

Thomas Nordahl Petersen

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

14,868
citations

430442

18
h-index

552369

26
g-index

29
all docs

29
docs citations

29
times ranked

26522
citing authors

#	ARTICLE	IF	CITATIONS
1	SignalP 4.0: discriminating signal peptides from transmembrane regions. <i>Nature Methods</i> , 2011, 8, 785-786.	9.0	8,521
2	SignalP 5.0 improves signal peptide predictions using deep neural networks. <i>Nature Biotechnology</i> , 2019, 37, 420-423.	9.4	3,317
3	Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. <i>Nature Communications</i> , 2019, 10, 1124.	5.8	612
4	A generic method for assignment of reliability scores applied to solvent accessibility predictions. <i>BMC Structural Biology</i> , 2009, 9, 51.	2.3	555
5	CPHmodels-3.0: remote homology modeling using structure-guided sequence profiles. <i>Nucleic Acids Research</i> , 2010, 38, W576-W581.	6.5	305
6	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.	1.3	274
7	Improved metagenome binning and assembly using deep variational autoencoders. <i>Nature Biotechnology</i> , 2021, 39, 555-560.	9.4	251
8	Abundance and diversity of the faecal resistome in slaughter pigs and broilers in nine European countries. <i>Nature Microbiology</i> , 2018, 3, 898-908.	5.9	230
9	The crystal structure of rhamnogalacturonase A from <i>Aspergillus aculeatus</i> : a right-handed parallel β helix. <i>Structure</i> , 1997, 5, 533-544.	1.6	145
10	Prediction of protein secondary structure at 80% accuracy. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 17-20.	1.5	112
11	A Systematic Study of Site-specific GalNAc-type O-Glycosylation Modulating Proprotein Convertase Processing. <i>Journal of Biological Chemistry</i> , 2011, 286, 40122-40132.	1.6	93
12	NetTurnP: Neural Network Prediction of Beta-turns by Use of Evolutionary Information and Predicted Protein Sequence Features. <i>PLoS ONE</i> , 2010, 5, e15079.	1.1	83
13	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.	1.6	74
14	MGMapper: Reference based mapping and taxonomy annotation of metagenomics sequence reads. <i>PLoS ONE</i> , 2017, 12, e0176469.	1.1	66
15	Cofactory: Sequence-based prediction of cofactor specificity of Rossmann folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1819-1828.	1.5	36
16	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, .	1.8	34
17	The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children. <i>Communications Biology</i> , 2020, 3, 155.	2.0	33
18	Metagenomics-Based Approach to Source-Attribution of Antimicrobial Resistance Determinants: Identification of Reservoir Resistome Signatures. <i>Frontiers in Microbiology</i> , 2020, 11, 601407.	1.5	29

#	ARTICLE	IF	CITATIONS
19	Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. PLoS ONE, 2013, 8, e68370.	1.1	20
20	Global Distribution of <i>mcr</i> Gene Variants in 214K Metagenomic Samples. MSystems, 2022, 7, e0010522.	1.7	17
21	Data integration for prediction of weight loss in randomized controlled dietary trials. Scientific Reports, 2020, 10, 20103.	1.6	10
22	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	1.5	7
23	Protein features as determinants of wild-type glycoside hydrolase thermostability. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2036-2044.	1.5	5
24	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	1.6	4