# Joseph Alexander Christie-Oleza

List of Publications by Year
in descending order



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|---|---|---|---|
| 46 papers | 3,187 citations | 257450 24 h-index | 214800 47 g-index |
| 54 all docs | 54 docs citations | 54 times ranked | 4002 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Lost, but Found with Nile Red: A Novel Method for Detecting and Quantifying Small Microplastics (1) Tj ETQq1 1 0.784314 rgBT /Ove | 10.0 | 519 |
| 2 | Distribution of plastic polymer types in the marine environment; A meta-analysis. Journal of Hazardous Materials, 2019, 369, 691-698. | 12.4 | 508 |
| 3 | Marine Plastic Debris: A New Surface for Microbial Colonization. Environmental Science & Technology, 2020, 54, 11657-11672. | 10.0 | 259 |
| 4 | Understanding microbial community dynamics to improve optimal microbiome selection. Microbiome, 2019, 7, 85. | 11.1 | 233 |
| 5 | Nutrient recycling facilitates long-term stability of marine microbial phototrophâ€“heterotroph interactions. Nature Microbiology, 2017, 2, 17100. | 13.3 | 181 |
| 6 | Proteomic insights into the lifestyle of an environmentally relevant marine bacterium. ISME Journal, 2012, 6, 124-135. | 9.8 | 100 |
| 7 | Plasticizer Degradation by Marine Bacterial Isolates: A Proteogenomic and Metabolomic Characterization. Environmental Science & Technology, 2020, 54, 2244-2256. | 10.0 | 97 |
| 8 | Early Colonization of Weathered Polyethylene by Distinct Bacteria in Marine Coastal Seawater. Microbial Ecology, 2020, 79, 517-526. | 2.8 | 96 |
| 9 | Environmental fate of microplastics in the world's third-largest river: Basin-wide investigation and microplastic community analysis. Water Research, 2022, 210, 118002. | 11.3 | 96 |
| 10 | Exoproteomics: exploring the world around biological systems. Expert Review of Proteomics, 2012, 9, 561-575. | 3.0 | 80 |
| 11 | Comparative Proteogenomics of Twelve Roseobacter Exoproteomes Reveals Different Adaptive Strategies Among These Marine Bacteria. Molecular and Cellular Proteomics, 2012, 11, M111.013110. | 3.8 | 73 |
| 12 | Bacterial Community Dynamics during Bioremediation of Diesel Oil-Contaminated Antarctic Soil. Microbial Ecology, 2009, 57, 598-610. | 2.8 | 61 |
| 13 | Characterization of bacterial consortia from diesel-contaminated Antarctic soils: Towards the design of tailored formulas for bioaugmentation. International Biodeterioration and Biodegradation, 2013, 77, 22-30. | 3.9 | 55 |
| 14 | Functional distinctness in the exoproteomes of marine <scp>S</scp>ynechococcus. Environmental Microbiology, 2015, 17, 3781-3794. | 3.8 | 55 |
| 15 | Beyond oil degradation: enzymatic potential of Alcanivorax to degrade natural and synthetic polyesters. Environmental Microbiology, 2020, 22, 1356-1369. | 3.8 | 53 |
| 16 | In-Depth Analysis of Exoproteomes from Marine Bacteria by Shotgun Liquid Chromatography-Tandem Mass Spectrometry: the Ruegeria pomeroyi DSS-3 Case-Study. Marine Drugs, 2010, 8, 2223-2239. | 4.6 | 52 |
| 17 | â€œYou produce while I clean upâ€, a strategy revealed by exoproteomics during Synechococcusâ€“Roseobacter interactions. Proteomics, 2015, 15, 3454-3462. | 2.2 | 50 |
| 18 | A multi-OMIC characterisation of biodegradation and microbial community succession within the PET plastisphere. Microbiome, 2021, 9, 141. | 11.1 | 49 |

