

Fan Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

397
citations

1040056

9
h-index

839539

18
g-index

20
all docs

20
docs citations

20
times ranked

400
citing authors

#	ARTICLE	IF	CITATIONS
1	Optimization and characterization of biosurfactant produced by indigenous <i>Brevibacillus borstelensis</i> isolated from a low permeability reservoir for application in MEOR. RSC Advances, 2022, 12, 2036-2047.	3.6	11
2	Elucidate microbial characteristics in a full-scale treatment plant for offshore oil produced wastewater. PLoS ONE, 2021, 16, e0255836.	2.5	3
3	Tracking alterations of alkyl side chains of N ¹ species in heavy crude oil after anaerobic biodegradation with negative-ion electrospray ionization coupled with high-field Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 875-882.	1.5	1
4	Dynamics of a microbial community during an effective boost MEOR trial using high-throughput sequencing. RSC Advances, 2018, 8, 690-697.	3.6	7
5	Shifts of the indigenous microbial communities from reservoir production water in crude oil- and asphaltene-degrading microcosms. International Biodeterioration and Biodegradation, 2018, 132, 18-29.	3.9	48
6	Anaerobic Microbial Diversity and Abundance in Xinjiang low-Temperature Water- Flooding Petroleum Reservoir. Journal of Engineering Science and Technology Review, 2017, 10, 129-135.	0.4	0
7	Deposit reduction in a high pour point oil reservoir due to the activity of indigenous bacterial communities. International Biodeterioration and Biodegradation, 2016, 110, 87-98.	3.9	9
8	Draft genome sequence of <i>Paenibacillus</i> sp. strain A2. Standards in Genomic Sciences, 2016, 11, 9.	1.5	2
9	High quality genome sequence and description of <i>Enterobacter mori</i> strain 5 ⁴ , isolated from a mixture of formation water and crude-oil. Standards in Genomic Sciences, 2015, 10, 9.	1.5	6
10	Isolation and characterization of a crude oil degrading bacteria from formation water: comparative genomic analysis of environmental <i>Ochrobactrum intermedium</i> isolate versus clinical strains. Journal of Zhejiang University: Science B, 2015, 16, 865-874.	2.8	15
11	Genome sequence of <i>Brevibacillus agri</i> strain 5-2, isolated from the formation water of petroleum reservoir. Marine Genomics, 2014, 18, 123-125.	1.1	9
12	Permanent draft genome sequence of <i>Geobacillus thermocatenulatus</i> strain GS-1. Marine Genomics, 2014, 18, 129-131.	1.1	7
13	Genomovar assignment of <i>Pseudomonas stutzeri</i> populations inhabiting produced oil reservoirs. MicrobiologyOpen, 2014, 3, 446-456.	3.0	8
14	Potential Microorganisms for Prevention of Paraffin Precipitation in a Hypersaline Oil Reservoir. Energy & Fuels, 2014, 28, 1191-1197.	5.1	24
15	Microbial diversity in long-term water-flooded oil reservoirs with different in situ temperatures in China. Scientific Reports, 2012, 2, 760.	3.3	68
16	Impact of an indigenous microbial enhanced oil recovery field trial on microbial community structure in a high pour-point oil reservoir. Applied Microbiology and Biotechnology, 2012, 95, 811-821.	3.6	46
17	Investigation of Biosurfactant-Producing Indigenous Microorganisms that Enhance Residue Oil Recovery in an Oil Reservoir After Polymer Flooding. Applied Biochemistry and Biotechnology, 2011, 163, 223-234.	2.9	68
18	Molecular biologic techniques applied to the microbial prospecting of oil and gas in the Ban 876 gas and oil field in China. Applied Microbiology and Biotechnology, 2010, 86, 1183-1194.	3.6	30

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19	Response of microbial community structure to microbial plugging in a mesothermic petroleum reservoir in China. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 1413-1422.	3.6	35
20	Microbial community diversity and potential bioremediation of drill cuttings in two oil reservoirs. <i>Petroleum Science and Technology</i> , 0, , 1-17.	1.5	0