

Peter N Golyshin

List of Publications by Year in descending order

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193
papers

13,069
citations

23567

58
h-index

27406

106
g-index

206
all docs

206
docs citations

206
times ranked

14222
citing authors

#	ARTICLE	IF	CITATIONS
1	Calm and Frenzy: marine obligate hydrocarbonoclastic bacteria sustain ocean wellness. <i>Current Opinion in Biotechnology</i> , 2022, 73, 337-345.	6.6	24
2	Identification of an Amylomaltase from the Halophilic Archaeon <i>Haloquadratum walsbyi</i> by Functional Metagenomics: Structural and Functional Insights. <i>Life</i> , 2022, 12, 85.	2.4	2
3	Anaerobic carboxydrotrophy in sulfur-respiring haloarchaea from hypersaline lakes. <i>ISME Journal</i> , 2022, 16, 1534-1546.	9.8	5
4	Field response of N ₂ O emissions, microbial communities, soil biochemical processes and winter barley growth to the addition of conventional and biodegradable microplastics. <i>Agriculture, Ecosystems and Environment</i> , 2022, 336, 108023.	5.3	26
5	A mechanistic understanding of polyethylene biodegradation by the marine bacterium <i>Alcanivorax</i> . <i>Journal of Hazardous Materials</i> , 2022, 436, 129278.	12.4	34
6	Structure and evolutionary trace-assisted screening of a residue swapping the substrate ambiguity and chiral specificity in an esterase. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2307-2317.	4.1	6
7	Land cover and nutrient enrichment regulates low-molecular weight dissolved organic matter turnover in freshwater ecosystems. <i>Limnology and Oceanography</i> , 2021, 66, 2979-2987.	3.1	10
8	Utilization of low-molecular-weight organic compounds by the filterable fraction of a lotic microbiome. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	0
9	Genetically engineered proteins with two active sites for enhanced biocatalysis and synergistic chemo- and biocatalysis. <i>Nature Catalysis</i> , 2020, 3, 319-328.	34.4	90
10	High Representation of Archaea Across All Depths in Oxic and Low-pH Sediment Layers Underlying an Acidic Stream. <i>Frontiers in Microbiology</i> , 2020, 11, 576520.	3.5	11
11	Symbiosis between nanohaloarchaeon and haloarchaeon is based on utilization of different polysaccharides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 20223-20234.	7.1	49
12	Degradation of Hydrocarbons and Heavy Metal Reduction by Marine Bacteria in Highly Contaminated Sediments. <i>Microorganisms</i> , 2020, 8, 1402.	3.6	34
13	Dissimilatory sulfate reduction in the archaeon <i>Candidatus Vulcanisaeta moutnovskia</i> TM sheds light on the evolution of sulfur metabolism. <i>Nature Microbiology</i> , 2020, 5, 1428-1438.	13.3	27
14	Rapid depletion of dissolved organic sulphur (DOS) in freshwaters. <i>Biogeochemistry</i> , 2020, 149, 105-113.	3.5	10
15	Protein expression in the obligate hydrocarbon-degrading psychrophile <i>Oleispira antarctica</i> during alkane degradation and cold tolerance. <i>Environmental Microbiology</i> , 2020, 22, 1870-1883.	3.8	27
16	Hydrocarbon-Degrading Bacteria <i>Alcanivorax</i> and <i>Marinobacter</i> Associated With Microalgae <i>Pavlova lutheri</i> and <i>Nannochloropsis oculata</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 572931.	3.5	35
17	Proteome Cold-Shock Response in the Extremely Acidophilic Archaeon, <i>Cuniculiplasma divulgatum</i> . <i>Microorganisms</i> , 2020, 8, 759.	3.6	3
18	Microbial uptake kinetics of dissolved organic carbon (DOC) compound groups from river water and sediments. <i>Scientific Reports</i> , 2019, 9, 11229.	3.3	31

