

# Mette Voldby Larsen

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17  
papers

6,062  
citations

14  
h-index

17  
g-index

17  
ext. papers

9,032  
ext. citations

4.4  
avg, IF

5.51  
L-index

#	Paper	IF	Citations
17	Identification of acquired antimicrobial resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2012</b> , 67, 2640-4	5.1	2855
16	In silico detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2014</b> , 58, 3895-903	5.9	1908
15	An integrative approach to CTL epitope prediction: a combined algorithm integrating MHC class I binding, TAP transport efficiency, and proteasomal cleavage predictions. <i>European Journal of Immunology</i> , <b>2005</b> , 35, 2295-303	6.1	229
14	Genotyping using whole-genome sequencing is a realistic alternative to surveillance based on phenotypic antimicrobial susceptibility testing. <i>Journal of Antimicrobial Chemotherapy</i> , <b>2013</b> , 68, 771-7	5.1	216
13	NetCTLpan: pan-specific MHC class I pathway epitope predictions. <i>Immunogenetics</i> , <b>2010</b> , 62, 357-68	3.2	205
12	PathogenFinder--distinguishing friend from foe using bacterial whole genome sequence data. <i>PLoS ONE</i> , <b>2013</b> , 8, e77302	3.7	178
11	Applying the ResFinder and VirulenceFinder web-services for easy identification of acquired antibiotic resistance and virulence genes in bacteriophage and prophage nucleotide sequences. <i>Bacteriophage</i> , <b>2014</b> , 4, e27943		155
10	A Bacterial Analysis Platform: An Integrated System for Analysing Bacterial Whole Genome Sequencing Data for Clinical Diagnostics and Surveillance. <i>PLoS ONE</i> , <b>2016</b> , 11, e0157718	3.7	103
9	HostPhinder: A Phage Host Prediction Tool. <i>Viruses</i> , <b>2016</b> , 8,	6.2	63
8	Metagenomic Analysis of Therapeutic PYO Phage Cocktails from 1997 to 2014. <i>Viruses</i> , <b>2017</b> , 9,	6.2	36
7	MetaPhinder-Identifying Bacteriophage Sequences in Metagenomic Data Sets. <i>PLoS ONE</i> , <b>2016</b> , 11, e0163111	3.7	32
6	Identification of CD8+ T cell epitopes in the West Nile virus polyprotein by reverse-immunology using NetCTL. <i>PLoS ONE</i> , <b>2010</b> , 5, e12697	3.7	29
5	Human leukocyte antigen (HLA) class I restricted epitope discovery in yellow fever and dengue viruses: importance of HLA binding strength. <i>PLoS ONE</i> , <b>2011</b> , 6, e26494	3.7	26
4	TAP-Independent MHC Class I Presentation. <i>Current Immunology Reviews</i> , <b>2006</b> , 2, 233-245	1.3	18
3	Internet-based solutions for analysis of next-generation sequence data. <i>Journal of Clinical Microbiology</i> , <b>2013</b> , 51, 3162	9.7	4
2	The CGE Tool Box <b>2017</b> , 65-90		3
1	Bioinformatics identification of antigenic peptide: predicting the specificity of major MHC class I and II pathway players. <i>Methods in Molecular Biology</i> , <b>2013</b> , 960, 247-260	1.4	2

