Posttranscriptional Regulator RsmA Modulates Production of Virulence Determinants and <i>N-</i> Acylhomoserine Lactones in <i>Pseudomonas aeruginosa</i>. Journal of Bacteriology, 2001, 183, 6676-6683.	2.2	344
4	Positive Control of Swarming, Rhamnolipid Synthesis, and Lipase Production by the Posttranscriptional RsmA/RsmZ System in<i>Pseudomonas aeruginosa</i>PAO1. Journal of Bacteriology, 2004, 186, 2936-2945.	2.2	275
5	Transcriptional Control of the Hydrogen Cyanide Biosynthetic Genes <i>hcnABC</i> by the Anaerobic Regulator ANR and the Quorum-Sensing Regulators LasR and RhlR in <i>Pseudomonas aeruginosa</i>. Journal of Bacteriology, 2000, 182, 6940-6949.	2.2	235
6	Chimeric peptidomimetic antibiotics against Gram-negative bacteria. Nature, 2019, 576, 452-458.	27.8	231
7	Genome-Wide Transcript Analysis of <i>Bradyrhizobium japonicum</i> Bacteroids in Soybean Root Nodules. Molecular Plant-Microbe Interactions, 2007, 20, 1353-1363.	2.6	187
8	A pathway for phosphatidylcholine biosynthesis in Plasmodium falciparum involving phosphoethanolamine methylation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6206-6211.	7.1	149
9	Cis-2-dodecenoic acid receptor RpfR links quorum-sensing signal perception with regulation of virulence through cyclic dimeric guanosine monophosphate turnover. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15479-15484.	7.1	145
10	Negative Control of Quorum Sensing by RpoN (Ïƒ 54) in Pseudomonas aeruginosa PAO1. Journal of Bacteriology, 2003, 185, 2227-2235.	2.2	140
11	GacS Sensor Domains Pertinent to the Regulation of Exoproduct Formation and to the Biocontrol Potential of Pseudomonas fluorescens CHA0. Molecular Plant-Microbe Interactions, 2003, 16, 634-644.	2.6	139
12	An integrated proteomics and transcriptomics reference data set provides new insights into the <i>Bradyrhizobium japonicum</i> bacteroid metabolism in soybean root nodules. Proteomics, 2010, 10, 1391-1400.	2.2	111
13	Thanatin targets the intermembrane protein complex required for lipopolysaccharide transport in <i>Escherichia coli</i>. Science Advances, 2018, 4, eaau2634.	10.3	109
14	Dissection of the Bradyrhizobium japonicum NifA+Ïƒ54 regulon, and identification of a ferredoxin gene (fdxN) for symbiotic nitrogen fixation. Molecular Genetics and Genomics, 2007, 278, 255-271.	2.1	107
15	Isovaleryl-homoserine lactone, an unusual branched-chain quorum-sensing signal from the soybean symbiont <i>Bradyrhizobium japonicum</i>. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16765-16770.	7.1	104
16	The PhyRâ€Ïƒ^{EcfG} signalling cascade is involved in stress response and symbiotic efficiency in <i>Bradyrhizobium japonicum</i>. Molecular Microbiology, 2009, 73, 291-305.	2.5	103
17	A Peptidomimetic Antibiotic Targets Outer Membrane Proteins and Disrupts Selectively the Outer Membrane in Escherichia coli. Journal of Biological Chemistry, 2016, 291, 1921-1932.	3.4	97
18	Biosynthesis of fragin is controlled by a novel quorum sensing signal. Nature Communications, 2018, 9, 1297.	12.8	91

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19	In Vivo Evidence for the Specificity of Plasmodium falciparum Phosphoethanolamine Methyltransferase and Its Coupling to the Kennedy Pathway. Journal of Biological Chemistry, 2005, 280, 12461-12466.	3.4	82
20	Dual control of hydrogen cyanide biosynthesis by the global activator GacA inPseudomonas aeruginosaPAO1. FEMS Microbiology Letters, 2001, 200, 73-78.	1.8	75
21	Disruption of the Plasmodium falciparum PfPMT Gene Results in a Complete Loss of Phosphatidylcholine Biosynthesis via the Serine-Decarboxylase-Phosphoethanolamine-Methyltransferase Pathway and Severe Growth and Survival Defects. Journal of Biological Chemistry, 2008, 283, 27636-27643.	3.4	75
22	New Target Genes Controlled by the <i>Bradyrhizobium japonicum</i> Two-Component Regulatory System RegSR. Journal of Bacteriology, 2007, 189, 8928-8943.	2.2	74
23	The AHL- and BDSF-Dependent Quorum Sensing Systems Control Specific and Overlapping Sets of Genes in Burkholderia cenocepacia H111. PLoS ONE, 2012, 7, e49966.	2.5	70
24	Genome-wide transcription start site mapping of Bradyrhizobium japonicum grown free-living or in symbiosis â€“ a rich resource to identify new transcripts, proteins and to study gene regulation. BMC Genomics, 2016, 17, 302.	2.8	70
25	Rhizobial Adaptation to Hosts, a New Facet in the Legume Root-Nodule Symbiosis. Molecular Plant-Microbe Interactions, 2010, 23, 784-790.	2.6	68
26	Two quorum sensing systems control biofilm formation and virulence in members of the<i>Burkholderia cepacia</i>complex. Virulence, 2013, 4, 400-409.	4.4	65
27	Metabolomic Profiling of Bradyrhizobium diazoefficiens-Induced Root Nodules Reveals Both Host Plant-Specific and Developmental Signatures. International Journal of Molecular Sciences, 2016, 17, 815.	4.1	52
28	Competition Experiments for Legume Infection Identify Burkholderia phymatum as a Highly Competitive Î²-Rhizobium. Frontiers in Microbiology, 2017, 8, 1527.	3.5	48
29	Response of Burkholderia cenocepacia H111 to Micro-Oxia. PLoS ONE, 2013, 8, e72939.	2.5	46
30	Ïƒ ⁵⁴ -Dependent Response to Nitrogen Limitation and Virulence in Burkholderia cenocepacia Strain H111. Applied and Environmental Microbiology, 2015, 81, 4077-4089.	3.1	44
31	Global transcriptome analysis of the heat shock response of Bifidobacterium longum. FEMS Microbiology Letters, 2007, 271, 136-145.	1.8	41
32	Small RNAs of theBradyrhizobium/Rhodopseudomonaslineage and their analysis. RNA Biology, 2012, 9, 47-58.	3.1	41
33	Host-specific symbiotic requirement of BdeAB, a RegR-controlled RND-type efflux system in Bradyrhizobium japonicum. FEMS Microbiology Letters, 2010, 312, 184-191.	1.8	39
34	Genome Sequence of Burkholderia cenocepacia H111, a Cystic Fibrosis Airway Isolate. Genome Announcements, 2014, 2, .	0.8	39
35	Localization of the Phosphoethanolamine Methyltransferase of the Human Malaria Parasite Plasmodium falciparum to the Golgi Apparatus. Journal of Biological Chemistry, 2006, 281, 21305-21311.	3.4	34
36	High intracellular c-di-GMP levels antagonize quorum sensing and virulence gene expression in Burkholderia cenocepacia H111. Microbiology (United Kingdom), 2017, 163, 754-764.	1.8	34

