

# Kyle R Pomraning

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11560815/publications.pdf>

Version: 2024-02-01

19  
papers

1,087  
citations

687363

13  
h-index

752698

20  
g-index

21  
all docs

21  
docs citations

21  
times ranked

1808  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetically Engineered Oleaginous Yeast <i>Lipomyces starkeyi</i> for Sesquiterpene $\hat{\pm}$ -Zingiberene Production. <i>ACS Synthetic Biology</i> , 2021, 10, 1000-1008.	3.8	5
2	Integration of Proteomics and Metabolomics Into the Design, Build, Test, Learn Cycle to Improve 3-Hydroxypropionic Acid Production in <i>Aspergillus pseudoterreus</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 603832.	4.1	12
3	Bayesian Inference for Integrating <i>Yarrowia lipolytica</i> Multiomics Datasets with Metabolic Modeling. <i>ACS Synthetic Biology</i> , 2021, 10, 2968-2981.	3.8	4
4	Deletion analysis of the itaconic acid biosynthesis gene cluster components in <i>Aspergillus pseudoterreus</i> ATCC32359. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 3981-3992.	3.6	10
5	Deletion of the KU70 homologue facilitates gene targeting in <i>Lipomyces starkeyi</i> strain NRRL Y-11558. <i>Current Genetics</i> , 2019, 65, 269-282.	1.7	9
6	Transcriptomic analysis of the oleaginous yeast <i>Lipomyces starkeyi</i> during lipid accumulation on enzymatically treated corn stover hydrolysate. <i>Biotechnology for Biofuels</i> , 2019, 12, 162.	6.2	24
7	A molecular genetic toolbox for <i>Yarrowia lipolytica</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 2.	6.2	62
8	Regulation of Nitrogen Metabolism by GATA Zinc Finger Transcription Factors in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2017, 2, .	2.9	29
9	Multimodal microfluidic platform for controlled culture and analysis of unicellular organisms. <i>Biomicrofluidics</i> , 2017, 11, 054104.	2.4	4
10	Omics Analyses of <i>Trichoderma reesei</i> CBS999.97 and QM6a Indicate the Relevance of Female Fertility to Carbohydrate-Active Enzyme and Transporter Levels. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	22
11	Multi-omics analysis reveals regulators of the response to nitrogen limitation in <i>Yarrowia lipolytica</i> . <i>BMC Genomics</i> , 2016, 17, 138.	2.8	62
12	The Genomes of Three Uneven Siblings: Footprints of the Lifestyles of Three <i>Trichoderma</i> Species. <i>Microbiology and Molecular Biology Reviews</i> , 2016, 80, 205-327.	6.6	194
13	Comprehensive Metabolomic, Lipidomic and Microscopic Profiling of <i>Yarrowia lipolytica</i> during Lipid Accumulation Identifies Targets for Increased Lipogenesis. <i>PLoS ONE</i> , 2015, 10, e0123188.	2.5	54
14	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	7.3	173
15	Bacterial Resistance to Antisense Peptide Phosphorodiamidate Morpholino Oligomers. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 6147-6153.	3.2	41
16	Library Preparation and Data Analysis Packages for Rapid Genome Sequencing. <i>Methods in Molecular Biology</i> , 2012, 944, 1-22.	0.9	17
17	Heterochromatin Is Required for Normal Distribution of <i>Neurospora crassa</i> CenH3. <i>Molecular and Cellular Biology</i> , 2011, 31, 2528-2542.	2.3	107
18	Bulk Segregant Analysis Followed by High-Throughput Sequencing Reveals the <i>Neurospora</i> Cell Cycle Gene, <i>ndc-1</i> , To Be Allelic with the Gene for Ornithine Decarboxylase, <i>spe-1</i> . <i>Eukaryotic Cell</i> , 2011, 10, 724-733.	3.4	67

#	ARTICLE	IF	CITATIONS
19	Genome-wide high throughput analysis of DNA methylation in eukaryotes. <i>Methods</i> , 2009, 47, 142-150.	3.8	178