

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	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	27.8	1,942
2	Obligate oil-degrading marine bacteria. <i>Current Opinion in Biotechnology</i> , 2007, 18, 257-266.	6.6	769
3	Genome sequence of the ubiquitous hydrocarbon-degrading marine bacterium <i>Alcanivorax borkumensis</i> . <i>Nature Biotechnology</i> , 2006, 24, 997-1004.	17.5	417
4	Polychlorinated biphenyl-degrading microbial communities in soils and sediments. <i>Current Opinion in Microbiology</i> , 2002, 5, 246-253.	5.1	263
5	<i>Oleispira antarctica</i> gen. nov., sp. nov., a novel hydrocarbonoclastic marine bacterium isolated from Antarctic coastal sea water. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 779-785.	1.7	259
6	Novel hydrolase diversity retrieved from a metagenome library of bovine rumen microflora. <i>Environmental Microbiology</i> , 2005, 7, 1996-2010.	3.8	258
7	Limits of life in MgCl ₂ -containing environments: chaotropicity defines the window. <i>Environmental Microbiology</i> , 2007, 9, 801-813.	3.8	254
8	Chaperonins govern growth of <i>Escherichia coli</i> at low temperatures. <i>Nature Biotechnology</i> , 2003, 21, 1266-1267.	17.5	228
9	Stratified prokaryote network in the oxic-anoxic transition of a deep-sea halocline. <i>Nature</i> , 2006, 440, 203-207.	27.8	215
10	Mining enzymes from extreme environments. <i>Current Opinion in Microbiology</i> , 2007, 10, 207-214.	5.1	213
11	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
12	Metagenomics for Mining New Genetic Resources of Microbial Communities. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 16, 109-123.	1.0	209
13	Natural microbial diversity in superficial sediments of Milazzo Harbor (Sicily) and community successions during microcosm enrichment with various hydrocarbons. <i>Environmental Microbiology</i> , 2005, 7, 1426-1441.	3.8	194
14	The ocean sampling day consortium. <i>GigaScience</i> , 2015, 4, 27.	6.4	185
15	Estimating the success of enzyme bioprospecting through metagenomics: current status and future trends. <i>Microbial Biotechnology</i> , 2016, 9, 22-34.	4.2	175
16	Novel Polyphenol Oxidase Mined from a Metagenome Expression Library of Bovine Rumen. <i>Journal of Biological Chemistry</i> , 2006, 281, 22933-22942.	3.4	168
17	<i>Thalassolituus oleivorans</i> gen. nov., sp. nov., a novel marine bacterium that obligately utilizes hydrocarbons. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2004, 54, 141-148.	1.7	160
18	Mining genomes and metagenomes for novel catalysts. <i>Current Opinion in Biotechnology</i> , 2005, 16, 588-593.	6.6	146

