

# Renato Fani

## List of Publications by Year in descending order

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177  
papers

5,557  
citations

66315

42  
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114418

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182  
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182  
docs citations

182  
times ranked

7014  
citing authors

#	ARTICLE	IF	CITATIONS
1	CO <sub>2</sub> biogeochemical investigation and microbial characterization of red wood ant mounds in a Southern Europe montane forest. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108536.	4.2	5
2	Effect of Non-Lethal Selection on Spontaneous Revertants of Frameshift Mutations: The <i>Escherichia coli</i> HisF Case. <i>Microorganisms</i> , 2022, 10, 692.	1.6	4
3	The Azurin Coding Gene: Origin and Phylogenetic Distribution. <i>Microorganisms</i> , 2022, 10, 9.	1.6	2
4	Genomic Analysis of Endophytic <i>Bacillus</i> -Related Strains Isolated from the Medicinal Plant <i>Origanum vulgare</i> L. Revealed the Presence of Metabolic Pathways Involved in the Biosynthesis of Bioactive Compounds. <i>Microorganisms</i> , 2022, 10, 919.	1.6	13
5	Microbial Genetics and Evolution. <i>Microorganisms</i> , 2022, 10, 1274.	1.6	0
6	Endophytic Bacteria and Essential Oil from <i>Origanum vulgare</i> ssp. <i>vulgare</i> Share Some VOCs with an Antibacterial Activity. <i>Microorganisms</i> , 2022, 10, 1424.	1.6	11
7	The art of adapting to extreme environments: The model system <i>Pseudoalteromonas</i> . <i>Physics of Life Reviews</i> , 2021, 36, 137-161.	1.5	53
8	Medicinal Plants and Their Bacterial Microbiota: A Review on Antimicrobial Compounds Production for Plant and Human Health. <i>Pathogens</i> , 2021, 10, 106.	1.2	38
9	Exploring the Gut Microbiome Alteration of the European Hare ( <i>Lepus europaeus</i> ) after Short-Term Diet Modifications. <i>Biology</i> , 2021, 10, 148.	1.3	0
10	The cypsel (achene) of <i>Echinacea purpurea</i> as a diffusion unit of a community of microorganisms. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2951-2965.	1.7	3
11	Antibacterial activity of bacteria isolated from <i>Phragmites australis</i> against multidrug-resistant human pathogens. <i>Future Microbiology</i> , 2021, 16, 291-303.	1.0	4
12	Volatile organic compounds: from figurants to leading actors in fungal symbiosis. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	1.3	12
13	Defining the resilience of the human salivary microbiota by a 520-day longitudinal study in a confined environment: the Mars500 mission. <i>Microbiome</i> , 2021, 9, 152.	4.9	5
14	The Histidine Biosynthetic Genes in the Superphylum Bacteroidota-Rhodothermota-Balneolota-Chlorobiota: Insights into the Evolution of Gene Structure and Organization. <i>Microorganisms</i> , 2021, 9, 1439.	1.6	4
15	Cross-Amplification in Strigiformes: A New STR Panel for Forensic Purposes. <i>Genes</i> , 2021, 12, 1721.	1.0	1
16	Biodiversity of Soil Bacterial Communities from the Sasso Fratino Integral Nature Reserve. <i>Microbiology Research</i> , 2021, 12, 862-877.	0.8	4
17	Volatile profile of <i>Echinacea purpurea</i> plants after <i>in vitro</i> endophyte infection. <i>Natural Product Research</i> , 2020, 34, 2232-2237.	1.0	14
18	Promoting Model Systems of Microbiota-Medicinal Plant Interactions. <i>Trends in Plant Science</i> , 2020, 25, 223-225.	4.3	20

