Michelle A O'malley

List of Publications by Year
in descending order

73 papers	4,121 citations	201674 27 h-index	133252 59 g-index
78 all docs	78 docs citations	78 times ranked	4918 citing authors

#	Article	IF	Citations
1	Identification of novel membrane proteins for improved lignocellulose conversion. Current Opinion in Biotechnology, 2022, 73, 198-204.	6.6	2
2	GPCR-FEX: A Fluoride-Based Selection System for Rapid GPCR Screening and Engineering. ACS Synthetic Biology, 2022, 11, 39-45.	3.8	1
3	Biofilm disruption enhances growth rate and carbohydrate-active enzyme production in anaerobic fungi. Bioresource Technology, 2022, 358, 127361.	9.6	5
4	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
5	Proteome specialization of anaerobic fungi during ruminal degradation of recalcitrant plant fiber. ISME Journal, 2021, 15, 421-434.	9.8	46
6	Genomic and functional analyses of fungal and bacterial consortia that enable lignocellulose breakdown in goat gut microbiomes. Nature Microbiology, 2021, 6, 499-511.	13.3	116
7	Oligomerization of the Human Adenosine A2AReceptor is Driven by the Intrinsically Disordered C-Terminus. Biophysical Journal, 2021, 120, 91a.	0.5	0
8	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. MSystems, 2021, 6, .	3.8	33
9	Integrating Systems and Synthetic Biology to Understand and Engineer Microbiomes. Annual Review of Biomedical Engineering, 2021, 23, 169-201.	12.3	23
10	The Anaerobic Fungi: Challenges and Opportunities for Industrial Lignocellulosic Biofuel Production. Microorganisms, 2021, 9, 694.	3.6	33
11	Anaerobic gut fungi are an untapped reservoir of natural products. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
12	Ecology and molecular targets of hypermutation in the global microbiome. Nature Communications, 2021, 12, 3076.	12.8	35
13	Cellulosome Localization Patterns Vary across Life Stages of Anaerobic Fungi. MBio, 2021, 12, e0083221.	4.1	8
14	A SWEET surprise: Anaerobic fungal sugar transporters and chimeras enhance sugar uptake in yeast. Metabolic Engineering, 2021, 66, 137-147.	7.0	19
15	A Genomic Catalog of Stress Response Genes in Anaerobic Fungi for Applications in Bioproduction. Frontiers in Fungal Biology, 2021, 2, .	2.0	1
16	Cocultivation of Anaerobic Fungi with Rumen Bacteria Establishes an Antagonistic Relationship. MBio, 2021, 12, e0144221.	4.1	12
17	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. Microbial Cell Factories, 2021, 20, 199.	4.0	7
18	Microbial communities and their enzymes facilitate degradation of recalcitrant polymers in anaerobic digestion. Current Opinion in Microbiology, 2021, 64, 100-108.	5.1	29