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19	Nutrient enrichment induces a shift in dissolved organic carbon (DOC) metabolism in oligotrophic freshwater sediments. <i>Science of the Total Environment</i> , 2019, 690, 1131-1139.	8.0	22
20	Microbial Communities of Polymetallic Depositsâ€™ Acidic Ecosystems of Continental Climatic Zone With High Temperature Contrasts. <i>Frontiers in Microbiology</i> , 2019, 10, 1573.	3.5	34
21	Archaea dominate the microbial community in an ecosystem with low-to-moderate temperature and extreme acidity. <i>Microbiome</i> , 2019, 7, 11.	11.1	58
22	Cuniculiplasmataceae, their ecogenomic and metabolic patterns, and interactions with â€™ARMANâ€™. <i>Extremophiles</i> , 2019, 23, 1-7.	2.3	15
23	Diversity of â€™Ca. Micrarchaeotaâ€™ in Two Distinct Types of Acidic Environments and Their Associations with Thermoplasmatales. <i>Genes</i> , 2019, 10, 461.	2.4	27
24	Reply to â€™Evolutionary placement of Methanonatronarchaeiaâ€™. <i>Nature Microbiology</i> , 2019, 4, 560-561.	13.3	7
25	Decoding the ocean's microbiological secrets for marine enzyme biodiscovery. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	26
26	Bioprospecting Reveals Class III Î‰-Transaminases Converting Bulky Ketones and Environmentally Relevant Polyamines. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	17
27	Marine, Aerobic Hydrocarbon-Degrading Gammaproteobacteria: The Family Alcanivoraceae. , 2019, , 1-13.		7
28	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 153-166.		1
29	Marine, Aerobic Hydrocarbon-Degrading Gammaproteobacteria: The Family Alcanivoraceae. , 2019, , 167-179.		10
30	Hydrocarbon-Degrading Microbes as Sources of New Biocatalysts. , 2019, , 353-373.		3
31	Aerobic Hydrocarbon-Degrading Gammaproteobacteria: Oleiphilaceae and Relatives. , 2019, , 1-14.		0
32	Draft Genome Sequence of <i>Monaibacterium marinum</i> C7 ^T , Isolated from Seawater from the Menai Straits, Wales, United Kingdom. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
33	Rational Engineering of Multiple Active Sites in an Ester Hydrolase. <i>Biochemistry</i> , 2018, 57, 2245-2255.	2.5	57
34	Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak Decline. <i>ISME Journal</i> , 2018, 12, 386-399.	9.8	75
35	Determinants and Prediction of Esterase Substrate Promiscuity Patterns. <i>ACS Chemical Biology</i> , 2018, 13, 225-234.	3.4	106
36	Proteogenomic Analysis of Epibacterium Mobile BBCC367, a Relevant Marine Bacterium Isolated From the South Pacific Ocean. <i>Frontiers in Microbiology</i> , 2018, 9, 3125.	3.5	4

