

Rupa Iyer

List of Publications by Year in descending order

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papers

226
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1307594

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#	ARTICLE	IF	CITATIONS
1	Functional Analysis of Chlorpyrifos Biodegradation in Agricultural Soils Augmented with a Three-Strain Bacterial Consortium. <i>Water, Air, and Soil Pollution</i> , 2021, 232, 1.	2.4	4
2	Shotgun metagenomics of indigenous bacteria collected from the banks of the San Jacinto River for biodegradation of aromatic waste. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	1
3	Genome data of <i>Stenotrophomonas maltophilia</i> DF07 collected from polluted river sediment reveals an opportunistic pathogen and a potential antibiotic reservoir. <i>Data in Brief</i> , 2019, 25, 104137.	1.0	1
4	Whole genome analysis of six organophosphate-degrading rhizobacteria reveals putative agrochemical degradation enzymes with broad substrate specificity. <i>Environmental Science and Pollution Research</i> , 2018, 25, 13660-13675.	5.3	15
5	Genome of <i>Pseudomonas nitroreducens</i> DF05 from dioxin contaminated sediment downstream of the San Jacinto River waste pits reveals a broad array of aromatic degradation gene determinants. <i>Genomics Data</i> , 2017, 14, 40-43.	1.3	8
6	Whole genome sequencing of <i>Microbacterium</i> sp. AISO3 from polluted San Jacinto River sediment reveals high bacterial mobility, metabolic versatility and heavy metal resistance. <i>Genomics Data</i> , 2017, 14, 10-13.	1.3	4
7	Whole genome of <i>Klebsiella aerogenes</i> PX01 isolated from San Jacinto River sediment west of Baytown, Texas reveals the presence of multiple antibiotic resistance determinants and mobile genetic elements. <i>Genomics Data</i> , 2017, 14, 7-9.	1.3	5
8	Draft Genome Sequence of the Broad-Spectrum Xenobiotic Degradier <i>Achromobacter xylosoxidans</i> ADAF13. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
9	Draft Genome Sequence of <i>Stenotrophomonas maltophilia</i> CBF10-1, an Organophosphate-Degrading Bacterium Isolated from Ranch Soil in Fairchilds, Texas. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
10	A review of the Texas, USA San Jacinto Superfund site and the deposition of polychlorinated dibenzo-p-dioxins and dibenzofurans in the San Jacinto River and Houston Ship Channel. <i>Environmental Science and Pollution Research</i> , 2016, 23, 23321-23338.	5.3	9
11	Draft Genome Sequence of <i>Pseudomonas putida</i> CBF10-2, a Soil Isolate with Bioremediation Potential in Agricultural and Industrial Environmental Settings. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
12	Draft Genome Sequence of <i>Exiguobacterium</i> sp. KKBO11, Isolated Downstream of a Wastewater Treatment Plant in Houston, Texas. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
13	Draft Genome Sequence of <i>Rhizobium</i> sp. GHKF11, Isolated from Farmland Soil in Pecan Grove, Texas. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
14	Draft Genome Sequence of Alkane-Degrading <i>Acinetobacter venetianus</i> JKSF02, Isolated from Contaminated Sediment of the San Jacinto River in Houston, Texas. <i>Genome Announcements</i> , 2016, 4, .	0.8	0
15	Draft Genome Sequence of <i>Pseudomonas stutzeri</i> ODKF13, Isolated from Farmland Soil in Alvin, Texas. <i>Genome Announcements</i> , 2016, 4, .	0.8	6
16	Draft Genome Sequence of Organophosphate-Degrading <i>Ochrobactrum anthropi</i> FRAF13. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
17	Characterization and comparison of putative <i>Stenotrophomonas maltophilia</i> methyl parathion hydrolases. <i>Bioremediation Journal</i> , 2016, 20, 71-79.	2.0	6
18	Developments in alternative treatments for organophosphate poisoning. <i>Toxicology Letters</i> , 2015, 233, 200-206.	0.8	46

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19	Detection and location of OP-degrading activity: A model to integrate education and research. <i>New Biotechnology</i> , 2015, 32, 403-411.	4.4	14
20	Protein engineering of representative hydrolytic enzymes for remediation of organophosphates. <i>Biochemical Engineering Journal</i> , 2015, 94, 134-144.	3.6	36
21	A comparison of organophosphate degradation genes and bioremediation applications. <i>Environmental Microbiology Reports</i> , 2013, 5, 787-798.	2.4	43