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19	Coâ€cultivation of the anaerobic fungus Caecomyces churrovis with Methanobacterium bryantii enhances transcription of carbohydrate binding modules, dockerins, and pyruvate formate lyases on specific substrates. Biotechnology for Biofuels, 2021, 14, 234.	6.2	21
20	Natureâ€™s recyclers: anaerobic microbial communities drive crude biomass deconstruction. Current Opinion in Biotechnology, 2020, 62, 38-47.	6.6	35
21	Genomic and proteomic biases inform metabolic engineering strategies for anaerobic fungi. Metabolic Engineering Communications, 2020, 10, e00107.	3.6	18
22	Lipo-chitooligosaccharides as regulatory signals of fungal growth and development. Nature Communications, 2020, 11, 3897.	12.8	65
23	Efficient and cost-effective bacterial mRNA sequencing from low input samples through ribosomal RNA depletion. BMC Genomics, 2020, 21, 717.	2.8	22
24	Engineered fluoride sensitivity enables biocontainment and selection of genetically-modified yeasts. Nature Communications, 2020, 11, 5459.	12.8	12
25	An Arduino based automatic pressure evaluation system to quantify growth of nonâ€model anaerobes in culture. AIChE Journal, 2020, 66, e16540.	3.6	6
26	Designing chimeric enzymes inspired by fungal cellulosomes. Synthetic and Systems Biotechnology, 2020, 5, 23-32.	3.7	34
27	Bridging non-overlapping reads illuminates high-order epistasis between distal protein sites in a GPCR. Nature Communications, 2020, 11, 690.	12.8	5
28	Human Adenosine A2AR Dimerization is Driven by a C-terminal Motif. Biophysical Journal, 2020, 118, 13a.	0.5	0
29	17 The Biotechnological Potential of Anaerobic Gut Fungi. , 2020, , 413-437.		3
30	Top-Down Enrichment Guides in Formation of Synthetic Microbial Consortia for Biomass Degradation. ACS Synthetic Biology, 2019, 8, 2174-2185.	3.8	74
31	Common principles and best practices for engineering microbiomes. Nature Reviews Microbiology, 2019, 17, 725-741.	28.6	324
32	Dimerization of Human Adenosine A2AReceptor - Impact of the C-Terminus. Biophysical Journal, 2019, 116, 52a-53a.	0.5	0
33	Co-cultivation of the anaerobic fungus <i>Anaeromyces robustus</i> with <i>Methanobacterium bryantii</i> enhances transcription of carbohydrate active enzymes. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1427-1433.	3.0	32
34	Heterologous transporters from anaerobic fungi bolster fluoride tolerance in Saccharomyces cerevisiae. Metabolic Engineering Communications, 2019, 9, e00091.	3.6	15
35	Harnessing Nature's Anaerobes for Biotechnology and Bioprocessing. Annual Review of Chemical and Biomolecular Engineering, 2019, 10, 105-128.	6.8	22
36	Linking â€˜omicsâ€™ to function unlocks the biotech potential of non-model fungi. Current Opinion in Systems Biology, 2019, 14, 9-17.	2.6	18

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37	Metabolic characterization of anaerobic fungi provides a path forward for bioprocessing of crude lignocellulose. Biotechnology and Bioengineering, 2018, 115, 874-884.	3.3	57
38	Substrate-based differential expression analysis reveals control of biomass degrading enzymes in Pycnoporus cinnabarinus. Biochemical Engineering Journal, 2018, 130, 83-89.	3.6	12
39	In Silico Identification of Microbial Partners to Form Consortia with Anaerobic Fungi. Processes, 2018, 6, 7.	2.8	17
40	Catabolic repression in early-diverging anaerobic fungi is partially mediated by natural antisense transcripts. Fungal Genetics and Biology, 2018, 121, 1-9.	2.1	8
41	Biomassâ€degrading enzymes are catabolite repressed in anaerobic gut fungi. AICHE Journal, 2018, 64, 4263-4270.	3.6	25
42	Tuning Vector Stability and Integration Frequency Elevates Functional GPCR Production and Homogeneity in <i>Saccharomyces cerevisiae</i>. ACS Synthetic Biology, 2018, 7, 1763-1772.	3.8	6
43	Methods for Genomic Characterization and Maintenance of Anaerobic Fungi. Methods in Molecular Biology, 2018, 1775, 53-67.	0.9	7
44	Engineering live cell surfaces with functional polymers via cytocompatible controlled radical polymerization. Nature Chemistry, 2017, 9, 537-545.	13.6	353
45	Widespread adenine N6-methylation of active genes in fungi. Nature Genetics, 2017, 49, 964-968.	21.4	292
46	A parts list for fungal cellulosomes revealed by comparative genomics. Nature Microbiology, 2017, 2, 17087.	13.3	183
47	The importance of sourcing enzymes from non-conventional fungi for metabolic engineering and biomass breakdown. Metabolic Engineering, 2017, 44, 45-59.	7.0	43
48	Emerging technologies for protease engineering: New tools to clear out disease. Biotechnology and Bioengineering, 2017, 114, 33-38.	3.3	19
49	Genomic analysis ofÂmethanogenic archaeaÂreveals a shift towards energy conservation. BMC Genomics, 2017, 18, 639.	2.8	41
50	PCR and Omics Based Techniques to Study the Diversity, Ecology and Biology of Anaerobic Fungi: Insights, Challenges and Opportunities. Frontiers in Microbiology, 2017, 8, 1657.	3.5	118
51	Transcriptomic characterization of Caecomyces churrovis: a novel, non-rhizoid-forming lignocellulolytic anaerobic fungus. Biotechnology for Biofuels, 2017, 10, 305.	6.2	70
52	Fungal diversity notes 253â€"366: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity, 2016, 78, 1-237.	12.3	239
53	Microbial communities for bioprocessing: lessons learned from nature. Current Opinion in Chemical Engineering, 2016, 14, 103-109.	7.8	57
54	Adenosine A2a receptors form distinct oligomers in protein detergent complexes. FEBS Letters, 2016, 590, 3295-3306.	2.8	12