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19	The environmental and biosecurity characteristics of livestock carcass disposal methods: A review. <i>Waste Management</i> , 2011, 31, 767-778.	7.4	143
20	Microbial Enzymes Mined from the Urania Deep-Sea Hypersaline Anoxic Basin. <i>Chemistry and Biology</i> , 2005, 12, 895-904.	6.0	142
21	Proteomic Insights into Metabolic Adaptations in <i>Alcanivorax borkumensis</i> Induced by Alkane Utilization. <i>Journal of Bacteriology</i> , 2006, 188, 3763-3773.	2.2	139
22	Analysis of Storage Lipid Accumulation in <i>Alcanivorax borkumensis</i> : Evidence for Alternative Triacylglycerol Biosynthesis Routes in Bacteria. <i>Journal of Bacteriology</i> , 2007, 189, 918-928.	2.2	133
23	Metagenomics approaches in systems microbiology. <i>FEMS Microbiology Reviews</i> , 2009, 33, 236-255.	8.6	130
24	Genome sequence completed of <i>Alcanivorax borkumensis</i> , a hydrocarbon-degrading bacterium that plays a global role in oil removal from marine systems. <i>Journal of Biotechnology</i> , 2003, 106, 215-220.	3.8	126
25	Oleiphilaceae fam. nov., to include <i>Oleiphilus messinensis</i> gen. nov., sp. nov., a novel marine bacterium that obligately utilizes hydrocarbons.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2002, 52, 901-911.	1.7	118
26	ARMAN™ archaea depend on association with euryarchaeal host in culture and in situ. <i>Nature Communications</i> , 2017, 8, 60.	12.8	116
27	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
28	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
29	Genomic and mechanistic insights into the biodegradation of organic pollutants. <i>Current Opinion in Biotechnology</i> , 2004, 15, 215-224.	6.6	113
30	Crude oil-induced structural shift of coastal bacterial communities of rod bay (Terra Nova Bay, Ross) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 <i>Microbiology Ecology</i> , 2004, 49, 419-432.	2.7	109
31	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
32	Microbial community of the deep-sea brine lake Karyos seawayer-brine interface is active below the chaotropy limit of life as revealed by recovery of mRNA. <i>Environmental Microbiology</i> , 2015, 17, 364-382.	3.8	109
33	Determinants and Prediction of Esterase Substrate Promiscuity Patterns. <i>ACS Chemical Biology</i> , 2018, 13, 225-234.	3.4	106
34	Primary producing prokaryotic communities of brine, interface and seawater above the halocline of deep anoxic lake L'Atalante, Eastern Mediterranean Sea. <i>ISME Journal</i> , 2007, 1, 743-755.	9.8	99
35	The novel extremely acidophilic, cell-wall-deficient archaeon <i>Cuniculiplasma divulgatum</i> gen. nov., sp. nov. represents a new family, <i>Cuniculiplasmataceae</i> fam. nov., of the order <i>Thermoplasmatales</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 332-340.	1.7	96
36	<i>Acidiplasma aeolicum</i> gen. nov., sp. nov., a euryarchaeon of the family <i>Ferropasmataceae</i> 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

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37	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
38	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
39	Bacterial population and biodegradation potential in chronically crude oil-contaminated marine sediments are strongly linked to temperature. <i>Scientific Reports</i> , 2015, 5, 11651.	3.3	91
40	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
41	The cellular machinery of <i>Ferroplasma acidiphilum</i> is iron-protein-dominated. <i>Nature</i> , 2007, 445, 91-94.	27.8	88
42	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
43	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
44	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
45	Mutation in a <i>tesB</i> -Like-Hydroxyacyl-Coenzyme A-Specific Thioesterase Gene Causes Hyperproduction of Extracellular Polyhydroxyalkanoates by <i>Alcanivorax borkumensis</i> SK2. <i>Journal of Bacteriology</i> , 2006, 188, 8452-8459.	2.2	79
46	Discovery of anaerobic lithoheterotrophic haloarchaea, ubiquitous in hypersaline habitats. <i>ISME Journal</i> , 2017, 11, 1245-1260.	9.8	79
47	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
48	Microbial life in the Lake Medee, the largest deep-sea salt-saturated formation. <i>Scientific Reports</i> , 2013, 3, 3554.	3.3	78
49	Microbiome and infectivity studies reveal complex polyspecies tree disease in Acute Oak Decline. <i>ISME Journal</i> , 2018, 12, 386-399.	9.8	75
50	Low temperature-induced systems failure in <i>Escherichia coli</i> : Insights from rescue by cold-adapted chaperones. <i>Proteomics</i> , 2006, 6, 193-206.	2.2	73
51	Expression of a Temperature-Sensitive Esterase in a Novel Chaperone-Based <i>Escherichia coli</i> Strain. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4499-4504.	3.1	71
52	Systems approaches to microbial communities and their functioning. <i>Current Opinion in Biotechnology</i> , 2010, 21, 532-538.	6.6	69
53	Activity screening of environmental metagenomic libraries reveals novel carboxylesterase families. <i>Scientific Reports</i> , 2017, 7, 44103.	3.3	67
54	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