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|---|---|---|---|
| 19 | High-throughput proteogenomics of Ruegeria pomeroyi: seeding a better genomic annotation for the whole marine Roseobacter clade. BMC Genomics, 2012, 13, 73. | 2.8 | 38 |
| 20 | N-Terminal-oriented Proteogenomics of the Marine Bacterium Roseobacter Denitrificans Och114 using and Diagonal Chromatography. Molecular and Cellular Proteomics, 2014, 13, 1369-1381. | 3.8 | 37 |
| 21 | A mechanistic understanding of polyethylene biodegradation by the marine bacterium Alcanivorax. Journal of Hazardous Materials, 2022, 436, 129278. | 12.4 | 34 |
| 22 | Riding the wave of genomics to investigate aquatic coliphage diversity and activity. Environmental Microbiology, 2019, 21, 2112-2128. | 3.8 | 33 |
| 23 | Mechanisms of silver nanoparticle toxicity on the marine cyanobacterium Prochlorococcus under environmentally-relevant conditions. Science of the Total Environment, 2020, 747, 141229. | 8.0 | 31 |
| 24 | Microbial pioneers of plastic colonisation in coastal seawaters. Marine Pollution Bulletin, 2022, 179, 113701. | 5.0 | 31 |
| 25 | Environmentally relevant concentrations of titanium dioxide nanoparticles pose negligible risk to marine microbes. Environmental Science: Nano, 2021, 8, 1236-1255. | 4.3 | 29 |
| 26 | Genome of Alcanivorax sp. 24: A hydrocarbon degrading bacterium isolated from marine plastic debris. Marine Genomics, 2020, 49, 100686. | 1.1 | 28 |
| 27 | A widely distributed phosphate-insensitive phosphatase presents a route for rapid organophosphorus remineralization in the biosphere. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, . | 7.1 | 26 |
| 28 | Shotgun nanoLCâ€MS/MS proteogenomics to document MALDIâ€TOF biomarkers for screening new members of the Ruegeria genus. Environmental Microbiology, 2013, 15, 133-147. | 3.8 | 25 |
| 29 | A Novel Ca2+ Signaling Pathway Coordinates Environmental Phosphorus Sensing and Nitrogen Metabolism in Marine Diatoms. Current Biology, 2021, 31, 978-989.e4. | 3.9 | 24 |
| 30 | Proteomics meets blue biotechnology: A wealth of novelties and opportunities. Marine Genomics, 2014, 17, 35-42. | 1.1 | 23 |
| 31 | Pili allow dominant marine cyanobacteria to avoid sinking and evade predation. Nature Communications, 2021, 12, 1857. | 12.8 | 22 |
| 32 | Cell size matters: Nano- and micro-plastics preferentially drive declines of large marine phytoplankton due to co-aggregation. Journal of Hazardous Materials, 2022, 424, 127488. | 12.4 | 20 |
| 33 | 100 Days of marine Synechococcusâ€“Ruegeria pomeroyi interaction: A detailed analysis of the exoproteome. Environmental Microbiology, 2018, 20, 785-799. | 3.8 | 19 |
| 34 | Physiological role of NahW, the additional salicylate hydroxylase found inPseudomonas stutzeriAN10. FEMS Microbiology Letters, 2009, 300, 265-272. | 1.8 | 18 |
| 35 | Conjugative Interaction Induces Transposition of IS Pst9 in Pseudomonas stutzeri AN10. Journal of Bacteriology, 2009, 191, 1239-1247. | 2.2 | 17 |
| 36 | Phytoplankton trigger the production of cryptic metabolites in the marine actinobacterium Salinispora tropica. Microbial Biotechnology, 2021, 14, 291-306. | 4.2 | 16 |

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|---|---|---|---|
| 37 | Proteogenomic Definition of Biomarkers for the Large Roseobacter Clade and Application for a Quick Screening of New Environmental Isolates. Journal of Proteome Research, 2013, 12, 5331-5339. | 3.7 | 15 |
| 38 | TnpR Encoded by an IS Ppu12 Isoform Regulates Transposition of Two Different IS L3 -Like Insertion Sequences in Pseudomonas stutzeri after Conjugative Interaction. Journal of Bacteriology, 2010, 192, 1423-1432. | 2.2 | 13 |
| 39 | Investigating the Impact of Cerium Oxide Nanoparticles Upon the Ecologically Significant Marine Cyanobacterium Prochlorococcus. Frontiers in Marine Science, 2021, 8, . | 2.5 | 13 |
| 40 | Proteomics of the Roseobacter clade, a window to the marine microbiology landscape. Proteomics, 2015, 15, 3928-3942. | 2.2 | 12 |
| 41 | Manganese Oxide Biomineralization Provides Protection against Nitrite Toxicity in a Cell-Density-Dependent Manner. Applied and Environmental Microbiology, 2019, 85, . | 3.1 | 12 |
| 42 | ISPst9, an ISL3-like insertion sequence from Pseudomonas stutzeri AN10 involved in catabolic gene inactivation. International Microbiology, 2008, 11, 101-10. | 2.4 | 12 |
| 43 | Assessing the Exoproteome of Marine Bacteria, Lesson from a RTX-Toxin Abundantly Secreted by Phaeobacter Strain DSM 17395. PLoS ONE, 2014, 9, e89691. | 2.5 | 10 |
| 44 | Draft Genome Sequence of Citreicella aestuarii Strain 357, a Member of the Roseobacter Clade Isolated without Xenobiotic Pressure from a Petroleum-Polluted Beach. Journal of Bacteriology, 2012, 194, 5464-5465. | 2.2 | 5 |
| 45 | MiniUIB, a Novel Minitransposon-Based System for Stable Insertion of Foreign DNA into the Genomes of Gram-Negative and Gram-Positive Bacteria. Applied and Environmental Microbiology, 2013, 79, 1629-1638. | 3.1 | 1 |
| 46 | Defining a Pipeline for Metaproteomic Analyses. Springer Protocols, 2015, , 99-110. | 0.3 | 1 |