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37	Differential Protein Expression During Growth on Medium Versus Long-Chain Alkanes in the Obligate Marine Hydrocarbon-Degrading Bacterium <i>Thalassolituus oleivorans</i> MIL-1. <i>Frontiers in Microbiology</i> , 2018, 9, 3130.	3.5	36
38	Members of the Uncultured Taxon OP1 (‘‘Acetothermia’’) Predominate in the Microbial Community of an Alkaline Hot Spring at East-Tuvianian Upland. <i>Microbiology</i> , 2018, 87, 783-795.	1.2	6
39	Sulfur Respiration in a Group of Facultatively Anaerobic Natronoarchaea Ubiquitous in Hypersaline Soda Lakes. <i>Frontiers in Microbiology</i> , 2018, 9, 2359.	3.5	30
40	Screening and Characterization of Novel Polyesterases from Environmental Metagenomes with High Hydrolytic Activity against Synthetic Polyesters. <i>Environmental Science & Technology</i> , 2018, 52, 12388-12401.	10.0	56
41	Hydrocarbon-Degrading Microbes as Sources of New Biocatalysts. , 2018, , 1-21.		1
42	A metagenomic collection of novel and highly efficient biocatalysts for industrial biotechnology. <i>Impact</i> , 2018, 2018, 82-84.	0.1	5
43	Relationships between Substrate Promiscuity and Chiral Selectivity of Esterases from Phylogenetically and Environmentally Diverse Microorganisms. <i>Catalysts</i> , 2018, 8, 10.	3.5	11
44	Nano-Sized and Filterable Bacteria and Archaea: Biodiversity and Function. <i>Frontiers in Microbiology</i> , 2018, 9, 1971.	3.5	51
45	Discovery of anaerobic lithoheterotrophic haloarchaea, ubiquitous in hypersaline habitats. <i>ISME Journal</i> , 2017, 11, 1245-1260.	9.8	79
46	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. <i>Scientific Reports</i> , 2017, 7, 44103.	3.3	67
47	Microbial use of low molecular weight DOM in filtered and unfiltered freshwater: Role of ultra-small microorganisms and implications for water quality monitoring. <i>Science of the Total Environment</i> , 2017, 598, 377-384.	8.0	27
48	Shotgun Metagenomic Sequencing Analysis of Soft-Rot Enterobacteriaceae in Polymicrobial Communities. <i>Methods in Molecular Biology</i> , 2017, 1539, 85-97.	0.9	2
49	Discovery of extremely halophilic, methyl-reducing euryarchaea provides insights into the evolutionary origin of methanogenesis. <i>Nature Microbiology</i> , 2017, 2, 17081.	13.3	213
50	Ferrous iron- and ammonium-rich diffuse vents support habitat-specific communities in a shallow hydrothermal field off the Basiluzzo Islet (Aeolian Volcanic Archipelago). <i>Geobiology</i> , 2017, 15, 664-677.	2.4	17
51	A communal catalogue reveals Earth’s multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
52	Subtle shifts in microbial communities occur alongside the release of carbon induced by drought and rewetting in contrasting peatland ecosystems. <i>Scientific Reports</i> , 2017, 7, 11314.	3.3	20
53	Metabolic and evolutionary patterns in the extremely acidophilic archaeon <i>Ferroplasma acidiphilum</i> YT. <i>Scientific Reports</i> , 2017, 7, 3682.	3.3	21
54	The genome analysis of <i>Oleiphilus messinensis</i> ME102 (DSM 13489 T) reveals backgrounds of its obligate alkane-devouring marine lifestyle. <i>Marine Genomics</i> , 2017, 36, 41-47.	1.1	18

