

Jochen Färster

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

1,324
citations

1040056

9
h-index

1372567

10
g-index

14
all docs

14
docs citations

14
times ranked

1812
citing authors

#	ARTICLE	IF	CITATIONS
1	Rational and evolutionary engineering of <i>Saccharomyces cerevisiae</i> for production of dicarboxylic acids from lignocellulosic biomass and exploring genetic mechanisms of the yeast tolerance to the biomass hydrolysate. , 2022, 15, 22.		8
2	Improving the Utilization of Isomaltose and Panose by Lager Yeast <i>Saccharomyces pastorianus</i> . Fermentation, 2021, 7, 107.	3.0	0
3	Never Change a Brewing Yeast? Why Not, There Are Plenty to Choose From. <i>Frontiers in Genetics</i> , 2020, 11, 582789.	2.3	8
4	Linking genetic, metabolic, and phenotypic diversity among <i>Saccharomyces cerevisiae</i> strains using multi-omics associations. <i>GigaScience</i> , 2019, 8, .	6.4	25
5	BachBerry: BACterial Hosts for production of Bioactive phenolics from bERRY fruits. <i>Phytochemistry Reviews</i> , 2018, 17, 291-326.	6.5	12
6	EasyCloneMulti: A Set of Vectors for Simultaneous and Multiple Genomic Integrations in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2016, 11, e0150394.	2.5	49
7	Highly Active and Specific Tyrosine Ammonia-Lyases from Diverse Origins Enable Enhanced Production of Aromatic Compounds in Bacteria and <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 4458-4476.	3.1	148
8	Assembly of a novel biosynthetic pathway for production of the plant flavonoid fisetin in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2015, 31, 84-93.	7.0	75
9	CRISPR-Cas system enables fast and simple genome editing of industrial <i>Saccharomyces cerevisiae</i> strains. <i>Metabolic Engineering Communications</i> , 2015, 2, 13-22.	3.6	154
10	EasyClone: method for iterative chromosomal integration of multiple genes <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014, 14, 238-248.	2.3	236
11	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005, 6, 308.	2.6	374
12	Modeling <i>Lactococcus lactis</i> using a genome-scale flux model. <i>BMC Microbiology</i> , 2005, 5, 39.	3.3	231