Jan Zrimec

List of Publications by Year
in descending order

17 papers	467 citations	1040056 9 h-index	940533 16 g-index
26 all docs	26 docs citations	26 times ranked	463 citing authors

#	Article	IF	Citations
1	Expanding functional protein sequence spaces using generative adversarial networks. Nature Machine Intelligence, 2021, 3, 324-333.	16.0	165
2	Deep learning suggests that gene expression is encoded in all parts of a co-evolving interacting gene regulatory structure. Nature Communications, 2020, 11, 6141.	12.8	83
3	Plastic-Degrading Potential across the Global Microbiome Correlates with Recent Pollution Trends. MBio, 2021, 12, e0215521.	4.1	51
4	Data mining of Saccharomyces cerevisiae mutants engineered for increased tolerance towards inhibitors in lignocellulosic hydrolysates. Biotechnology Advances, 2022, 57, 107947.	11.7	29
5	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. Nature Communications, 2021, 12, 190.	12.8	25
6	DNA structure at the plasmid origin-of-transfer indicates its potential transfer range. Scientific Reports, 2018, 8, 1820.	3.3	17
7	Learning the Regulatory Code of Gene Expression. Frontiers in Molecular Biosciences, 2021, 8, 673363.	3.5	17
8	Natural Microbial Communities Can Be Manipulated by Artificially Constructed Biofilms. Advanced Science, 2019, 6, 1901408.	11.2	16
9	Fast Prediction of DNA Melting Bubbles Using DNA Thermodynamic Stability. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 1137-1145.	3.0	9
10	Development of Highly Sensitive, Automatized and Portable Whole-Cell Hg Biosensor Based on Environmentally Relevant Microorganisms. Geomicrobiology Journal, 2017, 34, 596-605.	2.0	9
11	Performance of Regression Models as a Function of Experiment Noise. Bioinformatics and Biology Insights, 2021, 15, 117793222110203.	2.0	9
12	Determining the Virulence Properties of Escherichia coli ST131 Containing Bacteriocin-Encoding Plasmids Using Short- and Long-Read Sequencing and Comparing Them with Those of Other E. coli Lineages. Microorganisms, 2019, 7, 534.	3.6	7
13	Multiple plasmid origin‑of‑transfer regions might aid the spread of antimicrobial resistance to human pathogens. MicrobiologyOpen, 2020, 9, e1129.	3.0	7
14	Band smearing of PCR amplified bacterial 16S rRNA genes: Dependence on initial PCR target diversity. Journal of Microbiological Methods, 2013, 95, 186-194.	1.6	4
15	Bridge-Induced Translocation between NUP145 and TOP2 Yeast Genes Models the Genetic Fusion between the Human Orthologs Associated With Acute Myeloid Leukemia. Frontiers in Oncology, 2017, 7, 231.	2.8	3
16	Parallel Factor Analysis Enables Quantification and Identification of Highly Convolved Data-Independent-Acquired Protein Spectra. Patterns, 2020, 1, 100137.	5.9	2
17	Structural representations of DNA regulatory substrates can enhance sequence-based algorithms by associating functional sequence variants. , 2020, , .		2