

Michelle A O malley

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

72
papers

2,339
citations

23
h-index

47
g-index

78
ext. papers

3,355
ext. citations

8.4
avg, IF

5.07
L-index

#	Paper	IF	Citations
72	Biofilm disruption enhances growth rate and carbohydrate-active enzyme production in anaerobic fungi. <i>Bioresource Technology</i> , 2022 , 358, 127361	11	0
71	Non-destructive quantification of anaerobic gut fungi and methanogens in co-culture reveals increased fungal growth rate and changes in metabolic flux relative to mono-culture. <i>Microbial Cell Factories</i> , 2021 , 20, 199	6.4	2
70	Microbial communities and their enzymes facilitate degradation of recalcitrant polymers in anaerobic digestion. <i>Current Opinion in Microbiology</i> , 2021 , 64, 100-108	7.9	4
69	Integrating Systems and Synthetic Biology to Understand and Engineer Microbiomes. <i>Annual Review of Biomedical Engineering</i> , 2021 , 23, 169-201	12	9
68	The Anaerobic Fungi: Challenges and Opportunities for Industrial Lignocellulosic Biofuel Production. <i>Microorganisms</i> , 2021 , 9,	4.9	10
67	Anaerobic gut fungi are an untapped reservoir of natural products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	11
66	Ecology and molecular targets of hypermutation in the global microbiome. <i>Nature Communications</i> , 2021 , 12, 3076	17.4	9
65	Cellulosome Localization Patterns Vary across Life Stages of Anaerobic Fungi. <i>MBio</i> , 2021 , 12, e0083221	7.8	1
64	A SWEET surprise: Anaerobic fungal sugar transporters and chimeras enhance sugar uptake in yeast. <i>Metabolic Engineering</i> , 2021 , 66, 137-147	9.7	6
63	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021 , 39, 499-509	44.5	120
62	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. <i>ISME Journal</i> , 2021 , 15, 421-434	11.9	17
61	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. <i>Nature Microbiology</i> , 2021 , 6, 499-511	26.6	23
60	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. <i>MSystems</i> , 2021 , 6,	7.6	10
59	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. <i>MBio</i> , 2021 , 12, e0144221	7.8	0
58	Identification of novel membrane proteins for improved lignocellulose conversion. <i>Current Opinion in Biotechnology</i> , 2021 , 73, 198-204	11.4	1
57	Co-cultivation of the anaerobic fungus <i>Caecomyces churrovii</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. <i>Biotechnology for Biofuels</i> , 2021 , 14, 234	7.8	3
56	Efficient and cost-effective bacterial mRNA sequencing from low input samples through ribosomal RNA depletion. <i>BMC Genomics</i> , 2020 , 21, 717	4.5	3

