Mette Voldby Larsen

List of Publications by Year in Descending Order

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