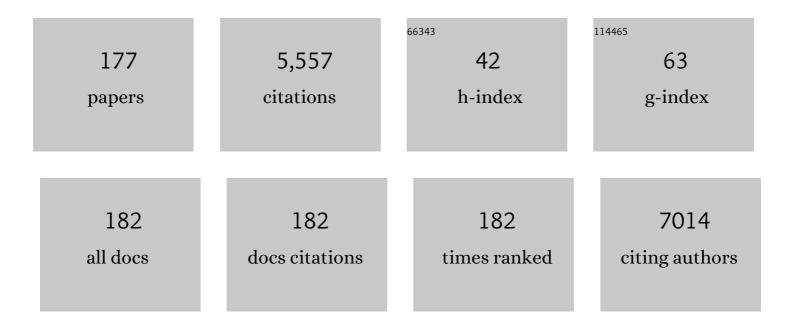
List of Publications by Year in descending order

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Ρενατό Γανι

#	Article	IF	CITATIONS
1	M <scp>e</scp> D <scp>u</scp> S <scp>a</scp> : a multi-draft based scaffolder. Bioinformatics, 2015, 31, 2443-2451.	4.1	359
2	Molecular Evolution of Nitrogen Fixation: The Evolutionary History of the nifD, nifK, nifE, and nifN Genes. Journal of Molecular Evolution, 2000, 51, 1-11.	1.8	141
3	Nitrogen Fixation Genes in an Endosymbiotic Burkholderia Strain. Applied and Environmental Microbiology, 2001, 67, 725-732.	3.1	134
4	Sponge-associated microbial Antarctic communities exhibiting antimicrobial activity against Burkholderia cepacia complex bacteria. Biotechnology Advances, 2012, 30, 272-293.	11.7	112
5	Identification ofAzospirillumstrains by restriction fragment length polymorphism of the 16S rDNA and of the histidine operon. FEMS Microbiology Letters, 1995, 127, 85-91.	1.8	108
6	Fluctuation of bacteria isolated from elm tissues during different seasons and from different plant organs. Research in Microbiology, 2003, 154, 105-114.	2.1	103
7	Origin and evolution of metabolic pathways. Physics of Life Reviews, 2009, 6, 23-52.	2.8	101
8	Antibiotics from Deep-Sea Microorganisms: Current Discoveries and Perspectives. Marine Drugs, 2018, 16, 355.	4.6	98
9	Large-Scale Analysis of Plasmid Relationships through Gene-Sharing Networks. Molecular Biology and Evolution, 2012, 29, 1225-1240.	8.9	94
10	Preliminary Comparison of Oral and Intestinal Human Microbiota in Patients with Colorectal Cancer: A Pilot Study. Frontiers in Microbiology, 2017, 8, 2699.	3.5	93
11	A novel resistance mechanism to triclosan that suggests horizontal gene transfer and demonstrates a potential selective pressure for reduced biocide susceptibility in clinical strains of Staphylococcus aureus. International Journal of Antimicrobial Agents, 2012, 40, 210-220.	2.5	92
12	Soil Bacterial Community Response to Differences in Agricultural Management along with Seasonal Changes in a Mediterranean Region. PLoS ONE, 2014, 9, e105515.	2.5	89
13	Exploring the evolutionary dynamics of plasmids: the Acinetobacter pan-plasmidome. BMC Evolutionary Biology, 2010, 10, 59.	3.2	87
14	Adhesion of <i>Acinetobacter venetianus</i> to Diesel Fuel Droplets Studied with In Situ Electrochemical and Molecular Probes. Applied and Environmental Microbiology, 1999, 65, 2041-2048.	3.1	85
15	"Every Gene Is Everywhere but the Environment Selects― Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. Genome Biology and Evolution, 2016, 8, 1388-1400.	2.5	82
16	Antagonistic interactions between psychrotrophic cultivable bacteria isolated from Antarctic sponges: a preliminary analysis. Research in Microbiology, 2009, 160, 27-37.	2.1	79
17	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic Vibrio cholerae Lineage. MBio, 2014, 5, .	4.1	78
18	Plant-endophytes interaction influences the secondary metabolism in Echinacea purpurea (L.) Moench: an in vitro model. Scientific Reports, 2017, 7, 16924.	3.3	74

#	Article	IF	CITATIONS
19	Biodiversity of cultivable psychrotrophic marine bacteria isolated from Terra Nova Bay (Ross Sea,) Tj ETQq1 1 0.78	4314 rgB1 1.8	72verlock
20	Thiophenecarboxamide Derivatives Activated by EthA Kill Mycobacterium tuberculosis by Inhibiting the CTP Synthetase PyrG. Chemistry and Biology, 2015, 22, 917-927.	6.0	72
