Hilal Taymaz-Nikerel

List of Publications by Year in descending order

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1307594 1281871 12 460 7 11 citations g-index h-index papers 12 12 12 679 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Development and application of a differential method for reliable metabolome analysis in Escherichia coli. Analytical Biochemistry, 2009, 386, 9-19.	2.4	145
2	Doxorubicin induces an extensive transcriptional and metabolic rewiring in yeast cells. Scientific Reports, 2018, 8, 13672.	3.3	104
3	Genomeâ€derived minimal metabolic models for <i>Escherichia coli</i> MG1655 with estimated in vivo respiratory ATP stoichiometry. Biotechnology and Bioengineering, 2010, 107, 369-381.	3.3	85
4	Escherichia coli responds with a rapid and large change in growth rate upon a shift from glucose-limited to glucose-excess conditions. Metabolic Engineering, 2011, 13, 307-318.	7.0	45
5	Changes in substrate availability in Escherichia coli lead to rapid metabolite, flux and growth rate responses. Metabolic Engineering, 2013, 16, 115-129.	7.0	35
6	Side effect prediction based on drug-induced gene expression profiles and random forest with iterative feature selection. Pharmacogenomics Journal, 2021, 21, 673-681.	2.0	14
7	Comparative fluxome and metabolome analysis for overproduction of succinate in <i>Escherichia coli</i> . Biotechnology and Bioengineering, 2016, 113, 817-829.	3.3	12
8	Vitreoscilla Haemoglobin: A Tool to Reduce Overflow Metabolism. Microorganisms, 2022, 10, 43.	3.6	7
9	Insights Into the Mechanism of Anticancer Drug Imatinib Revealed Through Multi-Omic Analyses in Yeast. OMICS A Journal of Integrative Biology, 2020, 24, 667-678.	2.0	6
10	Time-dependent re-organization of biological processes by the analysis of the dynamic transcriptional response of yeast cells to doxorubicin. Molecular Omics, 2021, 17, 572-582.	2.8	4
11	Integration of fluxome and transcriptome data in <i>Saccharomyces cerevisiae</i> offers unique features of doxorubicin and imatinib. Molecular Omics, 2021, 17, 783-789.	2.8	3
12	Fast Sampling of the Cellular Metabolome. Methods in Molecular Biology, 2022, 2349, 11-39.	0.9	0