Bertrand C Y Collard

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8409851/publications.pdf

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24 papers 3,470 citations

471509 17 h-index 26 g-index

27 all docs

27 docs citations

times ranked

27

4210 citing authors

#	Article	IF	CITATIONS
1	Identification and characterization of highâ€yielding, shortâ€duration rice genotypes for tropical Asia. Crop Science, 2020, 60, 2241-2250.	1.8	7
2	Use of NDVI for indirect selection of high yield in tropical rice breeding. Euphytica, 2020, 216, 1.	1.2	9
3	Increasing flooding tolerance in rice: combining tolerance of submergence and of stagnant flooding. Annals of Botany, 2019, 124, 1199-1209.	2.9	26
4	Review: Improving global food security through accelerated plant breeding. Plant Science, 2019, 287, 110207.	3.6	141
5	Global survey data on rice breeders' characteristics and willingness to adopt alternative breeding methods. Data in Brief, 2019, 23, 103782.	1.0	4
6	Global survey of rice breeders to investigate characteristics and willingness to adopt alternative breeding methods. Agriculture and Food Security, 2018, 7, 40.	4.2	12
7	Association mapping in rice: basic concepts and perspectives for molecular breeding. Plant Production Science, 2018, 21, 159-176.	2.0	28
8	Genetic Analysis and QTL Mapping for Agronomic and Yield-Related Traits in Ciherang-Sub1 Rice Backcross Populations. Plant Breeding and Biotechnology, 2018, 6, 177-192.	0.9	6
9	Mapping QTLs for submergence tolerance in rice using a population fixed for SUB1A tolerant allele. Molecular Breeding, 2017, 37, 1.	2.1	19
10	Physiological and morphological characterization of a high-yielding rice introgression line, YTH183, with genetic background of Indica Group cultivar, IR 64. Field Crops Research, 2017, 213, 89-99.	5.1	13
11	Revisiting rice breeding methods – evaluating the use of rapid generation advance (RGA) for routine rice breeding. Plant Production Science, 2017, 20, 337-352.	2.0	98
12	Identification of QTLs for yield and agronomic traits in rice under stagnant flooding conditions. Rice, 2017, 10, 15.	4.0	46
13	Development of early maturing submergence-tolerant rice varieties for Bangladesh. Field Crops Research, 2016, 190, 44-53.	5.1	24
14	Allelic diversity of newly characterized submergence-tolerant rice (Oryza sativa L.) germplasm from Bangladesh. Genetic Resources and Crop Evolution, 2016, 63, 859-867.	1.6	13
15	Improving yield potential of tropical rice: Achieved levels and perspectives through improved ideotypes. Field Crops Research, 2015, 182, 43-59.	5.1	66
16	Genomic Selection and Association Mapping in Rice (Oryza sativa): Effect of Trait Genetic Architecture, Training Population Composition, Marker Number and Statistical Model on Accuracy of Rice Genomic Selection in Elite, Tropical Rice Breeding Lines. PLoS Genetics, 2015, 11, e1004982.	3.5	425
17	Genome-Wide Association Mapping for Yield and Other Agronomic Traits in an Elite Breeding Population of Tropical Rice (Oryza sativa). PLoS ONE, 2015, 10, e0119873.	2.5	157
18	Accelerating the development of new submergence tolerant rice varieties: the case of Ciherang-Sub1 and PSB Rc18-Sub1. Euphytica, 2015, 202, 259-268.	1.2	66

#	Article	IF	CITATIONS
19	Evaluation of SSR and SNP Markers for Molecular Breeding in Rice. Plant Breeding and Biotechnology, 2015, 3, 139-152.	0.9	24
20	Physiological analyses of traits associated with tolerance of long-term partial submergence in rice. AoB PLANTS, 2014, 6, plu058-plu058.	2.3	59
21	Comparison of phenotypic versus marker-assisted background selection for the <i>SUB1</i> QTL during backcrossing in rice. Breeding Science, 2012, 62, 216-222.	1.9	17
22	Start Codon Targeted (SCoT) Polymorphism: A Simple, Novel DNA Marker Technique for Generating Gene-Targeted Markers in Plants. Plant Molecular Biology Reporter, 2009, 27, 86-93.	1.8	537
23	How accurate are the marker orders in crop linkage maps generated from large marker datasets?. Crop and Pasture Science, 2009, 60, 362.	1.5	16
24	Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. Philosophical Transactions of the Royal Society B: Biological Sciences, 2008, 363, 557-572.	4.0	1,568