

# Andrew J Gasparrini

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4574552/publications.pdf>

Version: 2024-02-01

11  
papers

1,197  
citations

933447

10  
h-index

1372567

10  
g-index

11  
all docs

11  
docs citations

11  
times ranked

1929  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tetracycline-inactivating enzymes from environmental, human commensal, and pathogenic bacteria cause broad-spectrum tetracycline resistance. <i>Communications Biology</i> , 2020, 3, 241.	4.4	97
2	Maternal activation of the EGFR prevents translocation of gut-residing pathogenic <i>Escherichia coli</i> in a model of late-onset neonatal sepsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7941-7949.	7.1	35
3	Persistent metagenomic signatures of early-life hospitalization and antibiotic treatment in the infant gut microbiota and resistome. <i>Nature Microbiology</i> , 2019, 4, 2285-2297.	13.3	191
4	Semisynthetic Analogues of Anhydrotetracycline as Inhibitors of Tetracycline Destructase Enzymes. <i>ACS Infectious Diseases</i> , 2019, 5, 618-633.	3.8	24
5	Adaptive Strategies of the Candidate Probiotic <i>E. coli</i> Nissle in the Mammalian Gut. <i>Cell Host and Microbe</i> , 2019, 25, 499-512.e8.	11.0	94
6	Multiscale Evolutionary Dynamics of Host-Associated Microbiomes. <i>Cell</i> , 2018, 172, 1216-1227.	28.9	85
7	Plasticity, dynamics, and inhibition of emerging tetracycline resistance enzymes. <i>Nature Chemical Biology</i> , 2017, 13, 730-736.	8.0	93
8	Next-generation approaches to understand and combat the antibiotic resistome. <i>Nature Reviews Microbiology</i> , 2017, 15, 422-434.	28.6	438
9	Genomic and functional techniques to mine the microbiome for novel antimicrobials and antimicrobial resistance genes. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 42-58.	3.8	38
10	Antibiotic perturbation of the preterm infant gut microbiome and resistome. <i>Gut Microbes</i> , 2016, 7, 443-449.	9.8	102
11	Identifying Potential Drivers of Differential DNA Methylation Patterns in Breast Cancer Cells. <i>FASEB Journal</i> , 2015, 29, LB143.	0.5	0