21	A Randomly Amplified Polymorphic DNA Marker Specific for the <i>Bacillus cereus</i> Group Is Diagnostic for <i>Bacillus anthracis</i> . Applied and Environmental Microbiology, 1999, 65, 1298-1303.	3.1	70
22	The evolution of the histidine biosynthetic genes in prokaryotes: A common ancestor for the hisA and hisF genes. Journal of Molecular Evolution, 1994, 38, 489-495.	1.8	69
23	Deciphering the Role of RND Efflux Transporters in Burkholderia cenocepacia. PLoS ONE, 2011, 6, e18902.	2.5	68
24	Molecular evolution of the histidine biosynthetic pathway. Journal of Molecular Evolution, 1995, 41, 760-74.	1.8	67
25	Genome of the Komodo dragon reveals adaptations in the cardiovascular and chemosensory systems of monitor lizards. Nature Ecology and Evolution, 2019, 3, 1241-1252.	7.8	67
26	Ecology of cold environments: new insights of bacterial metabolic adaptation through an integrated genomic-phenomic approach. Scientific Reports, 2017, 7, 839.	3.3	65
27	Origin and evolution of operons and metabolic pathways. Research in Microbiology, 2009, 160, 502-512.	2.1	63
28	Bioactive volatile organic compounds from Antarctic (sponges) bacteria. New Biotechnology, 2013, 30, 824-838.	4.4	62
29	The role of gene fusions in the evolution of metabolic pathways: the histidine biosynthesis case. BMC Evolutionary Biology, 2007, 7, S4.	3.2	59
30	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. BMC Bioinformatics, 2008, 9, 551.	2.6	57
31	The horizontal flow of the plasmid resistome: clues from interâ€generic similarity networks. Environmental Microbiology, 2010, 12, 3228-3242.	3.8	57
32	Bacterium–bacterium inhibitory interactions among psychrotrophic bacteria isolated from Antarctic seawater (Terra Nova Bay, Ross Sea). FEMS Microbiology Ecology, 2007, 60, 383-396.	2.7	55
33	Genomeâ€scale metabolic reconstruction and constraintâ€based modelling of the Antarctic bacterium <scp><i>P</i></scp> <i>seudoalteromonas haloplanktis</i> â€ <scp>TAC</scp> 125. Environmental Microbiology, 2015, 17, 751-766.	3.8	53
34	The art of adapting to extreme environments: The model system Pseudoalteromonas. Physics of Life Reviews, 2021, 36, 137-161.	2.8	53
35	Oil-degrading Acinetobacter strain RAG-1 and strains described as 'Acinetobacter venetianus sp. nov.' belong to the same genomic species. Research in Microbiology, 1999, 150, 69-73.	2.1	52
36	The Origin and Evolution of Operons: The Piecewise Building of the Proteobacterial Histidine Operon. Journal of Molecular Evolution, 2005, 60, 378-390.	1.8	52

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37	Diauxie and co-utilization of carbon sources can coexist during bacterial growth in nutritionally complex environments. Nature Communications, 2020, 11, 3135.	12.8	51
38	Antibiotic resistance differentiates Echinacea purpurea endophytic bacterial communities with respect to plant organs. Research in Microbiology, 2014, 165, 686-694.	2.1	50
39	Molecular and phenotypic characterization of Acinetobacter strains able to degrade diesel fuel. Research in Microbiology, 2012, 163, 161-172.	2.1	49
40	Characterization of the volatile profile of Antarctic bacteria by using solidâ€phase microextractionâ€gas chromatographyâ€mass spectrometry. Journal of Mass Spectrometry, 2011, 46, 1051-1059.	1.6	48
41	Antimicrobial Activity of Monoramnholipids Produced by Bacterial Strains Isolated from the Ross Sea (Antarctica). Marine Drugs, 2016, 14, 83.	4.6	48
42	Constraint-based modeling identifies new putative targets to fight colistin-resistant A. baumannii infections. Scientific Reports, 2017, 7, 3706.	3.3	47
