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List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

460
citations

1307594

7
h-index

1281871

11
g-index

12
all docs

12
docs citations

12
times ranked

679
citing authors

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