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55	The rumen microbiome: an underexplored resource for novel antimicrobial discovery. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 33.	6.4	51
56	â€˜ARMANâ€™™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	12.8	116
57	Functionalization and Modification of Hydrocarbon-Like Molecules Guided by Metagenomics: Enzymes Most Requested at the Industrial Scale for Chemical Synthesis as Study Cases. , 2017, , 309-329.		0
58	Buwchitin: A Ruminant Peptide with Antimicrobial Potential against <i>Enterococcus faecalis</i> . <i>Frontiers in Chemistry</i> , 2017, 5, 51.	3.6	19
59	Metagenomic Mining of Enzyme Diversity. , 2017, , 245-269.		2
60	Distribution of Hydrocarbon Degradation Pathways in the Sea. , 2017, , 629-651.		0
61	<i>Monaibacterium marinum</i> , gen. nov, sp. nov, a new member of the Alphaproteobacteria isolated from seawater of Menai Straits, Wales, UK. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2017, 67, 3310-3317.	1.7	18
62	The novel extremely acidophilic, cell-wall-deficient archaeon <i>Cuniculiplasma divulgatum</i> gen. nov., sp. nov. represents a new family, Cuniculiplasmataceae fam. nov., of the order Thermoplasmatales. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 332-340.	1.7	96
63	Combined Whole-Cell High-Throughput Functional Screening for Identification of New Nicotinamidases/Pyrazinamidases in Metagenomic/Polygenomic Libraries. <i>Frontiers in Microbiology</i> , 2016, 7, 1915.	3.5	5
64	Analysis of defence systems and a conjugative IncPâ€˜1 plasmid in the marine polyaromatic hydrocarbonsâ€˜degrading bacterium <i>Cycloclasticus</i> sp. 78â€˜ME. <i>Environmental Microbiology Reports</i> , 2016, 8, 508-519.	2.4	5
65	Biology of archaea from a novel family Cuniculiplasmataceae (Thermoplasmata) ubiquitous in hyperacidic environments. <i>Scientific Reports</i> , 2016, 6, 39034.	3.3	31
66	Estimating the success of enzyme bioprospecting through metagenomics: current status and future trends. <i>Microbial Biotechnology</i> , 2016, 9, 22-34.	4.2	175
67	Biochemical and Structural Insights into Enzymatic Depolymerization of Polylactic Acid and Other Polyesters by Microbial Carboxylesterases. <i>Biomacromolecules</i> , 2016, 17, 2027-2039.	5.4	114
68	Structural and Functional Characterization of a Ruminant Î²-Glycosidase Defines a Novel Subfamily of Glycoside Hydrolase Family 3 with Permuted Domain Topology. <i>Journal of Biological Chemistry</i> , 2016, 291, 24200-24214.	3.4	21
69	Insights into the degradation capacities of <i>Amycolatopsis tucumanensis</i> DSM 45259 guided by microarray data. <i>World Journal of Microbiology and Biotechnology</i> , 2016, 32, 201.	3.6	8
70	Genome sequence of obligate marine polycyclic aromatic hydrocarbons-degrading bacterium <i>Cycloclasticus</i> sp. 78-ME, isolated from petroleum deposits of the sunken tanker Amoco Milford Haven , Mediterranean Sea. <i>Marine Genomics</i> , 2016, 25, 11-13.	1.1	37
71	Elemental sulfur and acetate can support life of a novel strictly anaerobic haloarchaeon. <i>ISME Journal</i> , 2016, 10, 240-252.	9.8	62
72	Functionalization and Modification of Hydrocarbon-Like Molecules Guided by Metagenomics: Enzymes Most Requested at the Industrial Scale for Chemical Synthesis as Study Cases. , 2016, , 1-21.		1

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73	Diversity and Physiologies of Acidophilic Archaea. , 2016, , 93-106.		8
74	Metagenomic Mining of Enzyme Diversity. , 2016, , 1-25.		1
75	Distribution of Hydrocarbon Degradation Pathways in the Sea. , 2016, , 1-23.		0
76	Biodiversity for biocatalysis: A review of the α -hydrolase fold superfamily of esterases-lipases discovered in metagenomes. Biocatalysis and Biotransformation, 2015, 33, 235-249.	2.0	48
77	Metaproteomics and metabolomics analyses of chronically petroleum-polluted sites reveal the importance of general anaerobic processes uncoupled with degradation. Proteomics, 2015, 15, 3508-3520.	2.2	58
78	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. Frontiers in Bioengineering and Biotechnology, 2015, 3, 95.	4.1	26
79	Degradation Network Reconstruction in Uric Acid and Ammonium Amendments in Oil-Degrading Marine Microcosms Guided by Metagenomic Data. Frontiers in Microbiology, 2015, 6, 1270.	3.5	18
80	Metagenomics as a Tool for Enzyme Discovery: Hydrolytic Enzymes from Marine-Related Metagenomes. Advances in Experimental Medicine and Biology, 2015, 883, 1-20.	1.6	35
81	Microbial community of the deep-sea brine lake <i>Kryos</i> seawater-brine interface is active below the chaotropy limit of life as revealed by recovery of mRNA. Environmental Microbiology, 2015, 17, 364-382.	3.8	109
82	Identification and Characterization of Carboxyl Esterases of Gill Chamber-Associated Microbiota in the Deep-Sea Shrimp <i>Rimicaris exoculata</i> by Using Functional Metagenomics. Applied and Environmental Microbiology, 2015, 81, 2125-2136.	3.1	35
83	Pressure adaptation is linked to thermal adaptation in salt-saturated marine habitats. Environmental Microbiology, 2015, 17, 332-345.	3.8	40
84	Isolation and characterization of novel lipases/esterases from a bovine rumen metagenome. Applied Microbiology and Biotechnology, 2015, 99, 5475-5485.	3.6	59
85	Bacterial population and biodegradation potential in chronically crude oil-contaminated marine sediments are strongly linked to temperature. Scientific Reports, 2015, 5, 11651.	3.3	91
86	Conversion of Uric Acid into Ammonium in Oil-Degrading Marine Microbial Communities: a Possible Role of Halomonads. Microbial Ecology, 2015, 70, 724-740.	2.8	14
87	The ocean sampling day consortium. GigaScience, 2015, 4, 27.	6.4	185
88	Functional Screening of Metagenomic Libraries: Enzymes Acting on Greasy Molecules as Study Case. Springer Protocols, 2015, , 13-36.	0.3	1
89	Genomic Analysis of Pure Cultures and Communities. Springer Protocols, 2015, , 5-27.	0.3	16
90	Diversity of hydrolases from hydrothermal vent sediments of the Levante Bay, Vulcano Island (Aeolian) Tj ETQq0 0 0 rgBT /Overlock 10 T esterases and an arabinopyranosidase. Applied Microbiology and Biotechnology, 2015, 99, 10031-10046.	3.6	36

