MichaÅ, Burdukiewicz

List of Publications by Year in descending order

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687363 642732 28 621 13 23 citations g-index h-index papers 32 32 32 970 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	A systematic review and meta-analysis of the epidemiology of pathogenic Escherichia coli of calves and the role of calves as reservoirs for human pathogenic E. coli. Frontiers in Cellular and Infection Microbiology, 2015, 5, 23.	3.9	99
2	Genotypic and Phenotypic Characteristics Associated with Biofilm Formation by Human Clinical Escherichia coli Isolates of Different Pathotypes. Applied and Environmental Microbiology, 2017, 83, .	3.1	65
3	Proteomic Screening for Prediction and Design of Antimicrobial Peptides with AmpGram. International Journal of Molecular Sciences, 2020, 21, 4310.	4.1	59
4	Amyloidogenic motifs revealed by n-gram analysis. Scientific Reports, 2017, 7, 12961.	3.3	52
5	Classification of dead and living microalgae Chlorella vulgaris by bioimage informatics and machine learning. Algal Research, 2020, 48, 101908.	4.6	34
6	Simultaneous detection and quantification of DNA and protein biomarkers in spectrum of cardiovascular diseases in a microfluidic microbead chip. Analytical and Bioanalytical Chemistry, 2019, 411, 7725-7735.	3.7	32
7	Impact of Smoothing on Parameter Estimation in Quantitative DNA Amplification Experiments. Clinical Chemistry, 2015, 61, 379-388.	3.2	31
8	chipPCR: an R package to pre-process raw data of amplification curves. Bioinformatics, 2015, 31, 2900-2902.	4.1	29
9	PhyMet ² : a database and toolkit for phylogenetic and metabolic analyses of methanogens. Environmental Microbiology Reports, 2018, 10, 378-382.	2.4	24
10	Adhesion of Salmonella to Pancreatic Secretory Granule Membrane Major Glycoprotein GP2 of Human and Porcine Origin Depends on FimH Sequence Variation. Frontiers in Microbiology, 2018, 9, 1905.	3.5	21
11	MIRRAGGE – Minimum Information Required for Reproducible AGGregation Experiments. Frontiers in Molecular Neuroscience, 2020, 13, 582488.	2.9	19
12	CancerGram: An Effective Classifier for Differentiating Anticancer from Antimicrobial Peptides. Pharmaceutics, 2020, 12, 1045.	4.5	19
13	R as an Environment for Reproducible Analysis of DNA Amplification Experiments. R Journal, 2015, 7, 127.	1.8	19
14	System-specific periodicity in quantitative real-time polymerase chain reaction data questions threshold-based quantitation. Scientific Reports, 2016, 6, 38951.	3.3	16
15	HaDeX: an R package and web-server for analysis of data from hydrogen–deuterium exchange mass spectrometry experiments. Bioinformatics, 2020, 36, 4516-4518.	4.1	13
16	Algorithms for automated detection of hook effect-bearing amplification curves. Biomolecular Detection and Quantification, 2018, 16, 1-4.	7.0	12
17	Enabling reproducible real-time quantitative PCR research: the RDML package. Bioinformatics, 2017, 33, 4012-4014.	4.1	10
18	Prediction of Signal Peptides in Proteins from Malaria Parasites. International Journal of Molecular Sciences, 2018, 19, 3709.	4.1	10

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19	Variability of Amyloid Propensity in Imperfect Repeats of CsgA Protein of Salmonella enterica and Escherichia coli. International Journal of Molecular Sciences, 2021, 22, 5127.	4.1	9
20	Methods for comparing multiple digital PCR experiments. Biomolecular Detection and Quantification, 2016, 9, 14-19.	7.0	8
21	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. Journal of Proteome Research, 2021, 20, 2083-2088.	3.7	8
22	Role of recombination and faithfulness to partner in sex chromosome degeneration. Scientific Reports, 2018, 8, 8978.	3.3	7
23	Phylogenetic grouping and biofilm formation of multidrug resistant Escherichia coli isolates from humans, animals and food products in South-West Nigeria. Scientific African, 2019, 6, e00158.	1.5	7
24	Bioinformatics methods for identification of amyloidogenic peptides show robustness to misannotated training data. Scientific Reports, 2021, 11, 8934.	3.3	5
25	Identification of amyloidogenic proteins in the microbiomes of a rat Parkinson's disease model and wildâ€type rats. Protein Science, 2021, 30, 1854-1870.	7.6	5
26	Identification of Natural Mutations Responsible for Altered Infection Phenotypes of Salmonella enterica Clinical Isolates by Using Cell Line Infection Screens. Applied and Environmental Microbiology, 2021, 87, .	3.1	4
27	Genome placement of alpha-haemolysin cluster is associated with alpha-haemolysin sequence variation, adhesin and iron acquisition factor profile of Escherichia coli. Microbial Genomics, 2021, 7,	2.0	2
28	Intracellular Protein S-Nitrosylation—A Cells Response to Extracellular S100B and RAGE Receptor. Biomolecules, 2022, 12, 613.	4.0	2