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55	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
56	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
57	Microbial community of a saline mud volcano at San Biagio-Belpasso, Mt. Etna (Italy). <i>Environmental Microbiology</i> , 2002, 4, 249-256.	3.8	64
58	Metagenomic analysis of hadopelagic microbial assemblages thriving at the deepest part of Mediterranean Sea, Matapanâ€Vavilov Deep. <i>Environmental Microbiology</i> , 2013, 15, 167-182.	3.8	64
59	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
60	Elemental sulfur and acetate can support life of a novel strictly anaerobic haloarchaeon. <i>ISME Journal</i> , 2016, 10, 240-252.	9.8	62
61	Structural characterization of lichenysin A components by fast atom bombardment tandem mass spectrometry. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 1999, 1438, 273-280.	2.4	59
62	Isolation and characterization of novel lipases/esterases from a bovine rumen metagenome. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 5475-5485.	3.6	59
63	Recent trends in industrial microbiology. <i>Current Opinion in Microbiology</i> , 2008, 11, 240-248.	5.1	58
64	Metaproteomics and metabolomics analyses of chronically petroleumâ€Polluted sites reveal the importance of general anaerobic processes uncoupled with degradation. <i>Proteomics</i> , 2015, 15, 3508-3520.	2.2	58
65	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
66	â€Candidatus Lumbricincolaâ€™™, a novel lineage of uncultured Mollicutes from earthworms of family Lumbricidae. <i>Environmental Microbiology</i> , 2009, 11, 1016-1026.	3.8	57
67	Rational Engineering of Multiple Active Sites in an Ester Hydrolase. <i>Biochemistry</i> , 2018, 57, 2245-2255.	2.5	57
68	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
69	The rumen microbiome: an underexplored resource for novel antimicrobial discovery. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 33.	6.4	51
70	Nano-Sized and Filterable Bacteria and Archaea: Biodiversity and Function. <i>Frontiers in Microbiology</i> , 2018, 9, 1971.	3.5	51
71	Unveiling microbial life in the new deepâ€sea hypersaline Lake Thetis. Part II: a metagenomic study. <i>Environmental Microbiology</i> , 2012, 14, 268-281.	3.8	50
72	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

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73	The 'pH optimum anomaly' of intracellular enzymes of <i>Ferroplasma acidiphilum</i> . <i>Environmental Microbiology</i> , 2006, 8, 416-425.	3.8	48
74	Biodiversity for biocatalysis: A review of the β -hydrolase fold superfamily of esterases-lipases discovered in metagenomes. <i>Biocatalysis and Biotransformation</i> , 2015, 33, 235-249.	2.0	48
75	Microbial Community of a Hydrothermal Mud Vent Underneath the Deep-Sea Anoxic Brine Lake Urania (Eastern Mediterranean). <i>Origins of Life and Evolution of Biospheres</i> , 2007, 37, 177-188.	1.9	47
76	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
77	Functional consequences of single:double ring transitions in chaperonins: life in the cold. <i>Molecular Microbiology</i> , 2004, 53, 167-182.	2.5	42
78	A novel α -glucosidase from the acidophilic archaeon <i>Ferroplasma acidiphilum</i> strain Y with high transglycosylation activity and an unusual catalytic nucleophile. <i>Biochemical Journal</i> , 2005, 391, 269-276.	3.7	41
79	<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
80	Pressure adaptation is linked to thermal adaptation in salt-saturated marine habitats. <i>Environmental Microbiology</i> , 2015, 17, 332-345.	3.8	40
81	A putative lichenysin A synthetase operon in <i>Bacillus licheniformis</i> : initial characterization. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1998, 1399, 141-153.	2.4	39
82	Biochemical and structural features of a novel cyclodextrinase from cow rumen metagenome. <i>Biotechnology Journal</i> , 2007, 2, 207-213.	3.5	39
83	Reactome Array: Forging a Link Between Metabolome and Genome. <i>Science</i> , 2009, 326, 252-257.	12.6	39
84	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
85	Niche-specificity factors of a marine oil-degrading bacterium <i>Alcanivorax borkumensis</i> SK2. <i>FEMS Microbiology Letters</i> , 2008, 285, 89-96.	1.8	36
86	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. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10031-10046.	3.6	36
87	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
88	<i>Thermoleophilum album</i> and <i>Thermoleophilum minutum</i> are culturable representatives of group 2 of the Rubrobacteridae (Actinobacteria). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2003, 53, 377-380.	1.7	35
89	Metagenomics as a Tool for Enzyme Discovery: Hydrolytic Enzymes from Marine-Related Metagenomes. <i>Advances in Experimental Medicine and Biology</i> , 2015, 883, 1-20.	1.6	35
90	Identification and Characterization of Carboxyl Esterases of Gill Chamber-Associated Microbiota in the Deep-Sea Shrimp <i>Rimicaris exoculata</i> by Using Functional Metagenomics. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2125-2136.	3.1	35