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19	Temporal Evolution of Bacterial Endophytes Associated to the Roots of <i>Phragmites australis</i> Exploited in Phytodepuration of Wastewater. <i>Frontiers in Microbiology</i> , 2020, 11, 1652.	1.5	8
20	<i>In vivo</i> evaluation of the interaction between the <i>Escherichia coli</i> IGP synthase subunits using the Bacterial Two-Hybrid system. <i>FEMS Microbiology Letters</i> , 2020, 367, .	0.7	9
21	Exploring the role of the histidine biosynthetic <i>hisF</i> gene in cellular metabolism and in the evolution of (ancestral) genes: from LUCA to the extant (micro)organisms. <i>Microbiological Research</i> , 2020, 240, 126555.	2.5	14
22	Exploring the Diversity and Metabolic Profiles of Bacterial Communities Associated With Antarctic Sponges (Terra Nova Bay, Ross Sea). <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	14
23	The Role of Gene Elongation in the Evolution of Histidine Biosynthetic Genes. <i>Microorganisms</i> , 2020, 8, 732.	1.6	11
24	Diauxie and co-utilization of carbon sources can coexist during bacterial growth in nutritionally complex environments. <i>Nature Communications</i> , 2020, 11, 3135.	5.8	51
25	The Cultivable Bacterial Microbiota Associated to the Medicinal Plant <i>Origanum vulgare</i> L.: From Antibiotic Resistance to Growth-Inhibitory Properties. <i>Frontiers in Microbiology</i> , 2020, 11, 862.	1.5	19
26	Significant and Conflicting Correlation of IL-9 With <i>Prevotella</i> and <i>Bacteroides</i> in Human Colorectal Cancer. <i>Frontiers in Immunology</i> , 2020, 11, 573158.	2.2	37
27	The influence of <i>Echinacea purpurea</i> leaf microbiota on chicoric acid level. <i>Scientific Reports</i> , 2019, 9, 10897.	1.6	24
28	Genome of the Komodo dragon reveals adaptations in the cardiovascular and chemosensory systems of monitor lizards. <i>Nature Ecology and Evolution</i> , 2019, 3, 1241-1252.	3.4	67
29	Tissue specificity and differential effects on <i>in vitro</i> plant growth of single bacterial endophytes isolated from the roots, leaves and rhizospheric soil of <i>Echinacea purpurea</i> . <i>BMC Plant Biology</i> , 2019, 19, 284.	1.6	36
30	Bacterial Communities from Extreme Environments: Vulcano Island. <i>Diversity</i> , 2019, 11, 140.	0.7	9
31	Design and start-up of a constructed wetland as tertiary treatment for landfill leachates. <i>Water Science and Technology</i> , 2019, 79, 145-155.	1.2	18
32	<i>Pseudomonas</i> strains isolated from different environmental niches exhibit different antagonistic ability. <i>Ethology Ecology and Evolution</i> , 2019, 31, 399-420.	0.6	13
33	Microbial community composition of water samples stored inside the International Space Station. <i>Research in Microbiology</i> , 2019, 170, 230-234.	1.0	8
34	Harmful Effect of <i>Rheinheimera</i> sp. EpRS3 (Gammaproteobacteria) Against the Protist <i>Euplotes aediculatus</i> (Ciliophora, Spirotrichea): Insights Into the Ecological Role of Antimicrobial Compounds From Environmental Bacterial Strains. <i>Frontiers in Microbiology</i> , 2019, 10, 510.	1.5	16
35	Exploring the Bacterial Communities of Infernaccio Waterfalls: A Phenotypic and Molecular Characterization of <i>Acinetobacter</i> and <i>Pseudomonas</i> Strains Living in a Red Epilithic Biofilm. <i>Diversity</i> , 2019, 11, 175.	0.7	6
36	A Method for the Structure-Based, Genome-Wide Analysis of Bacterial Intergenic Sequences Identifies Shared Compositional and Functional Features. <i>Genes</i> , 2019, 10, 834.	1.0	0

