PlantTFDB 3.0: a portal for the functional and evolution factors

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Citation Report

#	ARTICLE	IF	CITATIONS
1	De Novo Transcriptome Assembly from Inflorescence of Orchis italica: Analysis of Coding and Non-Coding Transcripts. PLoS ONE, 2014, 9, e102155.	1.1	30
2	Genome-Wide Identification and Expression Analysis of the CaNAC Family Members in Chickpea during Development, Dehydration and ABA Treatments. PLoS ONE, 2014, 9, e114107.	1.1	49
3	Prioritization of candidate genes in QTL regions based on associations between traits and biological processes. BMC Plant Biology, 2014, 14, 330.	1.6	40
4	Transcriptome analysis of ripe and unripe fruit tissue of banana identifies major metabolic networks involved in fruit ripening process. BMC Plant Biology, 2014, 14, 316.	1.6	84
5	Overexpression of tomato SlNAC1transcription factor alters fruit pigmentation and softening. BMC Plant Biology, 2014, 14, 351.	1.6	155
6	Functional characterisation of a WRKY transcription factor of wheat and its expression analysis during leaf rust pathogenesis. Functional Plant Biology, 2014, 41, 1295.	1.1	13
7	The Role of cis Regulatory Evolution in Maize Domestication. PLoS Genetics, 2014, 10, e1004745.	1.5	144
8	De Novo Transcriptome Sequence Assembly and Identification of AP2/ERF Transcription Factor Related to Abiotic Stress in Parsley (Petroselinum crispum). PLoS ONE, 2014, 9, e108977.	1.1	21
9	Transcriptomic landscape of prophase I sunflower male meiocytes. Frontiers in Plant Science, 2014, 5, 277.	1.7	28
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11	Maize and millet transcription factors annotated using comparative genomic and transcriptomic data. BMC Genomics, 2014, 15, 818.	1.2	18
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14	Transcriptome-wide identification of bread wheat WRKY transcription factors in response to drought stress. Molecular Genetics and Genomics, 2014, 289, 765-781.	1.0	116
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16	Evaluation of abiotic stress tolerance and physiological characteristics of potato (Solanum) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Reports, 2014, 8, 295-304.	0.9	9
17	Evidence for Selection on Gene Expression in Cultivated Rice (Oryza sativa). Molecular Biology and Evolution, 2014, 31, 1514-1525.	3.5	29
18	The abiotic stress-responsive NAC-type transcription factor SlNAC4 regulates salt and drought tolerance and stress-related genes in tomato (Solanum lycopersicum). Plant Cell Reports, 2014, 33, 1851-1863.	2.8	132

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20	A robust chromatin immunoprecipitation protocol for studying transcription factorâ€"DNA interactions and histone modifications in wood-forming tissue. Nature Protocols, 2014, 9, 2180-2193.	5.5	63
21	The Potential of Transcription Factor-Based Genetic Engineering in Improving Crop Tolerance to Drought. OMICS A Journal of Integrative Biology, 2014, 18, 601-614.	1.0	79
22	Large-scale phosphoproteome analysis in seedling leaves of Brachypodium distachyon L.. BMC Genomics, 2014, 15, 375.	1.2	37
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