55	Engineered fluoride sensitivity enables biocontainment and selection of genetically-modified yeasts. <i>Nature Communications</i> , 2020 , 11, 5459	17.4	5
54	An Arduino based automatic pressure evaluation system to quantify growth of non-model anaerobes in culture. <i>AIChE Journal</i> , 2020 , 66, e16540	3.6	3
53	Designing chimeric enzymes inspired by fungal cellulosomes. <i>Synthetic and Systems Biotechnology</i> , 2020 , 5, 23-32	4.2	18
52	Bridging non-overlapping reads illuminates high-order epistasis between distal protein sites in a GPCR. <i>Nature Communications</i> , 2020 , 11, 690	17.4	1
51	The Biotechnological Potential of Anaerobic Gut Fungi 2020 , 413-437		1
50	Genomic and proteomic biases inform metabolic engineering strategies for anaerobic fungi. <i>Metabolic Engineering Communications</i> , 2020 , 10, e00107	6.5	10
49	Lipo-chitooligosaccharides as regulatory signals of fungal growth and development. <i>Nature Communications</i> , 2020 , 11, 3897	17.4	19
48	Nature's recyclers: anaerobic microbial communities drive crude biomass deconstruction. <i>Current Opinion in Biotechnology</i> , 2020 , 62, 38-47	11.4	16
47	Top-Down Enrichment Guides in Formation of Synthetic Microbial Consortia for Biomass Degradation. <i>ACS Synthetic Biology</i> , 2019 , 8, 2174-2185	5.7	30
46	Common principles and best practices for engineering microbiomes. <i>Nature Reviews Microbiology</i> , 2019 , 17, 725-741	22.2	144
45	Co-cultivation of the anaerobic fungus <i>Anaeromyces robustus</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate active enzymes. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2019 , 46, 1427-1433	4.2	19
44	Heterologous transporters from anaerobic fungi bolster fluoride tolerance in. <i>Metabolic Engineering Communications</i> , 2019 , 9, e00091	6.5	11
43	Harnessing Nature's Anaerobes for Biotechnology and Bioprocessing. <i>Annual Review of Chemical and Biomolecular Engineering</i> , 2019 , 10, 105-128	8.9	15
42	Linking omics to function unlocks the biotech potential of non-model fungi. <i>Current Opinion in Systems Biology</i> , 2019 , 14, 9-17	3.2	11
41	Tuning Vector Stability and Integration Frequency Elevates Functional GPCR Production and Homogeneity in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2018 , 7, 1763-1772	5.7	3
40	Methods for Genomic Characterization and Maintenance of Anaerobic Fungi. <i>Methods in Molecular Biology</i> , 2018 , 1775, 53-67	1.4	3
39	Metabolic characterization of anaerobic fungi provides a path forward for bioprocessing of crude lignocellulose. <i>Biotechnology and Bioengineering</i> , 2018 , 115, 874-884	4.9	42
38	Substrate-based differential expression analysis reveals control of biomass degrading enzymes in <i>Pycnoporus cinnabarinus</i> . <i>Biochemical Engineering Journal</i> , 2018 , 130, 83-89	4.2	8

37	In Silico Identification of Microbial Partners to Form Consortia with Anaerobic Fungi. <i>Processes</i> , 2018 , 6, 7	2.9	13
36	Catabolic repression in early-diverging anaerobic fungi is partially mediated by natural antisense transcripts. <i>Fungal Genetics and Biology</i> , 2018 , 121, 1-9	3.9	6
35	Biomass-degrading enzymes are catabolite repressed in anaerobic gut fungi. <i>AIChE Journal</i> , 2018 , 64, 4263-4270	3.6	17
34	Engineering live cell surfaces with functional polymers via cytocompatible controlled radical polymerization. <i>Nature Chemistry</i> , 2017 , 9, 537-545	17.6	273
33	Widespread adenine N6-methylation of active genes in fungi. <i>Nature Genetics</i> , 2017 , 49, 964-968	36.3	181
32	A parts list for fungal cellulosomes revealed by comparative genomics. <i>Nature Microbiology</i> , 2017 , 2, 17087	26.6	111
31	The importance of sourcing enzymes from non-conventional fungi for metabolic engineering and biomass breakdown. <i>Metabolic Engineering</i> , 2017 , 44, 45-59	9.7	29
30	Transcriptomic characterization of : a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus. <i>Biotechnology for Biofuels</i> , 2017 , 10, 305	7.8	33
29	Emerging technologies for protease engineering: New tools to clear out disease. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 33-38	4.9	9
28	Genomic analysis of [methanogenic archaea] reveals a shift towards energy conservation. <i>BMC Genomics</i> , 2017 , 18, 639	4.5	28
27	PCR and Omics Based Techniques to Study the Diversity, Ecology and Biology of Anaerobic Fungi: Insights, Challenges and Opportunities. <i>Frontiers in Microbiology</i> , 2017 , 8, 1657	5.7	64
26	Adenosine A2a receptors form distinct oligomers in protein detergent complexes. <i>FEBS Letters</i> , 2016 , 590, 3295-306	3.8	9
25	Mapping the membrane proteome of anaerobic gut fungi identifies a wealth of carbohydrate binding proteins and transporters. <i>Microbial Cell Factories</i> , 2016 , 15, 212	6.4	17
24	Mitochondrial targeting increases specific activity of a heterologous valine assimilation pathway in. <i>Metabolic Engineering Communications</i> , 2016 , 3, 68-75	6.5	2
23	Intracellular FRET-based Screen for Redesigning the Specificity of Secreted Proteases. <i>ACS Chemical Biology</i> , 2016 , 11, 961-70	4.9	16
22	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. <i>Science</i> , 2016 , 351, 1192-5	33.3	179
21	Robust and effective methodologies for cryopreservation and DNA extraction from anaerobic gut fungi. <i>Anaerobe</i> , 2016 , 38, 39-46	2.8	17
20	Mapping the Membrane Proteome of Anaerobic Gut Fungi using RNA-Seq. <i>Biophysical Journal</i> , 2016 , 110, 58a-59a	2.9	3