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37	Antimicrobial activity of six essential oils against <i>Burkholderia cepacia</i> complex: insights into mechanism(s) of action. <i>Future Microbiology</i> , 2018, 13, 59-67.	1.0	9
38	<i>Pseudoalteromonas haloplanktis</i> TAC125 produces 4-hydroxybenzoic acid that induces pyroptosis in human A459 lung adenocarcinoma cells. <i>Scientific Reports</i> , 2018, 8, 1190.	1.6	41
39	Genomic traits of <i>Klebsiella oxytoca</i> DSM 29614, an uncommon metal-nanoparticle producer strain isolated from acid mine drainages. <i>BMC Microbiology</i> , 2018, 18, 198.	1.3	5
40	Antibiotics from Deep-Sea Microorganisms: Current Discoveries and Perspectives. <i>Marine Drugs</i> , 2018, 16, 355.	2.2	98
41	Spatial structuring of bacterial communities in epilithic biofilms in the Acquarossa river (Italy). <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	15
42	Furnishing spaceship environment: evaluation of bacterial biofilms on different materials used inside International Space Station. <i>Research in Microbiology</i> , 2018, 169, 289-295.	1.0	19
43	Antagonism and antibiotic resistance drive a species-specific plant microbiota differentiation in <i>Echinacea</i> spp. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	19
44	The pangenome of (Antarctic) <i>Pseudoalteromonas</i> bacteria: evolutionary and functional insights. <i>BMC Genomics</i> , 2017, 18, 93.	1.2	46
45	Ecology of cold environments: new insights of bacterial metabolic adaptation through an integrated genomic-phenomic approach. <i>Scientific Reports</i> , 2017, 7, 839.	1.6	65
46	<i>Pseudoalteromonas haloplanktis</i> produces methylamine, a volatile compound active against <i>Burkholderia cepacia</i> complex strains. <i>New Biotechnology</i> , 2017, 35, 13-18.	2.4	23
47	Constraint-based modeling identifies new putative targets to fight colistin-resistant <i>A. baumannii</i> infections. <i>Scientific Reports</i> , 2017, 7, 3706.	1.6	47
48	Constraint-based metabolic modelling of marine microbes and communities. <i>Marine Genomics</i> , 2017, 34, 1-10.	0.4	6
49	Preliminary data on antibacterial activity of <i>Echinacea purpurea</i> -associated bacterial communities against <i>Burkholderia cepacia</i> complex strains, opportunistic pathogens of Cystic Fibrosis patients. <i>Microbiological Research</i> , 2017, 196, 34-43.	2.5	35
50	Plant-endophytes interaction influences the secondary metabolism in <i>Echinacea purpurea</i> (L.) Moench: an in vitro model. <i>Scientific Reports</i> , 2017, 7, 16924.	1.6	74
51	New Genome Sequence of an <i>Echinacea purpurea</i> Endophyte, <i>Arthrobacter</i> sp. Strain EpSL27, Able To Inhibit Human-Opportunistic Pathogens. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
52	Can an Imidazole Be Formed from an Alanyl-Seryl-Glycine Tripeptide under Possible Prebiotic Conditions?. <i>Origins of Life and Evolution of Biospheres</i> , 2017, 47, 345-354.	0.8	12
53	Is the plant-associated microbiota of <i>Thymus</i> spp. adapted to plant essential oil?. <i>Research in Microbiology</i> , 2017, 168, 276-282.	1.0	35
54	Phenotypic and genomic characterization of the antimicrobial producer <i>Rheinheimera</i> sp. EpRS3 isolated from the medicinal plant <i>Echinacea purpurea</i> : insights into its biotechnological relevance. <i>Research in Microbiology</i> , 2017, 168, 293-305.	1.0	39