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91	The intergenic transcribed spacer region 1 as a molecular marker for identification and discrimination of <i>Enterobacteriaceae</i> associated with acute oak decline. <i>Journal of Applied Microbiology</i> , 2015, 118, 193-201.	3.1	2
92	The environment shapes microbial enzymes: five cold-active and salt-resistant carboxylesterases from marine metagenomes. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2165-2178.	3.6	83
93	Metagenomics of Deep Hypersaline Anoxic Basins. , 2015, , 341-348.		0
94	Terrestrial Invertebrate Animal Metagenomics, Lumbricidae. , 2015, , 622-631.		0
95	Enzymes from Extreme Environments. , 2014, , 43-61.		1
96	<i>Halorhabdus tiamatea</i> proteogenomics and glycosidase activity measurements identify the first cultivated euryarchaeon from a deep-sea anoxic brine lake as potential polysaccharide degrader. <i>Environmental Microbiology</i> , 2014, 16, 2525-2537.	3.8	41
97	The gill chamber epibiosis of deep-sea shrimp <i>Rimicaris exoculata</i> : an in-depth metagenomic investigation and discovery of <i>Zetaproteobacteria</i> . <i>Environmental Microbiology</i> , 2014, 16, 2723-2738.	3.8	93
98	Effective bioremediation strategy for rapid in situ cleanup of anoxic marine sediments in mesocosm oil spill simulation. <i>Frontiers in Microbiology</i> , 2014, 5, 162.	3.5	62
99	<i>Alcanivorax borkumensis</i> produces an extracellular siderophore in iron-limitation condition maintaining the hydrocarbon-degradation efficiency. <i>Marine Genomics</i> , 2014, 17, 43-52.	1.1	27
100	Heterotrophic bicarbonate assimilation is the main process of <i>de novo</i> organic carbon synthesis in hadal zone of the Hellenic Trench, the deepest part of the Mediterranean Sea. <i>Environmental Microbiology Reports</i> , 2014, 6, 709-722.	2.4	23
101	The Family Oleiphilaceae. , 2014, , 529-533.		5
102	Metagenomic analysis of hadopelagic microbial assemblages thriving at the deepest part of Mediterranean Sea, Matapan-Vavilov Deep. <i>Environmental Microbiology</i> , 2013, 15, 167-182.	3.8	64
103	Genome sequence and functional genomic analysis of the oil-degrading bacterium <i>Oleispira antarctica</i> . <i>Nature Communications</i> , 2013, 4, 2156.	12.8	115
104	Single residues dictate the co-evolution of dual esterases: MCP hydrolases from the β hydrolase family. <i>Biochemical Journal</i> , 2013, 454, 157-166.	3.7	34
105	Bioremediation of Southern Mediterranean oil polluted sites comes of age. <i>New Biotechnology</i> , 2013, 30, 743-748.	4.4	32
106	Bioreduction of Sheep Carcasses Effectively Contains and Reduces Pathogen Levels under Operational and Simulated Breakdown Conditions. <i>Environmental Science & Technology</i> , 2013, 47, 5267-5275.	10.0	4
107	Microbial life in the Lake Medee, the largest deep-sea salt-saturated formation. <i>Scientific Reports</i> , 2013, 3, 3554.	3.3	78
108	Metagenomics of Deep Hypersaline Anoxic Basins. , 2013, , 1-9.		2

