Anthony V Palumbo

List of Publications by Year
in descending order

106 papers	7,795 citations	71102 41 h-index	53230 85 g-index
109 all docs	109 docs citations	109 times ranked	8144 citing authors

#	Article	IF	Citations
1	A Microbe Associated with Sleep Revealed by a Novel Systems Genetic Analysis of the Microbiome in Collaborative Cross Mice. Genetics, 2020, 214, 719-733.	2.9	20
2	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. Environmental Science & Technology, 2019, 53, 8649-8663.	10.0	99
3	Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. Applied and Environmental Microbiology, 2019, 85, .	3.1	233
4	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. Applied and Environmental Microbiology, 2018, 84, .	3.1	38
5	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. Environmental Science & Technology, 2017, 51, 2879-2889.	10.0	15
6	Development and Validation of Broad-Range Qualitative and Clade-Specific Quantitative Molecular Probes for Assessing Mercury Methylation in the Environment. Applied and Environmental Microbiology, 2016, 82, 6068-6078.	3.1	73
7	The impact of biotechnological advances on the future of <scp>US</scp> bioenergy. Biofuels, Bioproducts and Biorefining, 2015, 9, 454-467.	3.7	11
8	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	2.8	20
9	Changes in northern Gulf of Mexico sediment bacterial and archaeal communities exposed to hypoxia. Geobiology, 2015, 13, 478-493.	2.4	16
10	Global prevalence and distribution of genes and microorganisms involved in mercury methylation. Science Advances, 2015, 1, e1500675.	10.3	355
11	The Genetic Basis for Bacterial Mercury Methylation. Science, 2013, 339, 1332-1335.	12.6	778
12	Draft Genome Sequence for Ralstonia sp. Strain OR214, a Bacterium with Potential for Bioremediation. Genome Announcements, 2013, 1, .	0.8	12
13	Draft Genome Sequence for Caulobacter sp. Strain OR37, a Bacterium Tolerant to Heavy Metals. Genome Announcements, 2013, 1, .	0.8	11
14	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. PLoS ONE, 2013, 8, e83909.	2.5	36
15	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing Pelosinus spp. Applied and Environmental Microbiology, 2012, 78, 2082-2091.	3.1	42
16	Genome Sequences for Six Rhodanobacter Strains, Isolated from Soils and the Terrestrial Subsurface, with Variable Denitrification Capabilities. Journal of Bacteriology, 2012, 194, 4461-4462.	2.2	62
17	Draft Genome Sequences for Two Metal-Reducing Pelosinus fermentans Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7. Journal of Bacteriology, 2012, 194, 5147-5148.	2.2	24
18	Host genetic and environmental effects on mouse intestinal microbiota. ISME Journal, 2012, 6, 2033-2044.	9.8	206

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19	Draft Genome Sequence for Microbacterium laevaniformans Strain OR221, a Bacterium Tolerant to Metals, Nitrate, and Low pH. Journal of Bacteriology, 2012, 194, 3279-3280.	2.2	24
20	Role of Morphological Growth State and Gene Expression in Desulfovibrio africanus Strain Walvis Bay Mercury Methylation. Environmental Science & Technology, 2012, 46, 4926-4932.	10.0	14
21	Sequencing Intractable DNA to Close Microbial Genomes. PLoS ONE, 2012, 7, e41295.	2.5	11
22	Gene Expression Correlates with Process Rates Quantified for Sulfate- and Fe(III)-Reducing Bacteria in U(VI)-Contaminated Sediments. Frontiers in Microbiology, 2012, 3, 280.	3.5	13
23	Characterization of the Deltaproteobacteria in contaminated and uncontaminated stream sediments and identification of potential mercury methylators. Aquatic Microbial Ecology, 2012, 66, 271-282.	1.8	26
24	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. Applied and Environmental Microbiology, 2011, 77, 302-311.	3.1	137
25	Sulfate-Reducing Bacterium Desulfovibrio desulfuricans ND132 as a Model for Understanding Bacterial Mercury Methylation. Applied and Environmental Microbiology, 2011, 77, 3938-3951.	3.1	252
26	Genome Sequence of the Mercury-Methylating and Pleomorphic Desulfovibrio africanus Strain Walvis Bay. Journal of Bacteriology, 2011, 193, 4037-4038.	2.2	14
27	Complete Genome Sequence and Updated Annotation of Desulfovibrio alaskensis G20. Journal of Bacteriology, 2011, 193, 4268-4269.	2.2	56
28	Linking Specific Heterotrophic Bacterial Populations to Bioreduction of Uranium and Nitrate in Contaminated Subsurface Sediments by Using Stable Isotope Probing. Applied and Environmental Microbiology, 2011, 77, 8197-8200.	3.1	19
29	Genome Sequence of the Mercury-Methylating Strain Desulfovibrio desulfuricans ND132. Journal of Bacteriology, 2011, 193, 2078-2079.	2.2	41
30	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. Microbial Ecology, 2010, 60, 784-795.	2.8	51
31	Structural and functional diversity of soil bacterial and fungal communities following woody plant encroachment in the southern Great Plains. Soil Biology and Biochemistry, 2010, 42, 1816-1824.	8.8	72
32	Establishment and metabolic analysis of a model microbial community for understanding trophic and electron accepting interactions of subsurface anaerobic environments. BMC Microbiology, 2010, 10, 149.	3.3	36
33	Isolation and Physiology of Bacteria from Contaminated Subsurface Sediments. Applied and Environmental Microbiology, 2010, 76, 7413-7419.	3.1	76
34	Complete Genome Sequence of the Cellulolytic Thermophile Caldicellulosiruptor obsidiansis OB47 ^T. Journal of Bacteriology, 2010, 192, 6099-6100.	2.2	39
35	Denitrifying Bacteria Isolated from Terrestrial Subsurface Sediments Exposed to Mixed-Waste Contamination. Applied and Environmental Microbiology, 2010, 76, 3244-3254.	3.1	136
36	Microbial Community Changes in Response to Ethanol or Methanol Amendments for U(VI) Reduction. Applied and Environmental Microbiology, 2010, 76, 5728-5735.	3.1	38

