## Anthony V Palumbo

List of Publications by Year in descending order

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106 papers 7,795 citations

71102 41 h-index 85 g-index

109 all docs

109 docs citations

109 times ranked 8144 citing authors

#	Article	IF	CITATIONS
1	The Genetic Basis for Bacterial Mercury Methylation. Science, 2013, 339, 1332-1335.	12.6	778
2	Spatial and Resource Factors Influencing High Microbial Diversity in Soil. Applied and Environmental Microbiology, 2002, 68, 326-334.	3.1	599
3	Trichloroethylene Biodegradation by a Methane-Oxidizing Bacterium. Applied and Environmental Microbiology, 1988, 54, 951-956.	3.1	356
4	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
5	Global prevalence and distribution of genes and microorganisms involved in mercury methylation. Science Advances, 2015, 1, e1500675.	10.3	355
6	Simultaneous Recovery of RNA and DNA from Soils and Sediments. Applied and Environmental Microbiology, 2001, 67, 4495-4503.	3.1	341
7	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
8	Biogeochemical Dynamics in Zero-Valent Iron Columns:Â Implications for Permeable Reactive Barriers. Environmental Science & En	10.0	250
9	Soil Aggregate Microbial Communities: Towards Understanding Microbiome Interactions at Biologically Relevant Scales. Applied and Environmental Microbiology, 2019, 85, .	3.1	233
10	Host genetic and environmental effects on mouse intestinal microbiota. ISME Journal, 2012, 6, 2033-2044.	9.8	206
11	Role of Nutrient Cycling and Herbivory in Regulating Periphyton Communities in Laboratory Streams. Ecology, 1991, 72, 966-982.	3.2	180
12	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
13	Transcriptomic and metabolomic profiling of Zymomonas mobilis during aerobic and anaerobic fermentations. BMC Genomics, 2009, 10, 34.	2.8	138
14	Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Tennessee Streams. Applied and Environmental Microbiology, 2011, 77, 302-311.	3.1	137
15	Denitrifying Bacteria Isolated from Terrestrial Subsurface Sediments Exposed to Mixed-Waste Contamination. Applied and Environmental Microbiology, 2010, 76, 3244-3254.	3.1	136
16	Microbial Diversity and Heterogeneity in Sandy Subsurface Soils. Applied and Environmental Microbiology, 2004, 70, 1723-1734.	3.1	134
17	Mobility of natural organic matter in a study aquifer. Environmental Science &	10.0	123
18	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

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19	Determining the Reliability of Measuring Mercury Cycling Gene Abundance with Correlations with Mercury and Methylmercury Concentrations. Environmental Science & Eamp; Technology, 2019, 53, 8649-8663.	10.0	99
20	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
21	Laser-induced breakdown spectroscopy for the environmental determination of total carbon and nitrogen in soils. Applied Optics, 2003, 42, 2072.	2.1	91
22	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
23	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
24	Colloid transport through fractured and unfractured laboratory sand columns. Journal of Contaminant Hydrology, 1992, 9, 289-303.	3.3	83
25	Effect of Stream Acidification on Periphyton Composition, Chlorophyll, and Productivity. Canadian Journal of Fisheries and Aquatic Sciences, 1986, 43, 1846-1858.	1.4	82
26	Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. Environmental Science & Environmental Science & 2009, 43, 3529-3534.	10.0	80
27	Effects of Acidification on Leaf Decomposition in Streams. Journal of the North American Benthological Society, 1987, 6, 147-158.	3.1	76
28	Isolation and Physiology of Bacteria from Contaminated Subsurface Sediments. Applied and Environmental Microbiology, 2010, 76, 7413-7419.	3.1	76
29	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
30	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
31	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
32	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
33	Extraction with DMSO to simultaneously measure periphyton photosynthesis, chlorophyll, and ATP1,2. Limnology and Oceanography, 1987, 32, 464-471.	3.1	59
34	Snapshot of iron response in Shewanella oneidensis by gene network reconstruction. BMC Genomics, 2009, 10, 131.	2.8	56
35	Complete Genome Sequence and Updated Annotation of Desulfovibrio alaskensis G20. Journal of Bacteriology, 2011, 193, 4268-4269.	2.2	56
36	Characterization of the Shewanella oneidensis Fur gene: roles in iron and acid tolerance response. BMC Genomics, 2008, 9, S11.	2.8	55

