The Brassica oleracea genome reveals the asymmetrical

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Citation Report

#	Article	IF	Citations
1	A Complex Recombination Pattern in the Genome of Allotetraploid Brassica napus as Revealed by a High-Density Genetic Map. PLoS ONE, 2014, 9, e109910.	1.1	41
2	Functional Analysis of the Brassica napus L. Phytoene Synthase (PSY) Gene Family. PLoS ONE, 2014, 9, e114878.	1.1	26
3	Identification of three FLOWERING LOCUS C genes responsible for vernalization response in radish (Raphanus sativus L.). Horticulture Environment and Biotechnology, 2014, 55, 548-556.	0.7	22
4	Integration of a constraint-based metabolic model of Brassica napus developing seeds with 13C-metabolic flux analysis. Frontiers in Plant Science, 2014, 5, 724.	1.7	32
5	Neofunctionalization of Duplicated<i>Tic40</i>Genes Caused a Gain-of-Function Variation Related to Male Fertility in<i>Brassica oleracea</i>Lineages Â Â. Plant Physiology, 2014, 166, 1403-1419.	2.3	17
6	Quantitative trait loci analyses for resistance to Sclerotinia sclerotiorum and flowering time in Brassica napus. Molecular Breeding, 2014, 34, 1797-1804.	1.0	84
7	Mapping and analysis of a novel candidate Fusarium wilt resistance gene FOC1 in Brassica oleracea. BMC Genomics, 2014, 15, 1094.	1.2	74
8	A high-throughput SNP array in the amphidiploid species Brassica napus shows diversity in resistance genes. Functional and Integrative Genomics, 2014, 14, 643-655.	1.4	43
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15	Genome expansion of Arabis alpina linked with retrotransposition and reduced symmetric DNA methylation. Nature Plants, 2015, 1, 14023.	4.7	156
16	Linkage and regional association analysis reveal two new tightly-linked major-QTLs for pod number and seed number per pod in rapeseed (Brassica napus L.). Scientific Reports, 2015, 5, 14481.	1.6	79
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18	Comparative quantitative trait loci for silique length and seed weight in Brassica napus. Scientific Reports, 2015, 5, 14407.	1.6	65

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