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91	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
92	Single residues dictate the co-evolution of dual esterases: MCP hydrolases from the $\hat{\pm}/\hat{\iota}^2$ hydrolase family. <i>Biochemical Journal</i> , 2013, 454, 157-166.	3.7	34
93	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
94	Degradation of Hydrocarbons and Heavy Metal Reduction by Marine Bacteria in Highly Contaminated Sediments. <i>Microorganisms</i> , 2020, 8, 1402.	3.6	34
95	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
96	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
97	Conversion of a Carboxylesterase into a Triacylglycerol Lipase by a Random Mutation. <i>Angewandte Chemie - International Edition</i> , 2005, 44, 7553-7557.	13.8	32
98	Characterization of a chitinolytic enzyme from <i>Serratia</i> sp. KCK isolated from kimchi juice. <i>Applied Microbiology and Biotechnology</i> , 2007, 75, 1275-1283.	3.6	32
99	Bioremediation of Southern Mediterranean oil polluted sites comes of age. <i>New Biotechnology</i> , 2013, 30, 743-748.	4.4	32
100	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
101	Biology of archaea from a novel family Cuniculiplasmataceae (Thermoplasmata) ubiquitous in hyperacidic environments. <i>Scientific Reports</i> , 2016, 6, 39034.	3.3	31
102	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
103	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
104	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
105	A purple acidophilic di-ferric DNA ligase from <i>Ferroplasma</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8878-8883.	7.1	27
106	<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
107	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
108	Diversity of <i>Ca</i> . <i>Micrarchaeota</i> in Two Distinct Types of Acidic Environments and Their Associations with Thermoplasmatales. <i>Genes</i> , 2019, 10, 461.	2.4	27

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109	Dissimilatory sulfate reduction in the archaeon <i>Candidatus Vulcanisaeta moutnovskia</i> ™ sheds light on the evolution of sulfur metabolism. <i>Nature Microbiology</i> , 2020, 5, 1428-1438.	13.3	27
110	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
111	Functional Screening of Hydrolytic Activities Reveals an Extremely Thermostable Cellulase from a Deep-Sea Archaeon. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 95.	4.1	26
112	Decoding the ocean's microbiological secrets for marine enzyme biodiscovery. <i>FEMS Microbiology Letters</i> , 2019, 366, .	1.8	26
113	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
114	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
115	Calm and Frenzy: marine obligate hydrocarbonoclastic bacteria sustain ocean wellness. <i>Current Opinion in Biotechnology</i> , 2022, 73, 337-345.	6.6	24
116	ComA-Dependent Transcriptional Activation of Lichenysin A Synthetase Promoter in <i>Bacillus subtilis</i> cells. <i>Biotechnology Progress</i> , 1997, 13, 757-761.	2.6	23
117	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
118	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
119	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
120	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
121	<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
122	Structural and Functional Characterization of a Ruminal β -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
123	Metabolic and evolutionary patterns in the extremely acidophilic archaeon <i>Ferroplasma acidiphilum</i> YT. <i>Scientific Reports</i> , 2017, 7, 3682.	3.3	21
124	Genome Sequence of <i>Thalassolituus oleivorans</i> MIL-1 (DSM 14913 T). <i>Genome Announcements</i> , 2013, 1, e0014113.	0.8	20
125	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
126	Genomic signatures of fifth autotrophic carbon assimilation pathway in bathypelagic <i>Crenarchaeota</i> . <i>Microbial Biotechnology</i> , 2010, 3, 595-606.	4.2	19

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127	Buwchitin: A Ruminant Peptide with Antimicrobial Potential against <i>Enterococcus faecalis</i> . <i>Frontiers in Chemistry</i> , 2017, 5, 51.	3.6	19
128	Catalytic role of conserved HQGE motif in the CE6 carbohydrate esterase family. <i>FEBS Letters</i> , 2007, 581, 4657-4662.	2.8	18
129	Screening Metagenomic Libraries for Laccase Activities. <i>Methods in Molecular Biology</i> , 2010, 668, 189-202.	0.9	18
130	Degradation Network Reconstruction in Uric Acid and Ammonium Amendments in Oil-Degrading Marine Microcosms Guided by Metagenomic Data. <i>Frontiers in Microbiology</i> , 2015, 6, 1270.	3.5	18
131	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
132	<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
133	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
134	Bioprospecting Reveals Class III α -Transaminases Converting Bulky Ketones and Environmentally Relevant Polyamines. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	17
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