43	The pangenome of (Antarctic) Pseudoalteromonas bacteria: evolutionary and functional insights. BMC Genomics, 2017, 18, 93.	2.8	46
44	Endophytic and rhizospheric bacterial communities isolated from the medicinal plants Echinacea purpurea and Echinacea angustifolia. International Microbiology, 2014, 17, 165-74.	2.4	46
45	Antagonistic interactions between endophytic cultivable bacterial communities isolated from the medicinal plant <scp><i>E</i></scp> <i>chinacea purpurea</i> . Environmental Microbiology, 2016, 18, 2357-2365.	3.8	43
46	Identification of species of the Burkholderia cepacia complex by sequence analysis of the hisA gene. Journal of Medical Microbiology, 2010, 59, 1163-1170.	1.8	42
47	Molecular Evolution of hisB Genes. Journal of Molecular Evolution, 2004, 58, 225-237.	1.8	41
48	Pseudoalteromonas haloplanktis TAC125 produces 4-hydroxybenzoic acid that induces pyroptosis in human A459 lung adenocarcinoma cells. Scientific Reports, 2018, 8, 1190.	3.3	41
49	Phenotypic and genomic characterization of the antimicrobial producer Rheinheimera sp. EpRS3 isolated from the medicinal plant Echinacea purpurea: insights into its biotechnological relevance. Research in Microbiology, 2017, 168, 293-305.	2.1	39
50	Genomic analysis of three sponge-associated Arthrobacter Antarctic strains, inhibiting the growth of Burkholderia cepacia complex bacteria by synthesizing volatile organic compounds. Microbiological Research, 2014, 169, 593-601.	5.3	38
51	Medicinal Plants and Their Bacterial Microbiota: A Review on Antimicrobial Compounds Production for Plant and Human Health. Pathogens, 2021, 10, 106.	2.8	38
52	Biodiversity and horizontal gene transfer in culturable bacteria isolated from activated sludge enriched in nonylphenol ethoxylates. Research in Microbiology, 2001, 152, 105-112.	2.1	37
53	Molecular and physiological characterisation of psychrotrophic hydrocarbon-degrading bacteria isolated from Terra Nova Bay (Antarctica). European Journal of Soil Biology, 2007, 43, 368-379.	3.2	37
54	Significant and Conflicting Correlation of IL-9 With Prevotella and Bacteroides in Human Colorectal Cancer. Frontiers in Immunology, 2020, 11, 573158.	4.8	37

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55	Evolution of the structure and chromosomal distribution of histidine biosynthetic genes. Origins of Life and Evolution of Biospheres, 1998, 28, 555-570.	1.9	36
56	Tissue specificity and differential effects on in vitro plant growth of single bacterial endophytes isolated from the roots, leaves and rhizospheric soil of Echinacea purpurea. BMC Plant Biology, 2019, 19, 284.	3.6	36
57	Genetic Variability in European Populations of an Invasive American Crayfish: Preliminary Results. Biological Invasions, 2003, 5, 269-274.	2.4	35

Biochemical and microbial features of shallow marine sediments along the Terra Nova Bay (Ross Sea,) Tj ETQq0.0 rgBT /Overlock 10 Tf 1.8

59	Preliminary data on antibacterial activity of Echinacea purpurea -associated bacterial communities against Burkholderia cepacia complex strains, opportunistic pathogens of Cystic Fibrosis patients. Microbiological Research, 2017, 196, 34-43.	5.3	35
60	Is the plant-associated microbiota of Thymus spp. adapted to plant essential oil?. Research in Microbiology, 2017, 168, 276-282.	2.1	35
61	Cloning of histidine genes of Azospirillum brasilense: Organization of the ABFH gene cluster and nucleotide sequence of the hisB gene. Molecular Genetics and Genomics, 1989, 216, 224-229.	2.4	34