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109	Genome Sequence of <i>Thalassolituus oleivorans</i> MIL-1 (DSM 14913). <i>Genome Announcements</i> , 2013, 1, e0014113.	0.8	20
110	ULIXES, unravelling and exploiting Mediterranean Sea microbial diversity and ecology for xenobiotics and pollutants clean up. <i>Reviews in Environmental Science and Biotechnology</i> , 2012, 11, 207-211.	8.1	12
111	Fate of pathogens in a simulated bioreduction system for livestock carcasses. <i>Waste Management</i> , 2012, 32, 933-938.	7.4	14
112	<i>Methylorosula polaris</i> gen. nov., sp. nov., an aerobic, facultatively methylotrophic psychrotolerant bacterium from tundra wetland soil. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2012, 62, 638-646.	1.7	21
113	Microbial β -glucosidases from cow rumen metagenome enhance the saccharification of lignocellulose in combination with commercial cellulase cocktail. <i>Biotechnology for Biofuels</i> , 2012, 5, 73.	6.2	78
114	Temperature and water controls on vegetation emergence, microbial dynamics, and soil carbon and nitrogen fluxes in a high Arctic tundra ecosystem. <i>Functional Ecology</i> , 2012, 26, 1366-1380.	3.6	33
115	Structure and activity of the cold-active and anion-activated carboxyl esterase OLEI01171 from the oil-degrading marine bacterium <i>Oleispira antarctica</i> . <i>Biochemical Journal</i> , 2012, 445, 193-203.	3.7	31
116	Functional Metagenomics Unveils a Multifunctional Glycosyl Hydrolase from the Family 43 Catalysing the Breakdown of Plant Polymers in the Calf Rumen. <i>PLoS ONE</i> , 2012, 7, e38134.	2.5	83
117	Unveiling microbial life in the new deep-sea hypersaline Lake <i>Thetis</i> . Part II: a metagenomic study. <i>Environmental Microbiology</i> , 2012, 14, 268-281.	3.8	50
118	Composition and dynamics of biostimulated indigenous oil-degrading microbial consortia from the Irish, North and Mediterranean Seas: a mesocosm study. <i>FEMS Microbiology Ecology</i> , 2012, 81, 520-536.	2.7	29
119	Mineralization of low molecular weight carbon substrates in soil solution under laboratory and field conditions. <i>Soil Biology and Biochemistry</i> , 2012, 48, 88-95.	8.8	66
120	Gene Sets for Utilization of Primary and Secondary Nutrition Supplies in the Distal Gut of Endangered Iberian Lynx. <i>PLoS ONE</i> , 2012, 7, e51521.	2.5	23
121	The environmental and biosecurity characteristics of livestock carcass disposal methods: A review. <i>Waste Management</i> , 2011, 31, 767-778.	7.4	143
122	Unveiling microbial life in new deep-sea hypersaline Lake <i>Thetis</i> . Part I: Prokaryotes and environmental settings. <i>Environmental Microbiology</i> , 2011, 13, 2250-2268.	3.8	86
123	A novel platelet-activating factor acetylhydrolase discovered in a metagenome from the earthworm-associated microbial community. <i>Environmental Microbiology</i> , 2011, 13, 3036-3046.	3.8	8
124	Transcriptional profiling of the marine oil-degrading bacterium <i>Alcanivorax borkumensis</i> during growth on n-alkanes. <i>FEMS Microbiology Letters</i> , 2011, 319, 160-168.	1.8	65
125	Contribution of crenarchaeal autotrophic ammonia oxidizers to the dark primary production in Tyrrhenian deep waters (Central Mediterranean Sea). <i>ISME Journal</i> , 2011, 5, 945-961.	9.8	109
126	Molecular Methods to Study Complex Microbial Communities. <i>Methods in Molecular Biology</i> , 2010, 668, 1-37.	0.9	10