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37	Adhesion of Spores of Bacillus thuringiensis on a Planar Surface. Environmental Science & Technology, 2010, 44, 290-296.	10.0	20
38	Donorâ€dependent Extent of Uranium Reduction for Bioremediation of Contaminated Sediment Microcosms. Journal of Environmental Quality, 2009, 38, 53-60.	2.0	26
39	Controlled microfluidic production of alginate beads for in situ encapsulation of microbes. , 2009, , .		5
40	Snapshot of iron response in Shewanella oneidensis by gene network reconstruction. BMC Genomics, 2009, 10, 131.	2.8	56
41	Transcriptomic and metabolomic profiling of Zymomonas mobilis during aerobic and anaerobic fermentations. BMC Genomics, 2009, 10, 34.	2.8	138
42	Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. Environmental Science & Technology, 2009, 43, 3529-3534.	10.0	80
43	Multiphase, Microdispersion Reactor for the Continuous Production of Methane Gas Hydrate. Industrial & Engineering Chemistry Research, 2009, 48, 6448-6452.	3.7	10
44	Scanning Surface Potential Microscopy of Spores on Planar Surfaces. Microscopy and Microanalysis, 2009, 15, 1132-1133.	0.4	1
45	Functional Diversity and Electron Donor Dependence of Microbial Populations Capable of U(VI) Reduction in Radionuclide-Contaminated Subsurface Sediments. Applied and Environmental Microbiology, 2008, 74, 3159-3170.	3.1	97
46	Characterization of the Shewanella oneidensis Fur gene: roles in iron and acid tolerance response. BMC Genomics, 2008, 9, S11.	2.8	55
47	Micron-pore-sized metallic filter tube membranes for filtration of particulates and water purification. Journal of Microbiological Methods, 2008, 74, 10-16.	1.6	17
48	Comparing metal leaching and toxicity from high pH, low pH, and high ammonia fly ash. Fuel, 2007, 86, 1623-1630.	6.4	13
49	Confidence intervals of similarity values determined for cloned SSU rRNA genes from environmental samples. Journal of Microbiological Methods, 2006, 65, 144-152.	1.6	5
50	Laboratory studies identify a colloidal groundwater tracer: implications for bioremediation. FEMS Microbiology Letters, 2006, 148, 131-135.	1.8	7
51	Application of Nonlinear Analysis Methods for Identifying Relationships Between Microbial Community Structure and Groundwater Geochemistry. Microbial Ecology, 2006, 51, 177-188.	2.8	23
52	Elemental Analysis of Environmental and Biological Samples Using Laserâ€Induced Breakdown Spectroscopy and Pulsed Raman Spectroscopy. Journal of Dispersion Science and Technology, 2005, 25, 687-694.	2.4	23
53	Metal reduction at cold temperatures by Shewanella isolates from various marine environments. Aquatic Microbial Ecology, 2005, 38, 81-91.	1.8	34
54	Microbial Diversity and Heterogeneity in Sandy Subsurface Soils. Applied and Environmental Microbiology, 2004, 70, 1723-1734.	3.1	134