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37	Resilience of Lotic Ecosystems to a Light-Elimination Disturbance. Ecology, 1991, 72, 1299-1313.	3.2	52
38	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
39	Characterization of Archaeal Community in Contaminated and Uncontaminated Surface Stream Sediments. Microbial Ecology, 2010, 60, 784-795.	2.8	51
40	Coupling of Functional Gene Diversity and Geochemical Data from Environmental Samples. Applied and Environmental Microbiology, 2004, 70, 6525-6534.	3.1	48
41	Distribution of suspended bacteria in the Newport River estuary, North Carolina. Estuarine and Coastal Marine Science, 1978, 7, 521-529.	0.9	45
42	Effects of nutrient dosing on subsurface methanotrophic populations and trichloroethylene degradation. Journal of Industrial Microbiology and Biotechnology, 1997, 18, 204-212.	3.0	43
43	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
44	Genome Sequence of the Mercury-Methylating Strain Desulfovibrio desulfuricans ND132. Journal of Bacteriology, 2011, 193, 2078-2079.	2.2	41
45	Bioluminescent reporter bacteria detect contaminants in soil samples. Applied Biochemistry and Biotechnology, 1994, 45-46, 731-740.	2.9	40
46	Complete Genome Sequence of the Cellulolytic Thermophile <i>Caldicellulosiruptor obsidiansis</i> OB47 <sup>T</sup> . Journal of Bacteriology, 2010, 192, 6099-6100.	2.2	39
47	Distribution of suspended bacteria in neritic waters south of Long Island during stratified conditions1. Limnology and Oceanography, 1979, 24, 697-705.	3.1	38
48	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
49	Carbon Amendments Alter Microbial Community Structure and Net Mercury Methylation Potential in Sediments. Applied and Environmental Microbiology, 2018, 84, .	3.1	38
50	Resistance of Lotic Ecosystems to a Light Elimination Disturbance: A Laboratory Stream Study. Oikos, 1990, 58, 80.	2.7	36
51	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
52	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. PLoS ONE, 2013, 8, e83909.	2.5	36
53	Grain size and depth constraints on microbial variability in coastal plain subsurface sediments. Geomicrobiology Journal, 1998, 15, 171-185.	2.0	35
54	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

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55	Metal reduction at cold temperatures by Shewanella isolates from various marine environments. Aquatic Microbial Ecology, 2005, 38, 81-91.	1.8	34
56	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
57	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
58	Bacterial Communities in Acidic and Circumneutral Streams. Applied and Environmental Microbiology, 1987, 53, 337-344.	3.1	29
59	Methanotrophic TCE Biodegradation in a Multi-Stage Bioreactor. Environmental Science & Emp; Technology, 1995, 29, 2073-2082.	10.0	26
60	Donorâ€dependent Extent of Uranium Reduction for Bioremediation of Contaminated Sediment Microcosms. Journal of Environmental Quality, 2009, 38, 53-60.	2.0	26
61	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
62	Acid-base chemistry of high-elevation streams in the great smoky mountains. Water, Air, and Soil Pollution, 1994, 72, 331-356.	2.4	25
63	The effect of media composition on EDTA degradation by Agrobacterium sp Applied Biochemistry and Biotechnology, 1994, 45-46, 811-822.	2.9	24
64	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
65	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
66	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
67	Application of Nonlinear Analysis Methods for Identifying Relationships Between Microbial Community Structure and Groundwater Geochemistry. Microbial Ecology, 2006, 51, 177-188.	2.8	23
68	Bacterial sensitivity to UV light as a model for ionizing radiation resistance. Journal of Microbiological Methods, 1993, 18, 127-136.	1.6	22
69	Influence of media on measurement of bacterial populations in the subsurface. Applied Biochemistry and Biotechnology, 1996, 57-58, 905-914.	2.9	22
70	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
71	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
72	Iron reduction by psychrotrophic enrichment cultures. FEMS Microbiology Ecology, 1999, 30, 367-371.	2.7	21

