

rrnDB: documenting the number of rRNA and tRNA genes

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Visualization of ribosomal RNA operon copy number distribution. BMC Microbiology, 2009, 9, 208.	3.3	52
2	Microbial communities in iron-silica-rich microbial mats at deep-sea hydrothermal fields of the Southern Mariana Trough. Environmental Microbiology, 2009, 11, 2094-2111.	3.8	124
3	Real-time Polymerase Chain Reaction Quantification of Porphyromonas gingivalis and Tannerella forsythia in Primary Endodontic Infections. Journal of Endodontics, 2009, 35, 1518-1524.	3.1	27
4	Nucleic Acids Research annual Database Issue and the NAR online Molecular Biology Database Collection in 2009. Nucleic Acids Research, 2009, 37, D1-D4.	14.5	101
5	Constraints on the Biological Source(s) of the Orphan Branched Tetraether Membrane Lipids. Geomicrobiology Journal, 2009, 26, 402-414.	2.0	199
6	Identification of Active Microorganisms in Environmental Biofilms Using 16SrRNA Based Approaches: The Challenge of Obtaining Representative Information About the Microbial Community. Proceedings of the Water Environment Federation, 2010, 2010, 61-80.	0.0	0
7	Structure and dynamics of the microbial communities underlying the carboxylate platform for biofuel production. Applied Microbiology and Biotechnology, 2010, 88, 389-399.	3.6	32
8	Quantitative identification of fecal water pollution sources by TaqMan real-time PCR assays using Bacteroidales 16S rRNA genetic markers. Applied Microbiology and Biotechnology, 2010, 88, 1373-1383.	3.6	38
9	Culture-independent molecular techniques for soil microbial ecology. Soil Biology and Biochemistry, 2010, 42, 878-887.	8.8	193
10	Update of the All-Species Living Tree Project based on 16S and 23S rRNA sequence analyses. Systematic and Applied Microbiology, 2010, 33, 291-299.	2.8	441
11	Molecular analysis of bacterial population structure and dynamics during cold storage of untreated and treated milk. International Journal of Food Microbiology, 2010, 138, 108-118.	4.7	105
12	Human pathogens and tetracycline-resistant bacteria in bioaerosols of swine confinement buildings and in nasal flora of hog producers. International Journal of Hygiene and Environmental Health, 2010, 213, 444-449.	4.3	55
13	Diversity of nitrifying bacteria in a full-scale petroleum refinery wastewater treatment plant experiencing unstable nitrification. Journal of Hazardous Materials, 2010, 181, 281-288.	12.4	48
14	Characterization of microbial communities in the aqueous phase of a constructed model wetland treating 1,2-dichloroethene-contaminated groundwater. FEMS Microbiology Ecology, 2010, 72, 74-88.	2.7	30
15	Quantifying microbial communities with 454 pyrosequencing: does read abundance count?. Molecular Ecology, 2010, 19, 5555-5565.	3.9	468
16	Shifts in microbial community structure along an ecological gradient of hypersaline soils and sediments. ISME Journal, 2010, 4, 829-838.	9.8	289
17	A "rare biosphere" microorganism contributes to sulfate reduction in a peatland. ISME Journal, 2010, 4, 1591-1602.	9.8	303
18	Diversity and population structure of sewage-derived microorganisms in wastewater treatment plant influent. Environmental Microbiology, 2010, 12, 378-392.	3.8	342

