

Michał Burdukiewicz

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

621
citations

687363

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642732

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32
all docs

32
docs citations

32
times ranked

970
citing authors

#	ARTICLE	IF	CITATIONS
1	Intracellular Protein S-Nitrosylationâ€™s A Cells Response to Extracellular S100B and RAGE Receptor. <i>Biomolecules</i> , 2022, 12, 613.	4.0	2
2	Identification of Natural Mutations Responsible for Altered Infection Phenotypes of <i>Salmonella enterica</i> Clinical Isolates by Using Cell Line Infection Screens. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	4
3	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 2083-2088.	3.7	8
4	Bioinformatics methods for identification of amyloidogenic peptides show robustness to misannotated training data. <i>Scientific Reports</i> , 2021, 11, 8934.	3.3	5
5	Variability of Amyloid Propensity in Imperfect Repeats of CsgA Protein of <i>Salmonella enterica</i> and <i>Escherichia coli</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 5127.	4.1	9
6	Identification of amyloidogenic proteins in the microbiomes of a rat Parkinson's disease model and wildâ€™type rats. <i>Protein Science</i> , 2021, 30, 1854-1870.	7.6	5
7	Genome placement of alpha-haemolysin cluster is associated with alpha-haemolysin sequence variation, adhesin and iron acquisition factor profile of <i>Escherichia coli</i> . <i>Microbial Genomics</i> , 2021, 7, .	2.0	2
8	MIRRAGGE â€™ Minimum Information Required for Reproducible AGGregation Experiments. <i>Frontiers in Molecular Neuroscience</i> , 2020, 13, 582488.	2.9	19
9	CancerGram: An Effective Classifier for Differentiating Anticancer from Antimicrobial Peptides. <i>Pharmaceutics</i> , 2020, 12, 1045.	4.5	19
10	Classification of dead and living microalgae <i>Chlorella vulgaris</i> by bioimage informatics and machine learning. <i>Algal Research</i> , 2020, 48, 101908.	4.6	34
11	Proteomic Screening for Prediction and Design of Antimicrobial Peptides with AmpGram. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4310.	4.1	59
12	HaDeX: an R package and web-server for analysis of data from hydrogenâ€™ deuterium exchange mass spectrometry experiments. <i>Bioinformatics</i> , 2020, 36, 4516-4518.	4.1	13
13	Phylogenetic grouping and biofilm formation of multidrug resistant <i>Escherichia coli</i> isolates from humans, animals and food products in South-West Nigeria. <i>Scientific African</i> , 2019, 6, e00158.	1.5	7
14	Simultaneous detection and quantification of DNA and protein biomarkers in spectrum of cardiovascular diseases in a microfluidic microbead chip. <i>Analytical and Bioanalytical Chemistry</i> , 2019, 411, 7725-7735.	3.7	32
15	PhyMet²: a database and toolkit for phylogenetic and metabolic analyses of methanogens. <i>Environmental Microbiology Reports</i> , 2018, 10, 378-382.	2.4	24
16	Prediction of Signal Peptides in Proteins from Malaria Parasites. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3709.	4.1	10
17	Algorithms for automated detection of hook effect-bearing amplification curves. <i>Biomolecular Detection and Quantification</i> , 2018, 16, 1-4.	7.0	12
18	Adhesion of <i>Salmonella</i> to Pancreatic Secretory Granule Membrane Major Glycoprotein GP2 of Human and Porcine Origin Depends on FimH Sequence Variation. <i>Frontiers in Microbiology</i> , 2018, 9, 1905.	3.5	21

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19	Role of recombination and faithfulness to partner in sex chromosome degeneration. Scientific Reports, 2018, 8, 8978.	3.3	7
20	Amyloidogenic motifs revealed by n-gram analysis. Scientific Reports, 2017, 7, 12961.	3.3	52
21	Enabling reproducible real-time quantitative PCR research: the RDML package. Bioinformatics, 2017, 33, 4012-4014.	4.1	10
22	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
23	System-specific periodicity in quantitative real-time polymerase chain reaction data questions threshold-based quantitation. Scientific Reports, 2016, 6, 38951.	3.3	16
24	Methods for comparing multiple digital PCR experiments. Biomolecular Detection and Quantification, 2016, 9, 14-19.	7.0	8
25	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
26	Impact of Smoothing on Parameter Estimation in Quantitative DNA Amplification Experiments. Clinical Chemistry, 2015, 61, 379-388.	3.2	31
27	chipPCR: an R package to pre-process raw data of amplification curves. Bioinformatics, 2015, 31, 2900-2902.	4.1	29
28	R as an Environment for Reproducible Analysis of DNA Amplification Experiments. R Journal, 2015, 7, 127.	1.8	19