

# The banana (*Musa acuminata*) genome and the evolution

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Intelligent Control Using Neural Networks. , 1991, , .		14
2	Dynamic Modeling and Simulation of PEM Fuel Cells. , 2010, , .		1
3	Cytogenetic evidence of mixed disomic and polysomic inheritance in an allotetraploid (AABB) Musa genotype. <i>Annals of Botany</i> , 2012, 110, 1593-1606.	1.4	28
4	Plant & Cell Physiology Research Highlights. <i>Plant and Cell Physiology</i> , 2012, 53, 1985-1988.	1.5	1
5	Tibet is one of the centers of domestication of cultivated barley. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16969-16973.	3.3	221
6	PGDD: a database of gene and genome duplication in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1152-D1158.	6.5	544
7	Expression patterns of ethylene biosynthesis genes from bananas during fruit ripening and in relationship with finger drop. <i>AoB PLANTS</i> , 2012, 2012, pls041-pls041.	1.2	9
8	Induction, rapid fixation and retention of mutations in vegetatively propagated banana. <i>Plant Biotechnology Journal</i> , 2012, 10, 1056-1066.	4.1	83
9	The tomato genome: implications for plant breeding, genomics and evolution. <i>Genome Biology</i> , 2012, 13, 167.	13.9	37
10	De Novo characterization of the banana root transcriptome and analysis of gene expression under <i>Fusarium oxysporum</i> f. sp. <i>Cubense</i> tropical race 4 infection. <i>BMC Genomics</i> , 2012, 13, 650.	1.2	74
11	Exploring the genome of the salt-marsh <i>Spartina maritima</i> (Poaceae, Chloridoideae) through BAC end sequence analysis. <i>Plant Molecular Biology</i> , 2013, 83, 591-606.	2.0	11
12	Analysis of the leaf transcriptome of <i>Musa acuminata</i> during interaction with <i>Mycosphaerella musicola</i> : gene assembly, annotation and marker development. <i>BMC Genomics</i> , 2013, 14, 78.	1.2	46
13	Molecular cloning and expression of five glutathione S-transferase (GST) genes from Banana ( <i>Musa</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.8	18
14	The Ins and Outs of the Rice AGAMOUS Subfamily. <i>Molecular Plant</i> , 2013, 6, 650-664.	3.9	29
15	Assembly and Validation of the Genome of the Nonmodel Basal Angiosperm <i>Amborella</i> . <i>Science</i> , 2013, 342, 1516-1517.	6.0	89
17	Young, intact and nested retrotransposons are abundant in the onion and asparagus genomes. <i>Annals of Botany</i> , 2013, 112, 881-889.	1.4	29
18	â€œA draft <i>Musa balbisiana</i> genome sequence for molecular genetics in polyploid, inter- and intra-specific <i>Musa</i> hybridsâ€• <i>BMC Genomics</i> , 2013, 14, 683.	1.2	159
19	Proteomic analysis of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> tropical race 4-inoculated response to <i>Fusarium</i> wilts in the banana root cells. <i>Proteome Science</i> , 2013, 11, 41.	0.7	46

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20	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 202.	3.2	51
21	Analysis of banana transcriptome and global gene expression profiles in banana roots in response to infection by race 1 and tropical race 4 of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>BMC Genomics</i> , 2013, 14, 851.	1.2	112
22	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine ( <i>Pinus taeda</i> L.). <i>Tree Genetics and Genomes</i> , 2013, 9, 1529-1535.	0.6	23
23	Genomics reveals new landscapes for crop improvement. <i>Genome Biology</i> , 2013, 14, 206.	3.8	99
24	Regulation of ripening and opportunities for control in tomato and other fruits. <i>Plant Biotechnology Journal</i> , 2013, 11, 269-278.	4.1	156
25	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2898-2903.	3.3	351
26	Endogenous pararetroviruses as a reservoir of virus infection in plants. <i>Current Opinion in Virology</i> , 2013, 3, 615-620.	2.6	64
27	A Bountiful Harvest: Genomic Insights into Crop Domestication Phenotypes. <i>Annual Review of Plant Biology</i> , 2013, 64, 47-70.	8.6	326
28	Mango - Postharvest Biology and Biotechnology. <i>Critical Reviews in Plant Sciences</i> , 2013, 32, 217-236.	2.7	145
29	Fruit Development and Ripening. <i>Annual Review of Plant Biology</i> , 2013, 64, 219-241.	8.6	492
30	A decade of plant proteomics and mass spectrometry: Translation of technical advancements to food security and safety issues. <i>Mass Spectrometry Reviews</i> , 2013, 32, 335-365.	2.8	70
31	Genetic diversity and population structure of <i>Musa</i> accessions in ex situ conservation. <i>BMC Plant Biology</i> , 2013, 13, 41.	1.6	61
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34	Heavy traffic in the fast lane: long-distance signalling by macromolecules. <i>New Phytologist</i> , 2013, 198, 33-51.	3.5	82
35	Plant proteomics: Current status and future prospects. <i>Journal of Proteomics</i> , 2013, 88, 34-36.	1.2	4
36	Tapping the Promise of Genomics in Species with Complex, Nonmodel Genomes. <i>Annual Review of Plant Biology</i> , 2013, 64, 89-110.	8.6	53
37	Function of a citrate synthase gene ( <i>MaCCS</i> ) during postharvest banana fruit ripening. <i>Postharvest Biology and Technology</i> , 2013, 84, 43-50.	2.9	14

