

# Megan Bergkessel

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4564368/publications.pdf>

Version: 2024-02-01

20  
papers

1,230  
citations

623734

14  
h-index

752698

20  
g-index

24  
all docs

24  
docs citations

24  
times ranked

1842  
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity in Starvation Survival Strategies and Outcomes among Heterotrophic Proteobacteria. <i>Microbial Physiology</i> , 2021, 31, 146-162.	2.4	18
2	Bacterial defenses against a natural antibiotic promote collateral resilience to clinical antibiotics. <i>PLoS Biology</i> , 2021, 19, e3001093.	5.6	31
3	Bacterial transcription during growth arrest. <i>Transcription</i> , 2021, 12, 232-249.	3.1	7
4	Regulation of protein biosynthetic activity during growth arrest. <i>Current Opinion in Microbiology</i> , 2020, 57, 62-69.	5.1	12
5	Aggregation of Nontuberculous Mycobacteria Is Regulated by Carbon-Nitrogen Balance. <i>MBio</i> , 2019, 10, .	4.1	19
6	The dormancy-specific regulator, SutA, is intrinsically disordered and modulates transcription initiation in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2019, 112, 992-1009.	2.5	11
7	Identification of Fitness Determinants during Energy-Limited Growth Arrest in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2017, 8, .	4.1	45
8	The physiology of growth arrest: uniting molecular and environmental microbiology. <i>Nature Reviews Microbiology</i> , 2016, 14, 549-562.	28.6	176
9	Evolutionarily Conserved Polyadenosine RNA Binding Protein Nab2 Cooperates with Splicing Machinery To Regulate the Fate of Pre-mRNA. <i>Molecular and Cellular Biology</i> , 2016, 36, 2697-2714.	2.3	50
10	SutA is a bacterial transcription factor expressed during slow growth in <i>Pseudomonas aeruginosa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E597-605.	7.1	52
11	Enzymatic Degradation of Phenazines Can Generate Energy and Protect Sensitive Organisms from Toxicity. <i>MBio</i> , 2015, 6, e01520-15.	4.1	52
12	Colony PCR. <i>Methods in Enzymology</i> , 2013, 529, 299-309.	1.0	62
13	Yeast-Gene Replacement Using PCR Products. <i>Methods in Enzymology</i> , 2013, 533, 43-55.	1.0	4
14	Chemical Transformation of Yeast. <i>Methods in Enzymology</i> , 2013, 529, 311-320.	1.0	11
15	Diverse environmental stresses elicit distinct responses at the level of pre-mRNA processing in yeast. <i>Rna</i> , 2011, 17, 1461-1478.	3.5	55
16	SnapShot: Formation of mRNPs. <i>Cell</i> , 2009, 136, 794-794.e1.	28.9	2
17	A Genetic Interaction Map of RNA-Processing Factors Reveals Links between Sem1/Dss1-Containing Complexes and mRNA Export and Splicing. <i>Molecular Cell</i> , 2008, 32, 735-746.	9.7	221
18	Transcript Specificity in Yeast Pre-mRNA Splicing Revealed by Mutations in Core Spliceosomal Components. <i>PLoS Biology</i> , 2007, 5, e90.	5.6	168

#	ARTICLE	IF	CITATIONS
19	Rapid, Transcript-Specific Changes in Splicing in Response to Environmental Stress. <i>Molecular Cell</i> , 2007, 27, 928-937.	9.7	202
20	An Essential Role for the <i>Saccharomyces cerevisiae</i> DEAD-Box Helicase DHH1 in G1/S DNA-Damage Checkpoint Recovery. <i>Genetics</i> , 2004, 167, 21-33.	2.9	30