Ji-Nu Kim

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11943524/publications.pdf

Version: 2024-02-01

	933447	940533
616	10	16
citations	h-index	g-index
16	16	890
10	10	030
docs citations	times ranked	citing authors
	citations 16	616 10 citations h-index 16 16

#	Article	IF	CITATIONS
1	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	3.8	101
2	Mast cell recruitment is modulated by the hairless skin microbiome. Journal of Allergy and Clinical Immunology, 2019, 144, 330-333.e6.	2.9	6
3	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. PLoS Computational Biology, 2019, 15, e1006848.	3.2	46
4	Transcriptome analysis of wild-type and afsS deletion mutant strains identifies synergistic transcriptional regulator of afsS for a high antibiotic-producing strain of Streptomyces coelicolor A3(2). Applied Microbiology and Biotechnology, 2018, 102, 3243-3253.	3.6	9
5	Optimization of carbon and energy utilization through differential translational efficiency. Nature Communications, 2018, 9, 4474.	12.8	35
6	The dynamic transcriptional and translational landscape of the model antibiotic producer Streptomyces coelicolor A3(2). Nature Communications, 2016, 7, 11605.	12.8	201
7	Genome-scale analysis reveals a role for NdgR in the thiol oxidative stress response in Streptomyces coelicolor. BMC Genomics, 2015, 16, 116.	2.8	19
8	Comparative Genomics Reveals the Core and Accessory Genomes of Streptomyces Species. Journal of Microbiology and Biotechnology, 2015, 25, 1599-1605.	2.1	72
9	Reconstruction of a highâ€quality metabolic model enables the identification of gene overexpression targets for enhanced antibiotic production in <i>Streptomyces coelicolor</i> A3(2). Biotechnology Journal, 2014, 9, 1185-1194.	3.5	58
10	NdgR, a Common Transcriptional Activator for Methionine and Leucine Biosynthesis in Streptomyces coelicolor. Journal of Bacteriology, 2012, 194, 6837-6846.	2.2	13
11	A versatile PCR-based tandem epitope tagging system for Streptomyces coelicolor genome. Biochemical and Biophysical Research Communications, 2012, 424, 22-27.	2.1	4
12	Characterization of a new ScbR-like \hat{l}^3 -butyrolactone binding regulator (SlbR) in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2012, 96, 113-121.	3.6	19
13	Inactivation of phosphomannose isomerase gene abolishes sporulation and antibiotic production in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2012, 93, 1685-1693.	3.6	12
14	Loss of phosphomannomutase activity enhances actinorhodin production in Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2010, 86, 1485-1492.	3.6	9
15	An integrative approach for high-throughput screening and characterization of transcriptional regulators in Streptomyces coelicolor. Pure and Applied Chemistry, 2010, 82, 57-67.	1.9	1
16	Finding new pathway-specific regulators by clustering method using threshold standard deviation based on DNA chip data of Streptomyces coelicolor. Applied Microbiology and Biotechnology, 2008, 80, 709-717.	3.6	11