62	Nucleotide sequence of the gene encoding the nitrogenase iron protein (nifH) of Azospirillum brasilense and identification of a region controlling nifH transcription. Molecular Genetics and Genomics, 1989, 220, 81-87.	2.4	34
63	Exploring the HME and HAE1 efflux systems in the genus Burkholderia. BMC Evolutionary Biology, 2010, 10, 164.	3.2	32
64	Evaluation of Fluoroquinolone Resistance Mechanisms in <i>Pseudomonas aeruginosa</i> Multidrug Resistance Clinical Isolates. Microbial Drug Resistance, 2012, 18, 23-32.	2.0	31
65	The genome sequence of the hydrocarbon-degrading Acinetobacter venetianus VE-C3. Research in Microbiology, 2013, 164, 439-449.	2.1	30
66	Molecular nature of RAPD markers from Haemophilus influenzae Rd genome. Research in Microbiology, 1999, 150, 83-93.	2.1	29
67	Exploring the Anti- <i>Burkholderia cepacia</i> Complex Activity of Essential Oils: A Preliminary Analysis. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-10.	1.2	27
68	Restriction fragment length polymorphism of <i>Azospirillum</i> strains. FEMS Microbiology Letters, 1991, 83, 225-229.	1.8	26
69	Paralogous histidine biosynthetic genes: evolutionary analysis of the Saccharomyces cerevisiae HIS6 and HIS7 genes. Gene, 1997, 197, 9-17.	2.2	25
70	Polyphasic approach to the characterisation of marine luminous bacteria. Research in Microbiology, 1999, 150, 221-230.	2.1	25
71	Diversity of heterotrophic aerobic cultivable microbial communities of soils treated with fumigants and dynamics of metabolic, microbial, and mineralization quotients. Biology and Fertility of Soils, 2008, 44, 557-569.	4.3	24
72	Alteration of bacterial communities and organic matter in microbial fuel cells (MFCs) supplied with soil and organic fertilizer. Applied Microbiology and Biotechnology, 2013, 97, 1299-1315.	3.6	24

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73	The influence of Echinacea purpurea leaf microbiota on chicoric acid level. Scientific Reports, 2019, 9, 10897.	3.3	24
74	Organization and Evolution of the <i>cotG</i> and <i>cotH</i> Genes of Bacillus subtilis. Journal of Bacteriology, 2011, 193, 6664-6673.	2.2	23
75	Linking Bacterial Endophytic Communities to Essential Oils: Clues from <i>Lavandula angustifolia</i> Mill. Evidence-based Complementary and Alternative Medicine, 2014, 2014, 1-16.	1.2	23
76	Genomic and phenotypic characterization of the species Acinetobacter venetianus. Scientific Reports, 2016, 6, 21985.	3.3	23
77	Pseudoalteromonas haloplanktis produces methylamine, a volatile compound active against Burkholderia cepacia complex strains. New Biotechnology, 2017, 35, 13-18.	4.4	23
78	Phenotypic and genomic characterization of the Antarctic bacterium Gillisia sp. CAL575, a producer of antimicrobial compounds. Extremophiles, 2014, 18, 35-49.	2.3	22
79	Cold-adapted bacteria from a coastal area of the Ross Sea (Terra Nova Bay, Antarctica): linking microbial ecology to biotechnology. Hydrobiologia, 2015, 761, 417-441.	2.0	22
80	The origin and evolution of eucaryal HIS7 genes: from metabolon to bifunctional proteins?. Gene, 2004, 339, 149-160.	2.2	20
81	Use of the gyrB gene to discriminate among species of the Burkholderia cepacia complex. FEMS Microbiology Letters, 2008, 281, 175-182.	1.8	20
82	Promoting Model Systems of Microbiota–Medicinal Plant Interactions. Trends in Plant Science, 2020, 25, 223-225.	8.8	20
83	The Evolution of Histidine Biosynthesis in Archaea: Insights into the his Genes Structure and Organization in LUCA. Journal of Molecular Evolution, 2009, 69, 512-526.	1.8	19
