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List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The lack of a systematic validation of reference genes: a serious pitfall undervalued in reverse transcriptionâ€polymerase chain reaction (RTâ€PCR) analysis in plants. Plant Biotechnology Journal, 2008, 6, 609-618.	8.3	613
2	Normalization of qRT-PCR data: the necessity of adopting a systematic, experimental conditions-specific, validation of references. Journal of Experimental Botany, 2009, 60, 487-493.	4.8	481
3	Combined networks regulating seed maturation. Trends in Plant Science, 2007, 12, 294-300.	8.8	293
4	Towards a Systematic Validation of References in Real-Time RT-PCR. Plant Cell, 2008, 20, 1734-1735.	6.6	186
5	Characterization of an Iron-dependent Regulatory Sequence Involved in the Transcriptional Control of AtFer1and ZmFer1 Plant Ferritin Genes by Iron. Journal of Biological Chemistry, 2001, 276, 5584-5590.	3.4	121
6	Iron homeostasis alteration in transgenic tobacco overexpressing ferritin. Plant Journal, 1999, 17, 93-97.	5.7	120
7	The control of intracellular glycerol in Saccharomyces cerevisiae influences osmotic stress response and resistance to increased temperature. Molecular Microbiology, 2002, 36, 1381-1390.	2.5	94
8	Identification of pectin methylesterase 3 as a basic pectin methylesterase isoform involved in adventitious rooting in <i>Arabidopsis thaliana</i> . New Phytologist, 2011, 192, 114-126.	7.3	67
9	Development and validation of a flax (Linum usitatissimum L.) gene expression oligo microarray. BMC Genomics, 2010, 11, 592.	2.8	66
10	PME58 plays a role in pectin distribution during seed coat mucilage extrusion through homogalacturonan modification. Journal of Experimental Botany, 2016, 67, 2177-2190.	4.8	46
11	Unexpected effects of chitinases on the peach-potato aphid (Myzus persicae Sulzer) when delivered via transgenic potato plants (Solanum tuberosum Linn�) and in vitro. Transgenic Research, 2005, 14, 57-67.	2.4	44
12	PT-Flax (phenotyping and TILLinG of flax): development of a flax (Linum usitatissimumL.) mutant population and TILLinG platform for forward and reverse genetics. BMC Plant Biology, 2013, 13, 159.	3.6	44
13	Identification of new gene expression regulators specifically expressed during plant seed maturation. Journal of Experimental Botany, 2006, 57, 1919-1932.	4.8	36
14	Metabolite profiling of developing Camelina sativa seeds. Metabolomics, 2016, 12, 1.	3.0	20
15	Cytological Approaches Combined With Chemical Analysis Reveals the Layered Nature of Flax Mucilage. Frontiers in Plant Science, 2019, 10, 684.	3.6	14
16	MuSeeQ, a novel supervised image analysis tool for the simultaneous phenotyping of the soluble mucilage and seed morphometric parameters. Plant Methods, 2018, 14, 112.	4.3	10
17	Integument-Specific Transcriptional Regulation in the Mid-Stage of Flax Seed Development Influences the Release of Mucilage and the Seed Oil Content. Cells, 2021, 10, 2677.	4.1	2