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37	Disparate role of rhizobial ACC deaminase in root-nodule symbioses. Symbiosis, 2012, 57, 43-50.	2.3	33
38	An Integrated Systems Approach Unveils New Aspects of Microoxia-Mediated Regulation in Bradyrhizobium diazoefficiens. Frontiers in Microbiology, 2019, 10, 924.	3.5	31
39	Global consequences of phosphatidylcholine reduction in Bradyrhizobium japonicum. Molecular Genetics and Genomics, 2008, 280, 59-72.	2.1	30
40	Manipulating virulence factor availability can have complex consequences for infections. Evolutionary Applications, 2017, 10, 91-101.	3.1	29
41	Functional Genomics Approaches to Studying Symbioses between Legumes and Nitrogen-Fixing Rhizobia. High-Throughput, 2018, 7, 15.	4.4	29
42	A Link between Arabinose Utilization and Oxalotrophy in Bradyrhizobium japonicum. Applied and Environmental Microbiology, 2014, 80, 2094-2101.	3.1	28
43	Mutations in Two Paraburkholderia phymatum Type VI Secretion Systems Cause Reduced Fitness in Interbacterial Competition. Frontiers in Microbiology, 2017, 8, 2473.	3.5	27
44	Transcriptome Analysis of Paraburkholderia phymatum under Nitrogen Starvation and during Symbiosis with Phaseolus Vulgaris. Genes, 2017, 8, 389.	2.4	23
45	NtrC-dependent control of exopolysaccharide synthesis and motility in Burkholderia cenocepacia H111. PLoS ONE, 2017, 12, e0180362.	2.5	20
46	Pathways for phosphatidylcholine biosynthesis: targets and strategies for antimalarial drugs. Future Lipidology, 2006, 1, 173-180.	0.5	16
47	The Exopolysaccharide Cepacian Plays a Role in the Establishment of the Paraburkholderia phymatum â€" Phaseolus vulgaris Symbiosis. Frontiers in Microbiology, 2020, 11, 1600.	3.5	13
48	Metabolomics and Transcriptomics Identify Multiple Downstream Targets of Paraburkholderia phymatum Ïƒ54 During Symbiosis with Phaseolus vulgaris. International Journal of Molecular Sciences, 2018, 19, 1049.	4.1	11
49	Mapping of the Denitrification Pathway in Burkholderia thailandensis by Genome-Wide Mutant Profiling. Journal of Bacteriology, 2020, 202, .	2.2	10
50	Differential Expression of Paraburkholderia phymatum Type VI Secretion Systems (T6SS) Suggests a Role of T6SS-b in Early Symbiotic Interaction. Frontiers in Plant Science, 2021, 12, 699590.	3.6	10
51	The IclR-Family Regulator BapR Controls Biofilm Formation in B. cenocepacia H111. PLoS ONE, 2014, 9, e92920.	2.5	10
52	Paraburkholderia phymatum Homocitrate Synthase NifV Plays a Key Role for Nitrogenase Activity during Symbiosis with Papilionoids and in Free-Living Growth Conditions. Cells, 2021, 10, 952.	4.1	9
53	Identification of Genes Required for Resistance to Peptidomimetic Antibiotics by Transposon Sequencing. Frontiers in Microbiology, 2020, 11, 1681.	3.5	8
54	Cyanogenesis. , 2004, , 671-687.		7

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55	Microbial Biofilms and Quorum Sensing. , 2015, , 45-52.		4
56	Paraburkholderia phymatum STM815 Ïƒ54 Controls Utilization of Dicarboxylates, Motility, and T6SS-b Expression. Nitrogen, 2020, 1, 81-98.	1.3	3
57	Metabolomics and Dual RNA-Sequencing on Root Nodules Revealed New Cellular Functions Controlled by Paraburkholderia phymatum NifA. Metabolites, 2021, 11, 455.	2.9	3
58	Identification of AHL- and BDSF-Controlled Proteins in Burkholderia cenocepacia by Proteomics. Methods in Molecular Biology, 2018, 1673, 193-202.	0.9	2
59	Identification of Key Factors for Anoxic Survival of B. cenocepacia H111. International Journal of Molecular Sciences, 2022, 23, 4560.	4.1	1