84	Draft Genome Sequence of the Hydrocarbon-Degrading and Emulsan-Producing Strain Acinetobacter venetianus RAG-1T. Journal of Bacteriology, 2012, 194, 4771-4772.	2.2	19
85	Seasonal mercury transformation and surficial sediment detoxification by bacteria of Marano and Grado lagoons. Estuarine, Coastal and Shelf Science, 2012, 113, 105-115.	2.1	19
86	Furnishing spaceship environment: evaluation of bacterial biofilms on different materials used inside International Space Station. Research in Microbiology, 2018, 169, 289-295.	2.1	19
87	Antagonism and antibiotic resistance drive a species-specific plant microbiota differentiation in Echinacea spp. FEMS Microbiology Ecology, 2018, 94, .	2.7	19
88	The Cultivable Bacterial Microbiota Associated to the Medicinal Plant Origanum vulgare L.: From Antibiotic Resistance to Growth-Inhibitory Properties. Frontiers in Microbiology, 2020, 11, 862.	3.5	19
89	Envelope glycosylation determined by lectins in microscopy sections ofÂAcinetobacter venetianus induced by diesel fuel. Research in Microbiology, 2003, 154, 417-424.	2.1	18
90	Efflux-mediated resistance to a benzothiadiazol derivative effective against Burkholderia cenocepacia. Frontiers in Microbiology, 2015, 6, 815.	3.5	18

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91	Design and start-up of a constructed wetland as tertiary treatment for landfill leachates. Water Science and Technology, 2019, 79, 145-155.	2.5	18
92	The Origin and Evolution of Metabolic Pathways: Why and How did Primordial Cells Construct Metabolic Routes?. Evolution: Education and Outreach, 2012, 5, 367-381.	0.8	17
93	Network Analysis of Plasmidomes: The <i>Azospirillum brasilense</i> Sp245 Case. International Journal of Evolutionary Biology, 2014, 2014, 1-14.	1.0	17
94	Mechanism of Resistance to an Antitubercular 2-Thiopyridine Derivative That Is Also Active against Burkholderia cenocepacia. Antimicrobial Agents and Chemotherapy, 2014, 58, 2415-2417.	3.2	17
95	Draft genomes of three Antarctic Psychrobacter strains producing antimicrobial compounds against Burkholderia cepacia complex, opportunistic human pathogens. Marine Genomics, 2014, 13, 37-38.	1.1	17
96	Antimicrobial activity of Pseudoalteromonas strains isolated from the Ross Sea (Antarctica) versus Cystic Fibrosis opportunistic pathogens. Hydrobiologia, 2015, 761, 443-457.	2.0	17
97	Cloning of the histidine, pyrimidine and cysteine genes of Azospirillum brasilense: Expression of pyrimidine and three clustered histidine genes in Escherichia coli. Molecular Genetics and Genomics, 1987, 206, 76-80.	2.4	16
98	A plasmid vector for the selection and study of transcription promoters inAzospirillum brasilense. FEMS Microbiology Letters, 1988, 50, 271-276.	1.8	16
99	The mosaicism of plasmids revealed by atypical genes detection and analysis. BMC Genomics, 2011, 12, 403.	2.8	16
100	Harmful Effect of Rheinheimera sp. EpRS3 (Gammaproteobacteria) Against the Protist Euplotes aediculatus (Ciliophora, Spirotrichea): Insights Into the Ecological Role of Antimicrobial Compounds From Environmental Bacterial Strains. Frontiers in Microbiology, 2019, 10, 510.	3.5	16
101	A census of RND superfamily proteins in the <i>Burkholderia</i> genus. Future Microbiology, 2013, 8, 923-937.	2.0	15
102	Spatial structuring of bacterial communities in epilithic biofilms in the Acquarossa river (Italy). FEMS Microbiology Ecology, 2018, 94, .	2.7	15
