

Maize HapMap2 identifies extant variation from a geno

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Citation Report

#	ARTICLE	IF	CITATIONS
1	<i>ZmCCT</i> and the genetic basis of day-length adaptation underlying the postdomestication spread of maize. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1913-21.	3.3	290
3	Natural Variation in Maize Defense against Insect Herbivores. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 269-283.	2.0	81
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5	Genotyping-by-Sequencing for Plant Breeding and Genetics. Plant Genome, 2012, 5, .	1.6	703
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13	Choosing the Best Plant for the Job: A Cost-Effective Assay to Prescreen Ancient Plant Remains Destined for Shotgun Sequencing. PLoS ONE, 2012, 7, e45644.	1.1	16
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19	Comprehensive genotyping of the USA national maize inbred seed bank. Genome Biology, 2013, 14, R55.	3.8	458

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21	Meta-analysis combined with syntenic metaQTL mining dissects candidate loci for maize yield. <i>Molecular Breeding</i> , 2013, 31, 601-614.	1.0	33
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