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73	Biogeochemical cycling constraints on stream ecosystem recovery. Environmental Management, 1990, 14, 685-697.	2.7	20
74	Lotic Ecosystem Response to a Chlorine Disturbance. , 1992, 2, 341-355.		20
75	Adhesion of Spores of Bacillus thuringiensis on a Planar Surface. Environmental Science & Emp; Technology, 2010, 44, 290-296.	10.0	20
76	Community Analysis of Plant Biomass-Degrading Microorganisms from Obsidian Pool, Yellowstone National Park. Microbial Ecology, 2015, 69, 333-345.	2.8	20
77	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
78	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
79	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
80	Changes in northern Gulf of Mexico sediment bacterial and archaeal communities exposed to hypoxia. Geobiology, 2015, 13, 478-493.	2.4	16
81	Potential for microbial growth in arid subsurface sediments. Applied Biochemistry and Biotechnology, 1994, 45-46, 823-834.	2.9	15
82	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. Environmental Science & Eamp; Technology, 2017, 51, 2879-2889.	10.0	15
83	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
84	Genome Sequence of the Mercury-Methylating and Pleomorphic Desulfovibrio africanus Strain Walvis Bay. Journal of Bacteriology, 2011, 193, 4037-4038.	2.2	14
85	Role of Morphological Growth State and Gene Expression in <i>Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain Walvis Bay Mercury Methylation. Environmental Science & Expression in <i> Desulfovibrio africanus</i> Strain & Expression in	10.0	14
86	Comparing metal leaching and toxicity from high pH, low pH, and high ammonia fly ash. Fuel, 2007, 86, 1623-1630.	6.4	13
87	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
88	Draft Genome Sequence for $\langle i \rangle$ Ralstonia $\langle  i \rangle$ sp. Strain OR214, a Bacterium with Potential for Bioremediation. Genome Announcements, 2013, 1, .	0.8	12
89	Sequencing Intractable DNA to Close Microbial Genomes. PLoS ONE, 2012, 7, e41295.	2.5	11
90	Draft Genome Sequence for <i>Caulobacter</i> sp. Strain OR37, a Bacterium Tolerant to Heavy Metals. Genome Announcements, 2013, 1, .	0.8	11

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91	The impact of biotechnological advances on the future of <scp>US</scp> bioenergy. Biofuels, Bioproducts and Biorefining, 2015, 9, 454-467.	3.7	11
92	Biodegradation of NTA and <i>m</i>  i>â€eresol in coastal environments. Environmental Toxicology and Chemistry, 1988, 7, 573-585.	4.3	10
93	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
94	Multiphase, Microdispersion Reactor for the Continuous Production of Methane Gas Hydrate. Industrial & Samp; Engineering Chemistry Research, 2009, 48, 6448-6452.	3.7	10
95	An Intermediate-Scale Lysimeter Facility for Subsurface Bioremediation Research. Bioremediation Journal, 2000, 4, 69-79.	2.0	9
96	Laboratory studies identify a colloidal groundwater tracer: implications for bioremediation. FEMS Microbiology Letters, 2006, 148, 131-135.	1.8	7
97	Application of Emerging Tools and Techniques for Measuring Carbon and Microbial Communities in Reclaimed Mine Soils. Environmental Management, 2004, 33, S518.	2.7	6
98	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
99	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
100	Controlled microfluidic production of alginate beads for in situ encapsulation of microbes., 2009,,.		5
101	Phylogenetic Characterization of a Mixed Microbial Community Capable of Degrading Carbon Tetrachloride. Applied Biochemistry and Biotechnology, 1999, 80, 243-254.	2.9	4
102	Scanning Surface Potential Microscopy of Spores on Planar Surfaces. Microscopy and Microanalysis, 2009, 15, 1132-1133.	0.4	1
103	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
104	BIODEGRADATION OF NTA AND m-CRESOL IN COASTAL ENVIRONMENTS. Environmental Toxicology and Chemistry, 1988, 7, 573.	4.3	1
105	Biotransformations and biodegradation in extreme environments. Progress in Industrial Microbiology, 2002, , 549-571.	0.0	0
106	Spatial and Temporal Variations of Microbial Properties at Different Scales in Shallow Subsurface Sediments., 1997,, 797-808.		0