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19	Identification and Quantification of Genomic Repeats and Sample Contamination in Assemblies of 454 Pyrosequencing Reads. <i>Sequencing</i> , 2010, 2010, 1-12.	0.5	13
20	Novel Real-Time PCR Assay for Simultaneous Detection and Differentiation of <i>Clostridium chauvoei</i> and <i>Clostridium septicum</i> in Clostridial Myonecrosis. <i>Journal of Clinical Microbiology</i> , 2010, 48, 1093-1098.	3.9	13
21	Gut Microbiota in Human Adults with Type 2 Diabetes Differs from Non-Diabetic Adults. <i>PLoS ONE</i> , 2010, 5, e9085.	2.5	2,309
22	Diversity of 16S rRNA Genes within Individual Prokaryotic Genomes. <i>Applied and Environmental Microbiology</i> , 2010, 76, 3886-3897.	3.1	231
23	Transposases are the most abundant, most ubiquitous genes in nature. <i>Nucleic Acids Research</i> , 2010, 38, 4207-4217.	14.5	270
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25	Quantification of <i>Burkholderia coxL</i> Genes in Hawaiian Volcanic Deposits. <i>Applied and Environmental Microbiology</i> , 2010, 76, 2212-2217.	3.1	21
26	The effects of iron fortification on the gut microbiota in African children: a randomized controlled trial in CÔte d'Ivoire. <i>American Journal of Clinical Nutrition</i> , 2010, 92, 1406-1415.	4.7	413
27	The Systemic Imprint of Growth and Its Uses in Ecological (Meta)Genomics. <i>PLoS Genetics</i> , 2010, 6, e1000808.	3.5	286
28	Complete Genomic Structure of the Cultivated Rice Endophyte <i>Azospirillum</i> sp. B510. <i>DNA Research</i> , 2010, 17, 37-50.	3.4	148
29	The Complete Genome of <i>Propionibacterium freudenreichii</i> CIRM-BIA1T, a Hardy Actinobacterium with Food and Probiotic Applications. <i>PLoS ONE</i> , 2010, 5, e11748.	2.5	177
30	Linking Community Profiles, Gene Expression and N-Removal in Anammox Bioreactors Treating Municipal Anaerobic Digestion Reject Water. <i>Environmental Science & Technology</i> , 2010, 44, 6110-6116.	10.0	121
31	Comparison of Innovative Molecular Approaches and Standard Spore Assays for Assessment of Surface Cleanliness. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5438-5444.	3.1	27
32	Complete Debromination of Tetra- and Penta-Brominated Diphenyl Ethers by a Coculture Consisting of <i>Dehalococcoides</i> and <i>Desulfovibrio</i> Species. <i>Environmental Science & Technology</i> , 2011, 45, 8475-8482.	10.0	70
33	Influence of External Resistance on Electrogenesis, Methanogenesis, and Anode Prokaryotic Communities in Microbial Fuel Cells. <i>Applied and Environmental Microbiology</i> , 2011, 77, 564-571.	3.1	215
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36	The Use of rRNA Gene Sequence Data in the Classification and Identification of Prokaryotes. <i>Methods in Microbiology</i> , 2011, , 349-384.	0.8	4
37	Levels of periodontal pathogens in neonatal gastric aspirates and possible maternal sites of origin. <i>Molecular Oral Microbiology</i> , 2011, 26, 277-290.	2.7	22