103	The antimicrobial potential of algicolous marine fungi for counteracting multidrug-resistant bacteria: phylogenetic diversity and chemical profiling. Research in Microbiology, 2016, 167, 492-500.	2.1	14
104	Volatile profile of <i>Echinacea purpurea</i> plants after <i>in vitro</i> endophyte infection. Natural Product Research, 2020, 34, 2232-2237.	1.8	14
105	Exploring the role of the histidine biosynthetic hisF gene in cellular metabolism and in the evolution of (ancestral) genes: from LUCA to the extant (micro)organisms. Microbiological Research, 2020, 240, 126555.	5.3	14
106	Exploring the Diversity and Metabolic Profiles of Bacterial Communities Associated With Antarctic Sponges (Terra Nova Bay, Ross Sea). Frontiers in Ecology and Evolution, 2020, 8, .	2.2	14
107	Expression of horizontally transferred gene clusters: activation by promoter-generating mutations. Research in Microbiology, 2001, 152, 539-549.	2.1	13
108	On the origin and evolution of biosynthetic pathways: integrating microarray data with structure and organization of the Common Pathway genes. BMC Bioinformatics, 2007, 8, S12.	2.6	13

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109	Draft Genome Sequence of the Volatile Organic Compound-Producing Antarctic Bacterium Arthrobacter sp. Strain TB23, Able To Inhibit Cystic Fibrosis Pathogens Belonging to the Burkholderia cepacia Complex. Journal of Bacteriology, 2012, 194, 6334-6335.	2.2	13
110	<i>DprE1</i> , a new taxonomic marker in mycobacteria. FEMS Microbiology Letters, 2013, 348, 66-73.	1.8	13
111	Genome-scale phylogenetic and DNA composition analyses of Antarctic Pseudoalteromonas bacteria reveal inconsistencies in current taxonomic affiliation. Hydrobiologia, 2015, 761, 85-95.	2.0	13
112	Antimicrobial Potential of Cold-Adapted Bacteria and Fungi from Polar Regions. Grand Challenges in Biology and Biotechnology, 2016, , 83-115.	2.4	13
113	Pseudomonas strains isolated from different environmental niches exhibit different antagonistic ability. Ethology Ecology and Evolution, 2019, 31, 399-420.	1.4	13
114	Genomic Analysis of Endophytic Bacillus-Related Strains Isolated from the Medicinal Plant Origanum vulgare L. Revealed the Presence of Metabolic Pathways Involved in the Biosynthesis of Bioactive Compounds. Microorganisms, 2022, 10, 919.	3.6	13
115	Plasmid transformation of Azospirillum brasilense. FEMS Microbiology Letters, 1986, 35, 23-27.	1.8	12
116	Isolation and characterisation of a new antagonistic Burkholderia strain from the rhizosphere of healthy tomato plants. Research in Microbiology, 1999, 150, 45-59.	2.1	12
117	Long-term analysis of diesel fuel consumption in a co-culture of Acinetobacter venetianus, Pseudomonas putida and Alcaligenes faecalis. Antonie Van Leeuwenhoek, 2003, 83, 3-9.	1.7	12
118	From the primordial soup to the latest universal common ancestor. Research in Microbiology, 2009, 160, 437-440.	2.1	12
119	Application of multiplex single nucleotide primer extension (mSNuPE) to the identification of bacteria: The Burkholderia cepacia complex case. Journal of Microbiological Methods, 2010, 80, 251-256.	1.6	12
120	Modelling microbial metabolic rewiring during growth in a complex medium. BMC Genomics, 2016, 17, 970.	2.8	12
121	Draft genome sequence and overview of the purple non sulfur bacterium Rhodopseudomonas palustris 42OL. Standards in Genomic Sciences, 2016, 11, 24.	1.5	12
