Boris Zybailov

List of Publications by Year
in descending order

20 papers	1,821 citations	933447 10 h-index	752698 20 g-index
22 all docs	22 docs citations	22 times ranked	3317 citing authors

#	Article	IF	Citations
1	Metaproteomics—An Advantageous Option in Studies of Host-Microbiota Interaction. Microorganisms, 2021, 9, 980.	3.6	13
2	Domestication and microbiome. Holocene, 2021, 31, 1635-1645.	1.7	3
3	Milk Formula Diet Alters Bacterial and Host Protein Profile in Comparison to Human Milk Diet in Neonatal Piglet Model. Nutrients, 2021, 13, 3718.	4.1	2
4	Integration of Flow Cytometry and Single Cell Sequencing. Trends in Biotechnology, 2020, 38, 133-136.	9.3	7
5	Resistant starch slows the progression of CKD in the 5/6 nephrectomy mouse model. Physiological Reports, 2020, 8, e14610.	1.7	15
6	Leukocytosis and Expression of Bovine Leukemia Virus microRNAs in Cattle. Frontiers in Veterinary Science, 2020, 7, 272.	2.2	2
7	Proteome-transcriptome alignment of molecular portraits achieved by self-contained gene set analysis: Consensus colon cancer subtypes case study. PLoS ONE, 2019, 14, e0221444.	2.5	1
8	Metaproteomics reveals potential mechanisms by which dietary resistant starch supplementation attenuates chronic kidney disease progression in rats. PLoS ONE, 2019, 14, e0199274.	2.5	25
9	Chronic kidney disease and the gut microbiome. American Journal of Physiology - Renal Physiology, 2019, 316, F1211-F1217.	2.7	147
10	Domestication and mobile genetic elements. Holocene, 2019, 29, 518-522.	1.7	1
11	GSAR: Bioconductor package for Gene Set analysis in R. BMC Bioinformatics, 2017, 18, 61.	2.6	37
12	Extracting the Strongest Signals from Omics Data: Differentially Expressed Pathways and Beyond. Methods in Molecular Biology, 2017, 1613, 125-159.	0.9	3
13	Protein-protein interaction analysis for functional characterization of helicases. Methods, 2016, 108, 56-64.	3.8	8
14	Analysis of Protein-protein Interaction Interface between Yeast Mitochondrial Proteins Rim1 and Pif1 Using Chemical Cross-linking Mass Spectrometry. Journal of Proteomics and Bioinformatics, 2015, 8, 243-252.	0.4	9
15	Genomic Scanning Using Inverted Repeats of Microsatellites (GAG)6C, (AG)9C. Biogeosystem Technique, 2015, 4, 138-152.	0.1	2
16	Large Scale Chemical Cross-linking Mass Spectrometry Perspectives. Journal of Proteomics and Bioinformatics, 2013, 01, 001.	0.4	16
17	Computational Prediction of Polycomb-Associated Long Non-Coding RNAs. PLoS ONE, 2012, 7, e44878.	2.5	19
18	Quantitative shotgun proteomics using a protease with broad specificity and normalized spectral abundance factors. Molecular BioSystems, 2007, 3, 354.	2.9	144

#	Article	IF	Citations
19	Statistical Analysis of Membrane Proteome Expression Changes inSaccharomycescerevisiae. Journal of Proteome Research, 2006, 5, 2339-2347.	3.7	1,042
20	Correlation of Relative Abundance Ratios Derived from Peptide Ion Chromatograms and Spectrum Counting for Quantitative Proteomic Analysis Using Stable Isotope Labeling. Analytical Chemistry, 2005, 77, 6218-6224.	6.5	324