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55	Application of Emerging Tools and Techniques for Measuring Carbon and Microbial Communities in Reclaimed Mine Soils. Environmental Management, 2004, 33, S518.	2.7	6
56	Coupling of Functional Gene Diversity and Geochemical Data from Environmental Samples. Applied and Environmental Microbiology, 2004, 70, 6525-6534.	3.1	48
57	Microbial Population and Degradation Activity Changes Monitored During a Chlorinated Solvent Biovent Demonstration. Ground Water Monitoring and Remediation, 2004, 24, 102-110.	0.8	1
58	Bacterial phylogenetic diversity and a novel candidate division of two humid region, sandy surface soils. Soil Biology and Biochemistry, 2003, 35, 915-924.	8.8	64
59	Laser-induced breakdown spectroscopy for the environmental determination of total carbon and nitrogen in soils. Applied Optics, 2003, 42, 2072.	2.1	91
60	Molecular Diversity of Denitrifying Genes in Continental Margin Sediments within the Oxygen-Deficient Zone off the Pacific Coast of Mexico. Applied and Environmental Microbiology, 2003, 69, 3549-3560.	3.1	179
61	Biotransformations and biodegradation in extreme environments. Progress in Industrial Microbiology, 2002, , 549-571.	0.0	0
62	Spatial and Resource Factors Influencing High Microbial Diversity in Soil. Applied and Environmental Microbiology, 2002, 68, 326-334.	3.1	599
63	Metabolomics and microarrays for improved understanding of phenotypic characteristics controlled by both genomics and environmental constraints. Current Opinion in Biotechnology, 2002, 13, 20-24.	6.6	86
64	Introduction of a plasmid-encoded phoA gene for constitutive overproduction of alkaline phosphatase in three subsurface Pseudomonas isolates. FEMS Microbiology Ecology, 2002, 41, 115-123.	2.7	33
65	Simultaneous Recovery of RNA and DNA from Soils and Sediments. Applied and Environmental Microbiology, 2001, 67, 4495-4503.	3.1	341
66	Molecular characterization and diversity of thermophilic iron-reducing enrichment cultures from deep subsurface environments. Journal of Applied Microbiology, 2001, 90, 96-105.	3.1	111
67	Evaluation of PCR-Generated Chimeras, Mutations, and Heteroduplexes with 16S rRNA Gene-Based Cloning. Applied and Environmental Microbiology, 2001, 67, 880-887.	3.1	355
68	An Intermediate-Scale Lysimeter Facility for Subsurface Bioremediation Research. Bioremediation Journal, 2000, 4, 69-79.	2.0	9
69	Iron reduction by psychrotrophic enrichment cultures. FEMS Microbiology Ecology, 1999, 30, 367-371.	2.7	21
70	Phylogenetic Characterization of a Mixed Microbial Community Capable of Degrading Carbon Tetrachloride. Applied Biochemistry and Biotechnology, 1999, 80, 243-254.	2.9	4
71	Biogeochemical Dynamics in Zero-Valent Iron Columns:Â Implications for Permeable Reactive Barriers. Environmental Science & Technology, 1999, 33, 2170-2177.	10.0	250
72	Grain size and depth constraints on microbial variability in coastal plain subsurface sediments. Geomicrobiology Journal, 1998, 15, 171-185.	2.0	35