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38	Sulfur-Oxidizing Chemolithotrophic Proteobacteria Dominate the Microbiota in High Arctic Thermal Springs on Svalbard. <i>Astrobiology</i> , 2011, 11, 665-678.	3.0	36
39	Differential Growth Responses of Soil Bacterial Taxa to Carbon Substrates of Varying Chemical Recalcitrance. <i>Frontiers in Microbiology</i> , 2011, 2, 94.	3.5	504
40	The quantitative significance of <i>Syntrophaceae</i> and syntrophic partnerships in methanogenic degradation of crude oil alkanes. <i>Environmental Microbiology</i> , 2011, 13, 2957-2975.	3.8	217
41	Optimizing the analysis of human intestinal microbiota with phylogenetic microarray. <i>FEMS Microbiology Ecology</i> , 2011, 75, 332-342.	2.7	33
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48	A Closer Look at Bacteroides: Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. <i>Microbial Ecology</i> , 2011, 61, 473-485.	2.8	135
49	Identification of New Single Nucleotide Polymorphism-Based Markers for Inter- and Intraspecies Discrimination of Obligate Bacterial Parasites (<i>Pasteuria</i> spp.) of Invertebrates. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6388-6394.	3.1	10
50	Effects of stocking density on the growth performance and digestive microbiota of broiler chickens. <i>Poultry Science</i> , 2011, 90, 1878-1889.	3.4	103
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58	Intrinsic and acquired resistance mechanisms in enterococcus. <i>Virulence</i> , 2012, 3, 421-569.	4.4	529
59	Fundamentals of Microbial Community Resistance and Resilience. <i>Frontiers in Microbiology</i> , 2012, 3, 417.	3.5	1,131
60	Diversity of 5S rRNA genes within individual prokaryotic genomes. <i>FEMS Microbiology Letters</i> , 2012, 335, 11-18.	1.8	12
61	Molecular quantification of environmental DNA using microfluidics and digital PCR. <i>Systematic and Applied Microbiology</i> , 2012, 35, 390-395.	2.8	112
62	Abundance and Diversity of Microbial Inhabitants in European Spacecraft-Associated Clean Rooms. <i>Astrobiology</i> , 2012, 12, 572-585.	3.0	28
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71	Prokaryotic Abundance and Community Composition in a Freshwater Iron-Rich Microbial Mat at Circumneutral pH. <i>Geomicrobiology Journal</i> , 2012, 29, 896-905.	2.0	33
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80	Using electron balances and molecular techniques to assess trichloroethene-induced shifts to a dechlorinating microbial community. <i>Biotechnology and Bioengineering</i> , 2012, 109, 2230-2239.	3.3	27
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84	Investigation and quantification of key periodontal pathogens in patients with type 2 diabetes. <i>Journal of Periodontal Research</i> , 2012, 47, 470-478.	2.7	52
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91	The microbial diversity of a storm cloud as assessed by hailstones. <i>FEMS Microbiology Ecology</i> , 2012, 81, 684-695.	2.7	59

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109	Enrichment of specific protozoan populations during <i>in situ</i> bioremediation of uranium-contaminated groundwater. <i>ISME Journal</i> , 2013, 7, 1286-1298.	9.8	34
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112	Mobile Elements in a Single-Filament Orange Guaymas Basin Beggiatoa (‘Candidatus Maribeggiatoa’) sp. Draft Genome: Evidence for Genetic Exchange with Cyanobacteria. <i>Applied and Environmental Microbiology</i> , 2013, 79, 3974-3985.	3.1	33
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123	Ecological Drivers of Biogeographic Patterns of Soil Archaeal Community. <i>PLoS ONE</i> , 2013, 8, e63375.	2.5	39
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138	pH gradient and distribution of streptococci, lactobacilli, prevotellae, and fusobacteria in carious dentine. Clinical Oral Investigations, 2014, 18, 659-669.	3.0	16
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142	Stability of the Maternal Gut Microbiota During Late Pregnancy and Early Lactation. Current Microbiology, 2014, 68, 419-427.	2.2	126
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144	Abundance, diversity and seasonal dynamics of predatory bacteria in aquaculture zero discharge systems. FEMS Microbiology Ecology, 2014, 89, 149-161.	2.7	65
145	Hand bacterial communities vary across two different human populations. Microbiology (United Kingdom) 145, 1078-1087. doi:10.1093/aeg/kjv114	1.8	55
146	Draft Genome Sequence of <i>Williamsia</i> sp. Strain D3, Isolated From the Darwin Mountains, Antarctica. Genome Announcements, 2014, 2, .	0.8	9
147	Occurrence and distribution of <i>Vibrio vulnificus</i> and <i>Vibrio parahaemolyticus</i> and their potential roles for fish, oyster, sediment and water. Letters in Applied Microbiology, 2014, 58, 503-510.	2.2	68

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