Kanakachari Mogilicherla

List of Publications by Year
in descending order

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22 papers	1,000 citations	623734 14 h-index	713466 21 g-index
22 all docs	22 docs citations	22 times ranked	1040 citing authors

#	Article	IF	Citations
1	Caenorhabditis eleganssystemic RNA interference defective protein 1 enhances RNAi efficiency in a lepidopteran insect, the fall armyworm, in a tissue-specific manner. RNA Biology, 2021, 18, 1291-1299.	3.1	11
2	Improving RNA interference in the southern green stink bug, Nezara viridula. Journal of Pest Science, 2021, 94, 1461-1472.	3.7	8
3	Temporal expression profiling of GhNAC transcription factor genes in cotton cultivars under abiotic stresses. Plant Gene, 2021, 28, 100334.	2.3	1
4	RNA Interference-Based Forest Protection Products (FPPs) Against Wood-Boring Coleopterans: Hope or Hype?. Frontiers in Plant Science, 2021, 12, 733608.	3.6	2
5	Inhibitor of apoptosis is an effective target gene for RNAiâ€mediated control of Colorado potato beetle,Leptinotarsa decemlineata. Archives of Insect Biochemistry and Physiology, 2020, 104, e21685.	1.5	16
6	Development of RNAi methods to control the harlequin bug, Murgantia histrionica. Archives of Insect Biochemistry and Physiology, 2020, 104, e21690.	1.5	7
7	Chitosan nanoparticles help doubleâ€stranded RNA escape from endosomes and improve RNA interference in the fall armyworm, Spodoptera frugiperda. Archives of Insect Biochemistry and Physiology, 2020, 104, e21677.	1.5	36
8	Lipids help doubleâ€stranded RNA in endosomal escape and improve RNA interference in the fall armyworm, Spodoptera frugiperda. Archives of Insect Biochemistry and Physiology, 2020, 104, e21678.	1.5	33
9	Improving RNAi in the Brown Marmorated Stink Bug: Identification of target genes and reference genes for RT-qPCR. Scientific Reports, 2018, 8, 3720.	3.3	55
10	Double-stranded RNA binding protein, Staufen, is required for the initiation of RNAi in coleopteran insects. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8334-8339.	7.1	87
11	Development of RNAi method for screening candidate genes to control emerald ash borer, Agrilus planipennis. Scientific Reports, 2017, 7, 7379.	3.3	47
12	Comparative analysis of double-stranded RNA degradation and processing in insects. Scientific Reports, 2017, 7, 17059.	3.3	153
13	Genomeâ€wide transcriptomic and proteomic analyses of bollwormâ€infested developing cotton bolls revealed the genes and pathways involved in the insect pest defence mechanism. Plant Biotechnology Journal, 2016, 14, 1438-1455.	8.3	18
14	RNA interference in the Colorado potato beetle, Leptinotarsa decemlineata: Identification of key contributors. Insect Biochemistry and Molecular Biology, 2016, 78, 78-88.	2.7	81
15	Reduced stability and intracellular transport of dsRNA contribute to poor RNAi response in lepidopteran insects. RNA Biology, 2016, 13, 656-669.	3.1	194
16	Evaluation of Suitable Reference Genes for Normalization of qPCR Gene Expression Studies in Brinjal (Solanum melongena L.) During Fruit Developmental Stages. Applied Biochemistry and Biotechnology, 2016, 178, 433-450.	2.9	30
17	Delineating the glycoproteome of elongating cotton fiber cells. Data in Brief, 2015, 5, 717-725.	1.0	4
18	Evaluation of different carbon sources for high frequency callus culture with reduced phenolic secretion in cotton (Gossypium hirsutum L.) cv. SVPR-2. Biotechnology Reports (Amsterdam,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 57 T	4.1	37

#	Article	IF	Citations
19	A Gene Encoding Cold-Circadian Rhythm-RNA Binding-Like Protein (CCR-Like) from Upland Cotton (Gossypium hirsutum L.) Confers Tolerance to Abiotic Stresses in Transgenic Tobacco. Plant Molecular Biology Reporter, 2015, 33, 22-42.	1.8	7
20	Glycoproteome of Elongating Cotton Fiber Cells. Molecular and Cellular Proteomics, 2013, 12, 3677-3689.	3.8	53
21	Genome-wide transcriptomic analysis of cotton under drought stress reveal significant down-regulation of genes and pathways involved in fibre elongation and up-regulation of defense responsive genes. Plant Molecular Biology, 2012, 78, 223-246.	3.9	97
22	Genome-wide transcriptome and proteome analyses of tobacco psaA and psbA deletion mutants. Plant Molecular Biology, 2011, 76, 407-423.	3.9	28