

# Dante Travisany

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

904  
citations

471509

17  
h-index

477307

29  
g-index

30  
all docs

30  
docs citations

30  
times ranked

1423  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <i>Scientific Reports</i> , 2018, 8, 5875.	3.3	123
2	Whole genome comparison between table and wine grapes reveals a comprehensive catalog of structural variants. <i>BMC Plant Biology</i> , 2014, 14, 7.	3.6	115
3	Transcriptional response of Atlantic salmon families to <i>Piscirickettsia salmonis</i> infection highlights the relevance of the iron-deprivation defence system. <i>BMC Genomics</i> , 2015, 16, 495.	2.8	94
4	The bioleaching potential of a bacterial consortium. <i>Bioresource Technology</i> , 2016, 218, 659-666.	9.6	63
5	Complete genome sequence of <i>Piscirickettsia salmonis</i> LF-89 (ATCC VR-1361) a major pathogen of farmed salmonid fish. <i>Journal of Biotechnology</i> , 2015, 212, 30-31.	3.8	54
6	A new genome of <i>Acidithiobacillus thiooxidans</i> provides insights into adaptation to a bioleaching environment. <i>Research in Microbiology</i> , 2014, 165, 743-752.	2.1	48
7	Reconstruction of the microalga <i>Nannochloropsis salina</i> genome-scale metabolic model with applications to lipid production. <i>BMC Systems Biology</i> , 2017, 11, 66.	3.0	41
8	Transcriptome sequencing of <i>Prunus</i> sp. rootstocks roots to identify candidate genes involved in the response to root hypoxia. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	1.6	34
9	The Role of Fur in the Transcriptional and Iron Homeostatic Response of <i>Enterococcus faecalis</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1580.	3.5	32
10	Draft Genome Sequence of the <i>Sulfobacillus thermosulfidooxidans</i> Cutipay Strain, an Indigenous Bacterium Isolated from a Naturally Extreme Mining Environment in Northern Chile. <i>Journal of Bacteriology</i> , 2012, 194, 6327-6328.	2.2	30
11	Insights into neutralizing antibody responses in individuals exposed to SARS-CoV-2 in Chile. <i>Science Advances</i> , 2021, 7, .	10.3	29
12	Transcriptomic Changes of <i>Piscirickettsia salmonis</i> During Intracellular Growth in a Salmon Macrophage-Like Cell Line. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 426.	3.9	27
13	High-Throughput Single Nucleotide Polymorphism (SNP) Discovery and Validation Through Whole-Genome Resequencing in Nile Tilapia ( <i>Oreochromis niloticus</i> ). <i>Marine Biotechnology</i> , 2020, 22, 109-117.	2.4	25
14	<i>Piscirickettsia salmonis</i> Cryptic Plasmids: Source of Mobile DNA and Virulence Factors. <i>Pathogens</i> , 2019, 8, 269.	2.8	23
15	Global transcriptional responses of <i>Acidithiobacillus ferrooxidans</i> Wenelen under different sulfide minerals. <i>Bioresource Technology</i> , 2016, 200, 29-34.	9.6	21
16	A Multi-Serotype Approach Clarifies the Catabolite Control Protein A Regulon in the Major Human Pathogen Group A <i>Streptococcus</i> . <i>Scientific Reports</i> , 2016, 6, 32442.	3.3	19
17	Expression of two indole-3-acetic acid (IAA)-amido synthetase (GH3) genes during fruit development of raspberry ( <i>Rubus idaeus</i> Heritage). <i>Scientia Horticulturae</i> , 2019, 246, 168-175.	3.6	19
18	Analysis of <i>Piscirickettsia salmonis</i> Metabolism Using Genome-Scale Reconstruction, Modeling, and Testing. <i>Frontiers in Microbiology</i> , 2017, 8, 2462.	3.5	17

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19	Global Proteomic Profiling of <i>Piscirickettsia salmonis</i> and Salmon Macrophage-Like Cells during Intracellular Infection. <i>Microorganisms</i> , 2020, 8, 1845.	3.6	17
20	RNA-Seq analysis and transcriptome assembly of raspberry fruit ( <i>Rubus idaeus</i> "Heritage") revealed several candidate genes involved in fruit development and ripening. <i>Scientia Horticulturae</i> , 2019, 254, 26-34.	3.6	15
21	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. <i>Mycology</i> , 2018, 9, 59-69.	4.4	12
22	Whole Genome Sequence, Variant Discovery and Annotation in Mapuche-Huilliche Native South Americans. <i>Scientific Reports</i> , 2019, 9, 2132.	3.3	12
23	Global gene expression analysis provides insight into local adaptation to geothermal streams in tadpoles of the Andean toad <i>Rhinella spinulosa</i> . <i>Scientific Reports</i> , 2017, 7, 1966.	3.3	10
24	Comparative gene expression analysis of Dtg, a novel target gene of Dpp signaling pathway in the early <i>Drosophila melanogaster</i> embryo. <i>Gene</i> , 2014, 535, 210-217.	2.2	7
25	Genome Sequence of <i>Borrelia chilensis</i> VA1, a South American Member of the Lyme Borreliosis Group. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
26	Integration of Biological Networks for <i>Acidithiobacillus thiooxidans</i> Describes a Modular Gene Regulatory Organization of Bioleaching Pathways. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 155.	3.5	5
27	Generation and robustness of Boolean networks to model <i>Clostridium difficile</i> infection. <i>Natural Computing</i> , 2020, 19, 111-134.	3.0	2
28	First Identification of Reinfection by a Genetically Different Variant of SARS-CoV-2 in a Homeless Person from the Metropolitan Area of Santiago, Chile. <i>Journal of Environmental and Public Health</i> , 2022, 2022, 1-6.	0.9	2
29	Symbolic Extensions Applied to Multiscale Structure of Genomes. <i>Acta Biotheoretica</i> , 2014, 62, 145-169.	1.5	1