122	Can an Imidazole Be Formed from an Alanyl-Seryl-Glycine Tripeptide under Possible Prebiotic Conditions?. Origins of Life and Evolution of Biospheres, 2017, 47, 345-354.	1.9	12
123	Volatile organic compounds: from figurants to leading actors in fungal symbiosis. FEMS Microbiology Ecology, 2021, 97, .	2.7	12
124	Identification and Evolutionary Analysis of Putative Cytoplasmic McpA-Like Protein in a Bacterial Strain Living in Symbiosis with a Mycorrhizal Fungus. Journal of Molecular Evolution, 2002, 54, 815-824.	1.8	11
125	The Role of Gene Elongation in the Evolution of Histidine Biosynthetic Genes. Microorganisms, 2020, 8, 732.	3.6	11
126	Endophytic Bacteria and Essential Oil from Origanum vulgare ssp. vulgare Share Some VOCs with an Antibacterial Activity. Microorganisms, 2022, 10, 1424.	3.6	11

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127	Sequencing and analysis of plasmids pAV1 and pAV2 ofAcinetobacter venetianus VE-C3 involved in diesel fuel degradation. Annals of Microbiology, 2007, 57, 521-526.	2.6	10
128	Manila clams from Hg polluted sediments of Marano and Grado lagoons (Italy) harbor detoxifying Hg resistant bacteria in soft tissues. Environmental Research, 2013, 125, 188-196.	7.5	10
129	Genomes analysis and bacteria identification: The use of overlapping genes as molecular markers. Journal of Microbiological Methods, 2015, 117, 108-112.	1.6	9
130	A Systems Biology View on Bacterial Response to Temperature Shift. Grand Challenges in Biology and Biotechnology, 2016, , 597-618.	2.4	9
131	Antimicrobial activity of six essential oils againstBurkholderia cepaciacomplex: insights into mechanism(s) of action. Future Microbiology, 2018, 13, 59-67.	2.0	9
132	Bacterial Communities from Extreme Environments: Vulcano Island. Diversity, 2019, 11, 140.	1.7	9
133	<i>In vivo</i> evaluation of the interaction between the <i>Escherichia coli</i> IGP synthase subunits using the Bacterial Two-Hybrid system. FEMS Microbiology Letters, 2020, 367, .	1.8	9
134	Inference from Proteobacterial Operons Shows Piecewise Organization: A Reply to Price et al Journal of Molecular Evolution, 2006, 63, 577-580.	1.8	8
135	Chlor-alkali plant contamination of Aussa River sediments induced a large Hg-resistant bacterial community. Estuarine, Coastal and Shelf Science, 2012, 113, 96-104.	2.1	8
136	Essential Oil from <i>Origanum vulgare</i> Completely Inhibits the Growth of Multidrug-Resistant Cystic Fibrosis Pathogens. Natural Product Communications, 2016, 11, 1934578X1601100.	0.5	8
137	Microbial community composition of water samples stored inside the International Space Station. Research in Microbiology, 2019, 170, 230-234.	2.1	8
138	Temporal Evolution of Bacterial Endophytes Associated to the Roots of Phragmites australis Exploited in Phytodepuration of Wastewater. Frontiers in Microbiology, 2020, 11, 1652.	3.5	8
139	The CAI Analyser Package: inferring gene expressivity from raw genomic data. In Silico Biology, 2007, 7, 507-26.	0.9	8
140	Structural, evolutionary and genetic analysis of the histidine biosynthetic "core―in the genus Burkholderia. Gene, 2009, 448, 16-28.	2.2	7
141	Heterologous Gene Expression in an Escherichia coli Population Under Starvation Stress Conditions. Journal of Molecular Evolution, 1998, 47, 363-368.	1.8	6
142	Identification of alkane monoxygenase genes inAcinetobacter venetianus VE-C3 and analysis of mutants impaired in diesel fuel degradation. Annals of Microbiology, 2006, 56, 207-214.	2.6	6
143	Origin, duplication and reshuffling of plasmid genes: Insights from Burkholderia vietnamiensis G4 genome. Genomics, 2014, 103, 229-238.	2.9	6