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55	Mapping the membrane proteome of anaerobic gut fungi identifies a wealth of carbohydrate binding proteins and transporters. Microbial Cell Factories, 2016, 15, 212.	4.0	21
56	Mitochondrial targeting increases specific activity of a heterologous valine assimilation pathway in Saccharomyces cerevisiae. Metabolic Engineering Communications, 2016, 3, 68-75.	3.6	2
57	Intracellular FRET-based Screen for Redesigning the Specificity of Secreted Proteases. ACS Chemical Biology, 2016, 11, 961-970.	3.4	28
58	Early-branching gut fungi possess a large, comprehensive array of biomass-degrading enzymes. Science, 2016, 351, 1192-1195.	12.6	266
59	Robust and effective methodologies for cryopreservation and DNA extraction from anaerobic gut fungi. Anaerobe, 2016, 38, 39-46.	2.1	24
60	Mapping the Membrane Proteome of Anaerobic Gut Fungi using RNA-Seq. Biophysical Journal, 2016, 110, 58a-59a.	0.5	3
61	Driving biomass breakdown through engineered cellulosomes. Bioengineered, 2015, 6, 204-208.	3.2	37
62	Structure and function of G proteinâ€coupled receptor oligomers: implications for drug discovery. Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology, 2015, 7, 408-427.	6.1	22
63	Extracting data from the muck: deriving biological insight from complex microbial communities and non-model organisms with next generation sequencing. Current Opinion in Biotechnology, 2014, 28, 103-110.	6.6	31
64	Anaerobic gut fungi: Advances in isolation, culture, and cellulolytic enzyme discovery for biofuel production. Biotechnology and Bioengineering, 2014, 111, 1471-1482.	3.3	136
65	Evaluating expression and catalytic activity of anaerobic fungal fibrolytic enzymes native to<i>piromyces sp E2</i> in<i>Saccharomyces cerevisiae</i>. Environmental Progress and Sustainable Energy, 2012, 31, 37-46.	2.3	27
66	The Morphology and Composition of Cholesterol-Rich Micellar Nanostructures Determine Transmembrane Protein (GPCR) Activity. Biophysical Journal, 2011, 100, L11-L13.	0.5	39
67	Toward Rational Design of Protein Detergent Complexes: Determinants of Mixed Micelles That Are Critical for the InÂVitro Stabilization of a G-Protein Coupled Receptor. Biophysical Journal, 2011, 101, 1938-1948.	0.5	41
68	Analysis of Adenosine A₂a Receptor Stability: Effects of Ligands and Disulfide Bonds. Biochemistry, 2010, 49, 9181-9189.	2.5	20
69	Progress toward heterologous expression of active Gâ€proteinâ€coupled receptors in <i>Saccharomyces cerevisiae</i>: Linking cellular stress response with translocation and trafficking. Protein Science, 2009, 18, 2356-2370.	7.6	57
70	Optimization of the Human Adenosine A2a Receptor Yields in Saccharomyces cerevisiae. Biotechnology Progress, 2008, 22, 1249-1255.	2.6	14
71	Heterologous GPCR Expression: A Bottleneck to Obtaining Crystal Structures. Biotechnology Progress, 2008, 23, 540-547.	2.6	108
72	High-level expression in Saccharomyces cerevisiae enables isolation and spectroscopic characterization of functional human adenosine A2a receptor. Journal of Structural Biology, 2007, 159, 166-178.	2.8	75

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73	Optimization of the Human Adenosine A2a Receptor Yields inSaccharomyces cerevisiae. Biotechnology Progress, 2006, 22, 1249-1255.	2.6	31