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55	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 <i>Burkholderia cepacia</i> Complex. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
56	Subfunctionalization influences the expansion of bacterial multidrug antibiotic resistance. <i>BMC Genomics</i> , 2017, 18, 834.	1.2	5
57	Exploring the Effect of the Composition of Three Different <i>Oregano</i> Essential Oils on the Growth of Multidrug-Resistant Cystic Fibrosis <i>Pseudomonas aeruginosa</i> Strains. <i>Natural Product Communications</i> , 2017, 12, 1934578X1701201.	0.2	2
58	Preliminary Comparison of Oral and Intestinal Human Microbiota in Patients with Colorectal Cancer: A Pilot Study. <i>Frontiers in Microbiology</i> , 2017, 8, 2699.	1.5	93
59	Essential Oil from <i>Origanum vulgare</i> Completely Inhibits the Growth of Multidrug-Resistant Cystic Fibrosis Pathogens. <i>Natural Product Communications</i> , 2016, 11, 1934578X1601100.	0.2	8
60	<i>Arthrobacter</i> sp. EpRS66 and <i>Arthrobacter</i> sp. EpRS71: Draft Genome Sequences from Two Bacteria Isolated from <i>Echinacea purpurea</i> Rhizospheric Soil. <i>Frontiers in Microbiology</i> , 2016, 7, 1417.	1.5	3
61	Antimicrobial Activity of Monoramnholipids Produced by Bacterial Strains Isolated from the Ross Sea (Antarctica). <i>Marine Drugs</i> , 2016, 14, 83.	2.2	48
62	Antagonistic interactions between endophytic cultivable bacterial communities isolated from the medicinal plant <i>Echinacea purpurea</i> . <i>Environmental Microbiology</i> , 2016, 18, 2357-2365.	1.8	43
63	Modelling microbial metabolic rewiring during growth in a complex medium. <i>BMC Genomics</i> , 2016, 17, 970.	1.2	12
64	Draft Genome Sequences of the Antimicrobial Producers <i>Pseudomonas</i> sp. TAA207 and <i>Pseudomonas</i> sp. TAD18 Isolated from Antarctic Sediments. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
65	The antimicrobial potential of algicolous marine fungi for counteracting multidrug-resistant bacteria: phylogenetic diversity and chemical profiling. <i>Research in Microbiology</i> , 2016, 167, 492-500.	1.0	14
66	“Every Gene Is Everywhere but the Environment Selects” Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. <i>Genome Biology and Evolution</i> , 2016, 8, 1388-1400.	1.1	82
67	A new method for long-term storage of titred microbial standard solutions suitable for microbiologic quality control activities of pharmaceutical companies. <i>Journal of Microbiological Methods</i> , 2016, 127, 10-12.	0.7	0
68	Genomic and phenotypic characterization of the species <i>Acinetobacter venetianus</i> . <i>Scientific Reports</i> , 2016, 6, 21985.	1.6	23
69	Draft Genome Sequence of <i>Pseudomonas</i> sp. EpS/L25, Isolated from the Medicinal Plant <i>Echinacea purpurea</i> and Able To Synthesize Antimicrobial Compounds. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
70	Draft Genome Sequence of <i>Flavobacterium</i> sp. Strain TAB 87, Able To Inhibit the Growth of Cystic Fibrosis Bacterial Pathogens Belonging to the <i>Burkholderia cepacia</i> Complex. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
71	A Systems Biology View on Bacterial Response to Temperature Shift. <i>Grand Challenges in Biology and Biotechnology</i> , 2016, , 597-618.	2.4	9
72	Antimicrobial Potential of Cold-Adapted Bacteria and Fungi from Polar Regions. <i>Grand Challenges in Biology and Biotechnology</i> , 2016, , 83-115.	2.4	13