144	Constraint-based metabolic modelling of marine microbes and communities. Marine Genomics, 2017, 34, 1-10.	1.1	6

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145	Exploring the Bacterial Communities of Infernaccio Waterfalls: A Phenotypic and Molecular Characterization of Acinetobacter and Pseudomonas Strains Living in a Red Epilithic Biofilm. Diversity, 2019, 11, 175.	1.7	6
146	Factors affecting nitrogen fixation andnifgene transcription inAzospirillum brasilense. FEMS Microbiology Letters, 1994, 120, 133-136.	1.8	5
147	Subfunctionalization influences the expansion of bacterial multidrug antibiotic resistance. BMC Genomics, 2017, 18, 834.	2.8	5
148	Genomic traits of Klebsiella oxytoca DSM 29614, an uncommon metal-nanoparticle producer strain isolated from acid mine drainages. BMC Microbiology, 2018, 18, 198.	3.3	5
149	Defining the resilience of the human salivary microbiota by a 520-day longitudinal study in a confined environment: the Mars500 mission. Microbiome, 2021, 9, 152.	11.1	5
150	CO2 biogeochemical investigation and microbial characterization of red wood ant mounds in a Southern Europe montane forest. Soil Biology and Biochemistry, 2022, 166, 108536.	8.8	5
151	Current trends in the bioinformatic sequence analysis of metabolic pathways in prokaryotes. Briefings in Bioinformatics, 2007, 9, 34-45.	6.5	4
152	Investigating the Role of the Host Multidrug Resistance Associated Protein Transporter Family in Burkholderia cepacia Complex Pathogenicity Using a Caenorhabditis elegans Infection Model. PLoS ONE, 2015, 10, e0142883.	2.5	4
153	Draft Genome Sequences of the Antimicrobial Producers Pseudomonas sp. TAA207 and Pseudomonas sp. TAD18 Isolated from Antarctic Sediments. Genome Announcements, 2016, 4, .	0.8	4
154	Draft Genome Sequence of <i>Pseudomonas</i> sp. Strain Ep R1 Isolated from <i>Echinacea purpurea</i> Roots and Effective in the Growth Inhibition of Human Opportunistic Pathogens Belonging to the Burkholderia cepacia Complex. Genome Announcements, 2017, 5, .	0.8	4
155	Antibacterial activity of bacteria isolated from <i>Phragmites australis</i> against multidrug-resistant human pathogens. Future Microbiology, 2021, 16, 291-303.	2.0	4
156	The Histidine Biosynthetic Genes in the Superphylum Bacteroidota-Rhodothermota-Balneolota-Chlorobiota: Insights into the Evolution of Gene Structure and Organization. Microorganisms, 2021, 9, 1439.	3.6	4
157	Biodiversity of Soil Bacterial Communities from the Sasso Fratino Integral Nature Reserve. Microbiology Research, 2021, 12, 862-877.	1.9	4
158	Effect of Non-Lethal Selection on Spontaneous Revertants of Frameshift Mutations: The Escherichia coliÂhisF Case. Microorganisms, 2022, 10, 692.	3.6	4
159	Enly: Improving Draft Genomes through Reads Recycling. Journal of Genomics, 2014, 2, 89-93.	0.9	3
160	Arthrobacter sp. EpRS66 and Arthrobacter sp. EpRS71: Draft Genome Sequences from Two Bacteria Isolated from Echinacea purpurea Rhizospheric Soil. Frontiers in Microbiology, 2016, 7, 1417.	3.5	3
161	New Genome Sequence of an Echinacea purpurea Endophyte, Arthrobacter sp. Strain EpSL27, Able To Inhibit Human-Opportunistic Pathogens. Genome Announcements, 2017, 5, .	0.8	3
162	The cypsela (achene) of Echinacea purpurea as a diffusion unit of a community of microorganisms. Applied Microbiology and Biotechnology, 2021, 105, 2951-2965.	3.6	3

#	Article	IF	CITATIONS
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