

Boris Zybailov

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

1,821
citations

1051969

10
h-index

843174

20
g-index

22
all docs

22
docs citations

22
times ranked

3726
citing authors

#	ARTICLE	IF	CITATIONS
1	Metaproteomics – An Advantageous Option in Studies of Host-Microbiota Interaction. <i>Microorganisms</i> , 2021, 9, 980.	1.6	13
2	Domestication and microbiome. <i>Holocene</i> , 2021, 31, 1635-1645.	0.9	3
3	Milk Formula Diet Alters Bacterial and Host Protein Profile in Comparison to Human Milk Diet in Neonatal Piglet Model. <i>Nutrients</i> , 2021, 13, 3718.	1.7	2
4	Integration of Flow Cytometry and Single Cell Sequencing. <i>Trends in Biotechnology</i> , 2020, 38, 133-136.	4.9	7
5	Resistant starch slows the progression of CKD in the 5/6 nephrectomy mouse model. <i>Physiological Reports</i> , 2020, 8, e14610.	0.7	15
6	Leukocytosis and Expression of Bovine Leukemia Virus microRNAs in Cattle. <i>Frontiers in Veterinary Science</i> , 2020, 7, 272.	0.9	2
7	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. <i>PLoS ONE</i> , 2019, 14, e0221444.	1.1	1
8	Metaproteomics reveals potential mechanisms by which dietary resistant starch supplementation attenuates chronic kidney disease progression in rats. <i>PLoS ONE</i> , 2019, 14, e0199274.	1.1	25
9	Chronic kidney disease and the gut microbiome. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 316, F1211-F1217.	1.3	147
10	Domestication and mobile genetic elements. <i>Holocene</i> , 2019, 29, 518-522.	0.9	1
11	GSAR: Bioconductor package for Gene Set analysis in R. <i>BMC Bioinformatics</i> , 2017, 18, 61.	1.2	37
12	Extracting the Strongest Signals from Omics Data: Differentially Expressed Pathways and Beyond. <i>Methods in Molecular Biology</i> , 2017, 1613, 125-159.	0.4	3
13	Protein-protein interaction analysis for functional characterization of helicases. <i>Methods</i> , 2016, 108, 56-64.	1.9	8
14	Analysis of Protein-protein Interaction Interface between Yeast Mitochondrial Proteins Rim1 and Pif1 Using Chemical Cross-linking Mass Spectrometry. <i>Journal of Proteomics and Bioinformatics</i> , 2015, 8, 243-252.	0.4	9
15	Genomic Scanning Using Inverted Repeats of Microsatellites (GAG) ₆ C, (AG) ₉ C. <i>Biogeosystem Technique</i> , 2015, 4, 138-152.	0.5	2
16	Large Scale Chemical Cross-linking Mass Spectrometry Perspectives. <i>Journal of Proteomics and Bioinformatics</i> , 2013, 01, 001.	0.4	16
17	Computational Prediction of Polycomb-Associated Long Non-Coding RNAs. <i>PLoS ONE</i> , 2012, 7, e44878.	1.1	19
18	Quantitative shotgun proteomics using a protease with broad specificity and normalized spectral abundance factors. <i>Molecular BioSystems</i> , 2007, 3, 354.	2.9	144

#	ARTICLE	IF	CITATIONS
19	Statistical Analysis of Membrane Proteome Expression Changes in <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteome Research</i> , 2006, 5, 2339-2347.	1.8	1,042
20	Correlation of Relative Abundance Ratios Derived from Peptide Ion Chromatograms and Spectrum Counting for Quantitative Proteomic Analysis Using Stable Isotope Labeling. <i>Analytical Chemistry</i> , 2005, 77, 6218-6224.	3.2	324