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73	Draft genome sequence and overview of the purple non sulfur bacterium <i>Rhodospseudomonas palustris</i> 42OL. <i>Standards in Genomic Sciences</i> , 2016, 11, 24.	1.5	12
74	Efflux-mediated resistance to a benzothiadiazol derivative effective against <i>Burkholderia cenocepacia</i> . <i>Frontiers in Microbiology</i> , 2015, 6, 815.	1.5	18
75	Investigating the Role of the Host Multidrug Resistance Associated Protein Transporter Family in <i>Burkholderia cepacia</i> Complex Pathogenicity Using a <i>Caenorhabditis elegans</i> Infection Model. <i>PLoS ONE</i> , 2015, 10, e0142883.	1.1	4
76	Genomes analysis and bacteria identification: The use of overlapping genes as molecular markers. <i>Journal of Microbiological Methods</i> , 2015, 117, 108-112.	0.7	9
77	Thiophenecarboxamide Derivatives Activated by EthA Kill <i>Mycobacterium tuberculosis</i> by Inhibiting the CTP Synthetase PyrG. <i>Chemistry and Biology</i> , 2015, 22, 917-927.	6.2	72
78	Genome-scale phylogenetic and DNA composition analyses of Antarctic <i>Pseudoalteromonas</i> bacteria reveal inconsistencies in current taxonomic affiliation. <i>Hydrobiologia</i> , 2015, 761, 85-95.	1.0	13
79	Antimicrobial activity of <i>Pseudoalteromonas</i> strains isolated from the Ross Sea (Antarctica) versus <i>Cystic Fibrosis</i> opportunistic pathogens. <i>Hydrobiologia</i> , 2015, 761, 443-457.	1.0	17
80	MEDUSA: a multi-draft based scaffold. <i>Bioinformatics</i> , 2015, 31, 2443-2451.	1.8	359
81	Cold-adapted bacteria from a coastal area of the Ross Sea (Terra Nova Bay, Antarctica): linking microbial ecology to biotechnology. <i>Hydrobiologia</i> , 2015, 761, 417-441.	1.0	22
82	Genome-scale metabolic reconstruction and constraint-based modelling of the Antarctic bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Environmental Microbiology</i> , 2015, 17, 751-766.	1.8	53
83	Analysis of a Pool of Small Plasmids from Soil Heterotrophic Cultivable Bacterial Communities. <i>Open Microbiology Journal</i> , 2015, 9, 98-109.	0.2	1
84	Enly: Improving Draft Genomes through Reads Recycling. <i>Journal of Genomics</i> , 2014, 2, 89-93.	0.6	3
85	Exploring the Anti- <i>Burkholderia cepacia</i> Complex Activity of Essential Oils: A Preliminary Analysis. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-10.	0.5	27
86	Linking Bacterial Endophytic Communities to Essential Oils: Clues from <i>Lavandula angustifolia</i> Mill. <i>Evidence-based Complementary and Alternative Medicine</i> , 2014, 2014, 1-16.	0.5	23
87	Acquisition and Evolution of SXT-R391 Integrative Conjugative Elements in the Seventh-Pandemic <i>Vibrio cholerae</i> Lineage. <i>MBio</i> , 2014, 5, .	1.8	78
88	Soil Bacterial Community Response to Differences in Agricultural Management along with Seasonal Changes in a Mediterranean Region. <i>PLoS ONE</i> , 2014, 9, e105515.	1.1	89
89	Network Analysis of Plasmidomes: The <i>Azospirillum brasilense</i> Sp245 Case. <i>International Journal of Evolutionary Biology</i> , 2014, 2014, 1-14.	1.0	17
90	Phenotypic and genomic characterization of the Antarctic bacterium <i>Gillisia</i> sp. CAL575, a producer of antimicrobial compounds. <i>Extremophiles</i> , 2014, 18, 35-49.	0.9	22