19	Fungal diversity notes 253866: taxonomic and phylogenetic contributions to fungal taxa. <i>Fungal Diversity</i> , 2016 , 78, 1-237	17.6	174
18	Microbial communities for bioprocessing: lessons learned from nature. <i>Current Opinion in Chemical Engineering</i> , 2016 , 14, 103-109	5.4	41
17	Driving biomass breakdown through engineered cellulosomes. <i>Bioengineered</i> , 2015 , 6, 204-8	5.7	28
16	Structure and function of G protein-coupled receptor oligomers: implications for drug discovery. <i>Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology</i> , 2015 , 7, 408-27	9.2	18
15	Extracting data from the muck: deriving biological insight from complex microbial communities and non-model organisms with next generation sequencing. <i>Current Opinion in Biotechnology</i> , 2014 , 28, 103-114	11.4	26
14	Anaerobic gut fungi: Advances in isolation, culture, and cellulolytic enzyme discovery for biofuel production. <i>Biotechnology and Bioengineering</i> , 2014 , 111, 1471-82	4.9	84
13	Evaluating expression and catalytic activity of anaerobic fungal fibrolytic enzymes native to <i>Saccharomyces cerevisiae</i> . <i>Environmental Progress and Sustainable Energy</i> , 2012 , 31, 37-46	2.5	20
12	The morphology and composition of cholesterol-rich micellar nanostructures determine transmembrane protein (GPCR) activity. <i>Biophysical Journal</i> , 2011 , 100, L11-3	2.9	37
11	Toward rational design of protein detergent complexes: determinants of mixed micelles that are critical for the in vitro stabilization of a G-protein coupled receptor. <i>Biophysical Journal</i> , 2011 , 101, 1938-48	2.8	38
10	Analysis of adenosine A ₂ receptor stability: effects of ligands and disulfide bonds. <i>Biochemistry</i> , 2010 , 49, 9181-9	3.2	20
9	Progress toward heterologous expression of active G-protein-coupled receptors in <i>Saccharomyces cerevisiae</i> : Linking cellular stress response with translocation and trafficking. <i>Protein Science</i> , 2009 , 18, 2356-70	6.3	45
8	Heterologous GPCR expression: a bottleneck to obtaining crystal structures. <i>Biotechnology Progress</i> , 2007 , 23, 540-7	2.8	96
7	High-level expression in <i>Saccharomyces cerevisiae</i> enables isolation and spectroscopic characterization of functional human adenosine A ₂ receptor. <i>Journal of Structural Biology</i> , 2007 , 159, 166-78	3.4	68
6	Optimization of the human adenosine A ₂ receptor yields in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology Progress</i> , 2006 , 22, 1249-55	2.8	12
5	Optimization of the Human Adenosine A ₂ Receptor Yields in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology Progress</i> , 2006 , 22, 1249-1255	2.8	28
4	Oligomerization of the Human Adenosine A ₂ A Receptor is Driven by the Intrinsically Disordered C-terminus		1
3	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber		1
2	Ecology and molecular targets of hypermutation in the global microbiome		6

1 Co-cultivation of the anaerobic fungus *Caecomyces churrovis* with *Methanobacterium bryantii* enhances transcription of carbohydrate binding modules

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