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73	Effects of nutrient dosing on subsurface methanotrophic populations and trichloroethylene degradation. Journal of Industrial Microbiology and Biotechnology, 1997, 18, 204-212.	3.0	43
74	Spatial and temporal variations of microbial properties at different scales in shallow subsurface sediments. Applied Biochemistry and Biotechnology, 1997, 63-65, 797-808.	2.9	14
75	Spatial and Temporal Variations of Microbial Properties at Different Scales in Shallow Subsurface Sediments. , 1997, , 797-808.		0
76	Influence of media on measurement of bacterial populations in the subsurface. Applied Biochemistry and Biotechnology, 1996, 57-58, 905-914.	2.9	22
77	Methanotrophic TCE Biodegradation in a Multi-Stage Bioreactor. Environmental Science & Technology, 1995, 29, 2073-2082.	10.0	26
78	Acid-base chemistry of high-elevation streams in the great smoky mountains. Water, Air, and Soil Pollution, 1994, 72, 331-356.	2.4	25
79	Alternative method for rapidly screening microbial isolates for their potential to degrade volatile contaminants. Journal of Industrial Microbiology, 1994, 13, 361-366.	0.9	10
80	Bioluminescent reporter bacteria detect contaminants in soil samples. Applied Biochemistry and Biotechnology, 1994, 45-46, 731-740.	2.9	40
81	The effect of media composition on EDTA degradation byAgrobacterium sp.. Applied Biochemistry and Biotechnology, 1994, 45-46, 811-822.	2.9	24
82	Potential for microbial growth in arid subsurface sediments. Applied Biochemistry and Biotechnology, 1994, 45-46, 823-834.	2.9	15
83	Mobility of natural organic matter in a study aquifer. Environmental Science & Technology, 1993, 27, 667-676.	10.0	123
84	Bacterial sensitivity to UV light as a model for ionizing radiation resistance. Journal of Microbiological Methods, 1993, 18, 127-136.	1.6	22
85	Lotic Ecosystem Response to a Chlorine Disturbance. , 1992, 2, 341-355.		20
86	Relationships between stream acidity and bacteria, macroinvertebrates, and fish: a comparison of north temperate and south temperate mountain streams, USA. Hydrobiologia, 1992, 239, 7-24.	2.0	34
87	Colloid transport through fractured and unfractured laboratory sand columns. Journal of Contaminant Hydrology, 1992, 9, 289-303.	3.3	83
88	Role of Nutrient Cycling and Herbivory in Regulating Periphyton Communities in Laboratory Streams. Ecology, 1991, 72, 966-982.	3.2	180
89	Methanol Suppression of Trichloroethylene Degradation byMethylosinus trichosporium (OB3b) and Methane-Oxidizing Mixed Cultures. Applied Biochemistry and Biotechnology, 1991, 28-29, 887-899.	2.9	5
90	Resilience of Lotic Ecosystems to a Light-Elimination Disturbance. Ecology, 1991, 72, 1299-1313.	3.2	52

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91	Influence of Nutrients and Grazing on the Response of Stream Periphyton Communities to a Scour Disturbance. Journal of the North American Benthological Society, 1991, 10, 127-142.	3.1	52
92	Resistance of Lotic Ecosystems to a Light Elimination Disturbance: A Laboratory Stream Study. Oikos, 1990, 58, 80.	2.7	36
93	Biogeochemical cycling constraints on stream ecosystem recovery. Environmental Management, 1990, 14, 685-697.	2.7	20
94	Biodegradation of NTA and mâ€cresol in coastal environments. Environmental Toxicology and Chemistry, 1988, 7, 573-585.	4.3	10
95	Trichloroethylene Biodegradation by a Methane-Oxidizing Bacterium. Applied and Environmental Microbiology, 1988, 54, 951-956.	3.1	356
96	BIODEGRADATION OF NTA AND m-CRESOL IN COASTAL ENVIRONMENTS. Environmental Toxicology and Chemistry, 1988, 7, 573.	4.3	1
97	Extraction with DMSO to simultaneously measure periphyton photosynthesis, chlorophyll, and ATP1,2. Limnology and Oceanography, 1987, 32, 464-471.	3.1	59
98	Microbial Communities on Leaf Material Protected from Macroinvertebrate Grazing in Acidic and Circumneutral Streams. Canadian Journal of Fisheries and Aquatic Sciences, 1987, 44, 1064-1070.	1.4	33
99	Effects of Acidification on Leaf Decomposition in Streams. Journal of the North American Benthological Society, 1987, 6, 147-158.	3.1	76
100	Bacterial Communities in Acidic and Circumneutral Streams. Applied and Environmental Microbiology, 1987, 53, 337-344.	3.1	29
101	Effect of Stream Acidification on Periphyton Composition, Chlorophyll, and Productivity. Canadian Journal of Fisheries and Aquatic Sciences, 1986, 43, 1846-1858.	1.4	82
102	Biological consequences of hydrographic and atmospheric advection within the Gulf Loop Intrusion. Deep-sea Research Part A, Oceanographic Research Papers, 1984, 31, 1101-1120.	1.5	21
103	Size of Suspended Bacterial Cells and Association of Heterotrophic Activity with Size Fractions of Particles in Estuarine and Coastal Waters. Applied and Environmental Microbiology, 1984, 48, 157-164.	3.1	90
104	Efficient utilization of dissolved free amino acids by suspended marine bacteria. Journal of Experimental Marine Biology and Ecology, 1983, 69, 257-266.	1.5	21
105	Distribution of suspended bacteria in neritic waters south of Long Island during stratified conditions1. Limnology and Oceanography, 1979, 24, 697-705.	3.1	38
106	Distribution of suspended bacteria in the Newport River estuary, North Carolina. Estuarine and Coastal Marine Science, 1978, 7, 521-529.	0.9	45