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91	Genomic analysis of three sponge-associated <i>Arthrobacter</i> Antarctic strains, inhibiting the growth of <i>Burkholderia cepacia</i> complex bacteria by synthesizing volatile organic compounds. <i>Microbiological Research</i> , 2014, 169, 593-601.	2.5	38
92	Antibiotic resistance differentiates <i>Echinacea purpurea</i> endophytic bacterial communities with respect to plant organs. <i>Research in Microbiology</i> , 2014, 165, 686-694.	1.0	50
93	Mechanism of Resistance to an Antitubercular 2-Thiopyridine Derivative That Is Also Active against <i>Burkholderia cenocepacia</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2415-2417.	1.4	17
94	Modeling mutant distribution in a stressed <i>Escherichia coli</i> bacteria population using experimental data. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014, 393, 320-326.	1.2	1
95	Origin, duplication and reshuffling of plasmid genes: Insights from <i>Burkholderia vietnamiensis</i> G4 genome. <i>Genomics</i> , 2014, 103, 229-238.	1.3	6
96	Draft genomes of three Antarctic <i>Psychrobacter</i> strains producing antimicrobial compounds against <i>Burkholderia cepacia</i> complex, opportunistic human pathogens. <i>Marine Genomics</i> , 2014, 13, 37-38.	0.4	17
97	Endophytic and rhizospheric bacterial communities isolated from the medicinal plants <i>Echinacea purpurea</i> and <i>Echinacea angustifolia</i> . <i>International Microbiology</i> , 2014, 17, 165-74.	1.1	46
98	Alteration of bacterial communities and organic matter in microbial fuel cells (MFCs) supplied with soil and organic fertilizer. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1299-1315.	1.7	24
99	Manila clams from Hg polluted sediments of Marano and Grado lagoons (Italy) harbor detoxifying Hg resistant bacteria in soft tissues. <i>Environmental Research</i> , 2013, 125, 188-196.	3.7	10
100	The genome sequence of the hydrocarbon-degrading <i>Acinetobacter venetianus</i> VE-C3. <i>Research in Microbiology</i> , 2013, 164, 439-449.	1.0	30
101	<i>DprE1</i> , a new taxonomic marker in mycobacteria. <i>FEMS Microbiology Letters</i> , 2013, 348, 66-73.	0.7	13
102	Bioactive volatile organic compounds from Antarctic (sponges) bacteria. <i>New Biotechnology</i> , 2013, 30, 824-838.	2.4	62
103	A census of RND superfamily proteins in the <i>Burkholderia</i> genus. <i>Future Microbiology</i> , 2013, 8, 923-937.	1.0	15
104	RND-4 efflux transporter gene deletion in <i>Burkholderia cenocepacia</i> J2315: a proteomic analysis. <i>Journal of Proteome Science and Computational Biology</i> , 2013, 2, 1.	1.0	3
105	Draft Genome Sequence of the Volatile Organic Compound-Producing Antarctic Bacterium <i>Arthrobacter</i> sp. Strain TB23, Able To Inhibit Cystic Fibrosis Pathogens Belonging to the <i>Burkholderia cepacia</i> Complex. <i>Journal of Bacteriology</i> , 2012, 194, 6334-6335.	1.0	13
106	Draft Genome Sequence of the Hydrocarbon-Degrading and Emulsan-Producing Strain <i>Acinetobacter venetianus</i> RAG-1T. <i>Journal of Bacteriology</i> , 2012, 194, 4771-4772.	1.0	19
107	Large-Scale Analysis of Plasmid Relationships through Gene-Sharing Networks. <i>Molecular Biology and Evolution</i> , 2012, 29, 1225-1240.	3.5	94
108	Seasonal mercury transformation and surficial sediment detoxification by bacteria of Marano and Grado lagoons. <i>Estuarine, Coastal and Shelf Science</i> , 2012, 113, 105-115.	0.9	19

