

John P Mccrow

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

2,954
citations

331670

21
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377865

34
g-index

39
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docs citations

39
times ranked

4198
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Microbial communities associated with sinking particles across an environmental gradient from coastal upwelling to the oligotrophic ocean. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2022, 179, 103668. | 1.4 | 11 |
| 2 | Proteomic analysis of metabolic pathways supports chloroplast-mitochondria cross-talk in a Cu-limited diatom. <i>Plant Direct</i> , 2022, 6, e376. | 1.9 | 6 |
| 3 | Molecular underpinnings and biogeochemical consequences of enhanced diatom growth in a warming Southern Ocean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 7.1 | 17 |
| 4 | Relating sinking and suspended microbial communities in the California Current Ecosystem: digestion resistance and the contributions of phytoplankton taxa to export. <i>Environmental Microbiology</i> , 2021, 23, 6734-6748. | 3.8 | 8 |
| 5 | Dinoflagellates alter their carbon and nutrient metabolic strategies across environmental gradients in the central Pacific Ocean. <i>Nature Microbiology</i> , 2021, 6, 173-186. | 13.3 | 45 |
| 6 | Hydrothermal trace metal release and microbial metabolism in the northeastern Lau Basin of the South Pacific Ocean. <i>Biogeosciences</i> , 2021, 18, 5397-5422. | 3.3 | 11 |
| 7 | Sierra Nevada mountain lake microbial communities are structured by temperature, resources and geographic location. <i>Molecular Ecology</i> , 2020, 29, 2080-2093. | 3.9 | 14 |
| 8 | Silicon limitation facilitates virus infection and mortality of marine diatoms. <i>Nature Microbiology</i> , 2019, 4, 1790-1797. | 13.3 | 64 |
| 9 | Evolution and regulation of nitrogen flux through compartmentalized metabolic networks in a marine diatom. <i>Nature Communications</i> , 2019, 10, 4552. | 12.8 | 116 |
| 10 | Molecular Approaches for an Operational Marine Biodiversity Observation Network. , 2019, , 613-631. | | 5 |
| 11 | Carbonate-sensitive phytoferritin controls high-affinity iron uptake in diatoms. <i>Nature</i> , 2018, 555, 534-537. | 27.8 | 106 |
| 12 | Biosynthesis of the neurotoxin domoic acid in a bloom-forming diatom. <i>Science</i> , 2018, 361, 1356-1358. | 12.6 | 124 |
| 13 | Colony formation in <i>Phaeocystis antarctica</i> : connecting molecular mechanisms with iron biogeochemistry. <i>Biogeosciences</i> , 2018, 15, 4923-4942. | 3.3 | 44 |
| 14 | Tracking the rise of eukaryotes to ecological dominance with zinc isotopes. <i>Geobiology</i> , 2018, 16, 341-352. | 2.4 | 65 |
| 15 | The Baltic Sea Virome: Diversity and Transcriptional Activity of DNA and RNA Viruses. <i>MSystems</i> , 2017, 2, . | 3.8 | 80 |
| 16 | Nitrate Reductase Knockout Uncouples Nitrate Transport from Nitrate Assimilation and Drives Repartitioning of Carbon Flux in a Model Pennate Diatom. <i>Plant Cell</i> , 2017, 29, 2047-2070. | 6.6 | 102 |
| 17 | Contrasting effects of copper limitation on the photosynthetic apparatus in two strains of the open ocean diatom <i>Thalassiosira oceanica</i> . <i>PLoS ONE</i> , 2017, 12, e0181753. | 2.5 | 24 |
| 18 | Genetic Manipulation of Competition for Nitrate between Heterotrophic Bacteria and Diatoms. <i>Frontiers in Microbiology</i> , 2016, 7, 880. | 3.5 | 55 |

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|----|---|------|-----------|
| 19 | Diversity and Expression of Bacterial Metacaspases in an Aquatic Ecosystem. <i>Frontiers in Microbiology</i> , 2016, 7, 1043. | 3.5 | 37 |
| 20 | Genome and methylome of the oleaginous diatom <i>Cyclotella cryptica</i> reveal genetic flexibility toward a high lipid phenotype. <i>Biotechnology for Biofuels</i> , 2016, 9, 258. | 6.2 | 87 |
| 21 | Spectrum of mitochondrial genomic variation and associated clinical presentation of prostate cancer in South African men. <i>Prostate</i> , 2016, 76, 349-358. | 2.3 | 26 |
| 22 | Transcriptional Orchestration of the Global Cellular Response of a Model Pennate Diatom to Diel Light Cycling under Iron Limitation. <i>PLoS Genetics</i> , 2016, 12, e1006490. | 3.5 | 129 |
| 23 | Patterns of Transcript Abundance of Eukaryotic Biogeochemically-Relevant Genes in the Amazon River Plume. <i>PLoS ONE</i> , 2016, 11, e0160929. | 2.5 | 17 |
| 24 | Phytoplankton-bacterial interactions mediate micronutrient colimitation at the coastal Antarctic sea ice edge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9938-9943. | 7.1 | 202 |
| 25 | Genomes and gene expression across light and productivity gradients in eastern subtropical Pacific microbial communities. <i>ISME Journal</i> , 2015, 9, 1076-1092. | 9.8 | 108 |
| 26 | Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. <i>PLoS ONE</i> , 2014, 9, e89549. | 2.5 | 184 |
| 27 | Lineage specific gene family enrichment at the microscale in marine systems. <i>Current Opinion in Microbiology</i> , 2013, 16, 605-617. | 5.1 | 16 |
| 28 | Influence of nutrients and currents on the genomic composition of microbes across an upwelling mosaic. <i>ISME Journal</i> , 2012, 6, 1403-1414. | 9.8 | 120 |
| 29 | Metagenomic Exploration of Viruses throughout the Indian Ocean. <i>PLoS ONE</i> , 2012, 7, e42047. | 2.5 | 113 |
| 30 | A rapid fingerprinting approach to distinguish between closely related strains of <i>Shewanella</i> . <i>Journal of Microbiological Methods</i> , 2011, 86, 62-68. | 1.6 | 5 |
| 31 | Evolution and metabolic significance of the urea cycle in photosynthetic diatoms. <i>Nature</i> , 2011, 473, 203-207. | 27.8 | 453 |
| 32 | Genomic and functional adaptation in surface ocean planktonic prokaryotes. <i>Nature</i> , 2010, 468, 60-66. | 27.8 | 280 |
| 33 | Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14679-14684. | 7.1 | 257 |
| 34 | Alignment of Phylogenetically Unambiguous Indels in <i>Shewanella</i> . <i>Journal of Computational Biology</i> , 2009, 16, 1517-1528. | 1.6 | 3 |