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127	Effect of the Earthworms <i>Lumbricus terrestris</i> and <i>Aporrectodea caliginosa</i> on Bacterial Diversity in Soil. <i>Microbial Ecology</i> , 2010, 59, 574-587.	2.8	92
128	A Mesocosm Study of the Changes in Marine Flagellate and Ciliate Communities in a Crude Oil Bioremediation Trial. <i>Microbial Ecology</i> , 2010, 60, 180-191.	2.8	23
129	Fate of prions in soil: Degradation of recombinant prion in aqueous extracts from soil and casts of two earthworm species. <i>Soil Biology and Biochemistry</i> , 2010, 42, 1168-1171.	8.8	10
130	Interconversion of catalytic abilities in a bifunctional carboxyl/feruloyl esterase from earthworm gut metagenome. <i>Microbial Biotechnology</i> , 2010, 3, 48-58.	4.2	15
131	Genomic signatures of fifth autotrophic carbon assimilation pathway in bathypelagic <i>Crenarchaeota</i> . <i>Microbial Biotechnology</i> , 2010, 3, 595-606.	4.2	19
132	Novel Hybrid Esterase-Haloacid Dehalogenase Enzyme. <i>ChemBioChem</i> , 2010, 11, 1975-1978.	2.6	16
133	Systems approaches to microbial communities and their functioning. <i>Current Opinion in Biotechnology</i> , 2010, 21, 532-538.	6.6	69
134	Diversity of Glycosyl Hydrolases from Cellulose-Depleting Communities Enriched from Casts of Two Earthworm Species. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5934-5946.	3.1	65
135	Screening Metagenomic Libraries for Laccase Activities. <i>Methods in Molecular Biology</i> , 2010, 668, 189-202.	0.9	18
136	Metagenomics for Mining New Genetic Resources of Microbial Communities. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 109-123.	1.0	209
137	<i>Acidiplasma aeolicum</i> gen. nov., sp. nov., a euryarchaeon of the family Ferroplasmaceae isolated from a hydrothermal pool, and transfer of <i>Ferroplasma cupricumulans</i> to <i>Acidiplasma cupricumulans</i> comb. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2009, 59, 2815-2823.	1.7	93
138	Metagenomics as a new technological tool to gain scientific knowledge. <i>World Journal of Microbiology and Biotechnology</i> , 2009, 25, 945-954.	3.6	25
139	Bacterial consortium proteomics under 4-chlorosalicylate carbon-limiting conditions. <i>Proteomics</i> , 2009, 9, 2273-2285.	2.2	14
140	Metagenomics approaches in systems microbiology. <i>FEMS Microbiology Reviews</i> , 2009, 33, 236-255.	8.6	130
141	Microbial consortia in mesocosm bioremediation trial using oil sorbents, slow-release fertilizer and bioaugmentation. <i>FEMS Microbiology Ecology</i> , 2009, 69, 288-300.	2.7	44
142	<i>Candidatus Lumbricincola</i> TM , a novel lineage of uncultured <i>Mollicutes</i> from earthworms of family <i>Lumbricidae</i> . <i>Environmental Microbiology</i> , 2009, 11, 1016-1026.	3.8	57
143	Reactome Array: Forging a Link Between Metabolome and Genome. <i>Science</i> , 2009, 326, 252-257.	12.6	39
144	Rare Metabolic Conversions—Harvesting Diversity through Nature. , 2009, , .		0

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145	Niche-specificity factors of a marine oil-degrading bacterium <i>Alcanivorax borkumensis</i> SK2. FEMS Microbiology Letters, 2008, 285, 89-96.	1.8	36
146	Recent trends in industrial microbiology. Current Opinion in Microbiology, 2008, 11, 240-248.	5.1	58
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