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109	Evaluation of Fluoroquinolone Resistance Mechanisms in <i>Pseudomonas aeruginosa</i> Multidrug Resistance Clinical Isolates. <i>Microbial Drug Resistance</i> , 2012, 18, 23-32.	0.9	31
110	Molecular and phenotypic characterization of <i>Acinetobacter</i> strains able to degrade diesel fuel. <i>Research in Microbiology</i> , 2012, 163, 161-172.	1.0	49
111	The Origin and Evolution of Metabolic Pathways: Why and How did Primordial Cells Construct Metabolic Routes?. <i>Evolution: Education and Outreach</i> , 2012, 5, 367-381.	0.3	17
112	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 <i>Staphylococcus aureus</i> . <i>International Journal of Antimicrobial Agents</i> , 2012, 40, 210-220.	1.1	92
113	Chlor-alkali plant contamination of Aussa River sediments induced a large Hg-resistant bacterial community. <i>Estuarine, Coastal and Shelf Science</i> , 2012, 113, 96-104.	0.9	8
114	Sponge-associated microbial Antarctic communities exhibiting antimicrobial activity against <i>Burkholderia cepacia</i> complex bacteria. <i>Biotechnology Advances</i> , 2012, 30, 272-293.	6.0	112
115	The mosaicism of plasmids revealed by atypical genes detection and analysis. <i>BMC Genomics</i> , 2011, 12, 403.	1.2	16
116	Characterization of the volatile profile of Antarctic bacteria by using solid-phase microextraction-gas chromatography-mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2011, 46, 1051-1059.	0.7	48
117	Organization and Evolution of the <i>cotG</i> and <i>cotH</i> Genes of <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 6664-6673.	1.0	23
118	Deciphering the Role of RND Efflux Transporters in <i>Burkholderia cenocepacia</i> . <i>PLoS ONE</i> , 2011, 6, e18902.	1.1	68
119	The Gene Flow between Plasmids and Chromosomes: Insights from Bioinformatics Analyses. <i>The Open Applied Informatics Journal</i> , 2011, 5, 62-76.	1.0	3
120	Exploring the HME and HAE1 efflux systems in the genus <i>Burkholderia</i> . <i>BMC Evolutionary Biology</i> , 2010, 10, 164.	3.2	32
121	Exploring the evolutionary dynamics of plasmids: the <i>Acinetobacter</i> pan-plasmidome. <i>BMC Evolutionary Biology</i> , 2010, 10, 59.	3.2	87
122	The horizontal flow of the plasmid resistome: clues from intergeneric similarity networks. <i>Environmental Microbiology</i> , 2010, 12, 3228-3242.	1.8	57
123	Identification of species of the <i>Burkholderia cepacia</i> complex by sequence analysis of the <i>hisA</i> gene. <i>Journal of Medical Microbiology</i> , 2010, 59, 1163-1170.	0.7	42
124	Application of multiplex single nucleotide primer extension (mSNUPE) to the identification of bacteria: The <i>Burkholderia cepacia</i> complex case. <i>Journal of Microbiological Methods</i> , 2010, 80, 251-256.	0.7	12
125	Biochemical and microbial features of shallow marine sediments along the Terra Nova Bay (Ross Sea). <i>Journal of Microbiological Methods</i> , 2010, 80, 251-256.	0.9	35
126	Evolution of Metabolic Pathways and Evolution of Genomes. , 2010, , 37-68.		1



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127	The Evolution of Histidine Biosynthesis in Archaea: Insights into the his Genes Structure and Organization in LUCA. <i>Journal of Molecular Evolution</i> , 2009, 69, 512-526.	0.8	19
128	Origin and evolution of metabolic pathways. <i>Physics of Life Reviews</i> , 2009, 6, 23-52.	1.5	101
129	Structural, evolutionary and genetic analysis of the histidine biosynthetic "core" in the genus <i>Burkholderia</i> . <i>Gene</i> , 2009, 448, 16-28.	1.0	7
130	Antagonistic interactions between psychrotrophic cultivable bacteria isolated from Antarctic sponges: a preliminary analysis. <i>Research in Microbiology</i> , 2009, 160, 27-37.	1.0	79
131	Origin and evolution of operons and metabolic pathways. <i>Research in Microbiology</i> , 2009, 160, 502-512.	1.0	63
132	From the primordial soup to the latest universal common ancestor. <i>Research in Microbiology</i> , 2009, 160, 437-440.	1.0	12
133	Diversity of heterotrophic aerobic cultivable microbial communities of soils treated with fumigants and dynamics of metabolic, microbial, and mineralization quotients. <i>Biology and Fertility of Soils</i> , 2008, 44, 557-569.	2.3	24
134	Use of the <i>gyrB</i> gene to discriminate among species of the <i>Burkholderia cepacia</i> complex. <i>FEMS Microbiology Letters</i> , 2008, 281, 175-182.	0.7	20
135	Analysis of plasmid genes by phylogenetic profiling and visualization of homology relationships using Blast2Network. <i>BMC Bioinformatics</i> , 2008, 9, 551.	1.2	57
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