

Thomas Nordahl Petersen

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

14,868
citations

430874

18
h-index

552781

26
g-index

29
all docs

29
docs citations

29
times ranked

26522
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Distribution of <i>mcr</i> Gene Variants in 214K Metagenomic Samples. <i>MSystems</i> , 2022, 7, e0010522.	3.8	17
2	Detection of mobile genetic elements associated with antibiotic resistance in <i>Salmonella enterica</i> using a newly developed web tool: MobileElementFinder. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 101-109.	3.0	274
3	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	17.5	251
4	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. <i>Microorganisms</i> , 2020, 8, 1861.	3.6	4
5	Data integration for prediction of weight loss in randomized controlled dietary trials. <i>Scientific Reports</i> , 2020, 10, 20103.	3.3	10
6	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. <i>Frontiers in Microbiology</i> , 2020, 11, 575377.	3.5	7
7	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. <i>Communications Biology</i> , 2020, 3, 155.	4.4	33
8	Metagenomics-Based Approach to Source-Attribution of Antimicrobial Resistance Determinants – Identification of Reservoir Resistome Signatures. <i>Frontiers in Microbiology</i> , 2020, 11, 601407.	3.5	29
9	Proficiency Testing of Virus Diagnostics Based on Bioinformatics Analysis of Simulated <i>In Silico</i> High-Throughput Sequencing Data Sets. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	34
10	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	12.8	612
11	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	17.5	3,317
12	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. <i>Nature Microbiology</i> , 2018, 3, 898-908.	13.3	230
13	Protein features as determinants of wild-type glycoside hydrolase thermostability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2036-2044.	2.6	5
14	MGmapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. <i>PLoS ONE</i> , 2017, 12, e0176469.	2.5	66
15	Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance. <i>Scientific Reports</i> , 2015, 5, 11444.	3.3	74
16	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1819-1828.	2.6	36
17	Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. <i>PLoS ONE</i> , 2013, 8, e68370.	2.5	20
18	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011, 8, 785-786.	19.0	8,521

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19	A Systematic Study of Site-specific GalNAc-type O-Glycosylation Modulating Proprotein Convertase Processing. <i>Journal of Biological Chemistry</i> , 2011, 286, 40122-40132.	3.4	93
20	NetTurnP – Neural Network Prediction of Beta-turns by Use of Evolutionary Information and Predicted Protein Sequence Features. <i>PLoS ONE</i> , 2010, 5, e15079.	2.5	83
21	CPHmodels-3.0 – remote homology modeling using structure-guided sequence profiles. <i>Nucleic Acids Research</i> , 2010, 38, W576-W581.	14.5	305
22	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009, 9, 51.	2.3	555
23	Prediction of protein secondary structure at 80% accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 17-20.	2.6	112
24	The crystal structure of rhamnogalacturonase A from <i>Aspergillus aculeatus</i> : a right-handed parallel β^2 helix. <i>Structure</i> , 1997, 5, 533-544.	3.3	145