

# Ruth R Miller

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10410582/publications.pdf>

Version: 2024-02-01

17  
papers

1,064  
citations

759233

12  
h-index

888059

17  
g-index

17  
all docs

17  
docs citations

17  
times ranked

2039  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole blood human transcriptome and virome analysis of ME/CFS patients experiencing post-exertional malaise following cardiopulmonary exercise testing. <i>PLoS ONE</i> , 2019, 14, e0212193.	2.5	22
2	Immunosignature Analysis of Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS). <i>Molecular Neurobiology</i> , 2019, 56, 4249-4257.	4.0	17
3	RNA-Seq Analysis of Gene Expression, Viral Pathogen, and B-Cell/T-Cell Receptor Signatures in Complex Chronic Disease. <i>Clinical Infectious Diseases</i> , 2017, 64, 476-481.	5.8	21
4	Genomic Analysis of a Serotype 5 <i>Streptococcus pneumoniae</i> Outbreak in British Columbia, Canada, 2005–2009. <i>Canadian Journal of Infectious Diseases and Medical Microbiology</i> , 2016, 2016, 1-7.	1.9	6
5	Metagenomic Investigation of Plasma in Individuals with ME/CFS Highlights the Importance of Technical Controls to Elucidate Contamination and Batch Effects. <i>PLoS ONE</i> , 2016, 11, e0165691.	2.5	15
6	Brain-derived neurotrophic factor concentration may not be depressed in chronic fatigue syndrome. <i>Fatigue: Biomedicine, Health and Behavior</i> , 2015, 3, 122-125.	1.9	1
7	Submaximal exercise testing with near-infrared spectroscopy in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome patients compared to healthy controls: a case–control study. <i>Journal of Translational Medicine</i> , 2015, 13, 159.	4.4	4
8	Lyme Disease Diagnosed by Alternative Methods: A Phenotype Similar to That of Chronic Fatigue Syndrome. <i>Clinical Infectious Diseases</i> , 2015, 61, 1084-1091.	5.8	38
9	Whole-Genome Sequencing of Three Clonal Clinical Isolates of <i>B. cenocepacia</i> from a Patient with Cystic Fibrosis. <i>PLoS ONE</i> , 2015, 10, e0143472.	2.5	9
10	Carriage of Methicillin-Resistant <i>Staphylococcus aureus</i> by Wild Urban Norway Rats ( <i>Rattus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 382 T	2.5	46
11	Mobile elements drive recombination hotspots in the core genome of <i>Staphylococcus aureus</i> . <i>Nature Communications</i> , 2014, 5, 3956.	12.8	128
12	Dynamics of acquisition and loss of carriage of <i>Staphylococcus aureus</i> strains in the community: The effect of clonal complex. <i>Journal of Infection</i> , 2014, 68, 426-439.	3.3	42
13	Prevalence of <i>Staphylococcus aureus</i> protein A ( <i>spa</i> ) mutants in the community and hospitals in Oxfordshire. <i>BMC Microbiology</i> , 2014, 14, 63.	3.3	72
14	Metagenomics for pathogen detection in public health. <i>Genome Medicine</i> , 2013, 5, 81.	8.2	202
15	A metagenomic approach to investigate the microbial causes of myalgic encephalomyelitis/chronic fatigue syndrome: moving beyond XMRV. <i>Fatigue: Biomedicine, Health and Behavior</i> , 2013, 1, 185-189.	1.9	3
16	Within-Host Evolution of <i>Staphylococcus aureus</i> during Asymptomatic Carriage. <i>PLoS ONE</i> , 2013, 8, e61319.	2.5	194
17	Evolutionary dynamics of <i>Staphylococcus aureus</i> during progression from carriage to disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4550-4555.	7.1	244