

David Parker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10438893/publications.pdf>

Version: 2024-02-01

13
papers

1,184
citations

759233

12
h-index

1125743

13
g-index

13
all docs

13
docs citations

13
times ranked

1781
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Design, Sustainability Analysis and Multiobjective Optimisation of Ethanol Production via Syngas Fermentation. <i>Waste and Biomass Valorization</i> , 2019, 10, 865-876. | 3.4 | 30 |
| 2 | Comparative Analysis of Synthetic Natural Gas versus Hydrogen Production from Bagasse. <i>Chemical Engineering and Technology</i> , 2017, 40, 546-554. | 1.5 | 4 |
| 3 | A multicriteria comparison of utilizing sugar cane bagasse for methanol to gasoline and butanol production. <i>Biomass and Bioenergy</i> , 2016, 95, 436-448. | 5.7 | 32 |
| 4 | Simulation Studies on Ethanol Production from Sugar Cane Residues. <i>Industrial & Engineering Chemistry Research</i> , 2016, 55, 5173-5179. | 3.7 | 14 |
| 5 | UbiX is a flavin prenyltransferase required for bacterial ubiquinone biosynthesis. <i>Nature</i> , 2015, 522, 502-506. | 27.8 | 168 |
| 6 | New cofactor supports $\hat{1}\pm, \hat{1}^2$ -unsaturated acid decarboxylation via 1,3-dipolar cycloaddition. <i>Nature</i> , 2015, 522, 497-501. | 27.8 | 197 |
| 7 | Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for Plant Metabolite Profiling and Metabolite Identification. <i>Methods in Molecular Biology</i> , 2011, 860, 157-176. | 0.9 | 20 |
| 8 | Metabolite signal identification in accurate mass metabolomics data with MZedDB, an interactive m/z annotation tool utilising predicted ionisation behaviour 'rules'. <i>BMC Bioinformatics</i> , 2009, 10, 227. | 2.6 | 142 |
| 9 | Metabolomic analysis reveals a common pattern of metabolic reprogramming during invasion of three host plant species by <i>Magnaporthe grisea</i> . <i>Plant Journal</i> , 2009, 59, 723-737. | 5.7 | 209 |
| 10 | Rice blast infection of <i>Brachypodium distachyon</i> as a model system to study dynamic host/pathogen interactions. <i>Nature Protocols</i> , 2008, 3, 435-445. | 12.0 | 95 |
| 11 | High-throughput, nontargeted metabolite fingerprinting using nominal mass flow injection electrospray mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 486-504. | 12.0 | 115 |
| 12 | Preprocessing, classification modeling and feature selection using flow injection electrospray mass spectrometry metabolite fingerprint data. <i>Nature Protocols</i> , 2008, 3, 446-470. | 12.0 | 114 |
| 13 | Explanatory signal interpretation and metabolite identification strategies for nominal mass FIE-MS metabolite fingerprints. <i>Nature Protocols</i> , 2008, 3, 471-485. | 12.0 | 44 |