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38	Biology and biotechnology of fruit flavor and aroma volatiles. <i>Stewart Postharvest Review</i> , 0, 9, 1-13.	0.7	1
39	Wound-induced pectin methylesterases enhance banana ( <i>Musa</i> spp. AAA) susceptibility to <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . <i>Journal of Experimental Botany</i> , 2013, 64, 2219-2229.	2.4	33
40	Three Infectious Viral Species Lying in Wait in the Banana Genome. <i>Journal of Virology</i> , 2013, 87, 8624-8637.	1.5	80
41	Molecular Evolution and Patterns of Duplication in the SEP/AGL6-Like Lineage of the Zingiberales: A Proposed Mechanism for Floral Diversification. <i>Molecular Biology and Evolution</i> , 2013, 30, 2401-2422.	3.5	42
42	The Banana Genome Hub. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat035.	1.4	151
43	Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research. <i>International Journal of Molecular Sciences</i> , 2013, 14, 11444-11483.	1.8	8
44	Crop plants as models for understanding plant adaptation and diversification. <i>Frontiers in Plant Science</i> , 2013, 4, 290.	1.7	80
45	Functional Diversification of FD Transcription Factors in Rice, Components of Florigen Activation Complexes. <i>Plant and Cell Physiology</i> , 2013, 54, 385-397.	1.5	69
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47	Oil palm genome sequence reveals divergence of interfertile species in Old and New worlds. <i>Nature</i> , 2013, 500, 335-339.	13.7	468
48	Recent Advances in Temperate Fruit Crops. , 2013, , 251-284.		0
49	Melhoramento genotico da bananeira: estratogias e tecnologias disponaveis. <i>Revista Brasileira De Fruticultura</i> , 2013, 35, 919-931.	0.2	16
50	BANANA IN LATIN AMERICA AND THE CARIBBEAN: CURRENT STATE, CHALLENGES AND PERSPECTIVES. <i>Acta Horticulturae</i> , 2013, , 365-380.	0.1	19
51	Germplasm diversity and genetics to drive plant breeding for Africa. , 0, , 82-94.		0
52	The First 50 Plant Genomes. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0001in.	1.6	228
53	Molecular Analysis and Genomic Organization of Major DNA Satellites in Banana ( <i>Musa</i> spp.). <i>PLoS ONE</i> , 2013, 8, e54808.	1.1	49
54	Phylogenomic Analyses of Nuclear Genes Reveal the Evolutionary Relationships within the BEP Clade and the Evidence of Positive Selection in Poaceae. <i>PLoS ONE</i> , 2013, 8, e64642.	1.1	37
55	Phylogenomics of MADS-Box Genes in Plants â€” Two Opposing Life Styles in One Gene Family. <i>Biology</i> , 2013, 2, 1150-1164.	1.3	70

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56	Annotation of Differentially Expressed Genes in the Somatic Embryogenesis of <i>Musa</i> and Their Location in the Banana Genome. <i>Scientific World Journal</i> , The, 2013, 2013, 1-7.	0.8	10
58	A Draft Genome Sequence for <i>Ensete ventricosum</i> , the Drought-Tolerant "Tree Against Hunger". <i>Agronomy</i> , 2014, 4, 13-33.	1.3	21
59	Evaluation of four different strategies to characterize plasma membrane proteins from banana roots. <i>Ciencia E Agrotecnologia</i> , 2014, 38, 424-434.	1.5	1
60	Targeted parallel sequencing of the <i>Musa</i> species: Searching for an alternative model system for polyploidy studies. <i>African Journal of Biotechnology</i> , 2014, 13, 4052-4060.	0.3	0
61	<i>Musa</i> spp. Germplasm Management: Microsatellite Fingerprinting of USDA-ARS National Plant Germplasm System Collection. <i>Crop Science</i> , 2014, 54, 2140-2151.	0.8	12
63	Phylogenetic analysis of the expansion of the MATH-BTB gene family in the grasses. <i>Plant Signaling and Behavior</i> , 2014, 9, e28242.	1.2	13
64	Evolution of endogenous non-retroviral genes integrated into plant genomes. <i>Current Plant Biology</i> , 2014, 1, 55-59.	2.3	20
66	Lineage-Specific Conserved Noncoding Sequences of Plant Genomes: Their Possible Role in Nucleosome Positioning. <i>Genome Biology and Evolution</i> , 2014, 6, 2527-2542.	1.1	15
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74	Bayesian phylogeny of sucrose transporters: ancient origins, differential expansion and convergent evolution in monocots and dicots. <i>Frontiers in Plant Science</i> , 2014, 5, 615.	1.7	41
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76	The Evolution of Plant Gene and Genome Sequencing. <i>Advances in Botanical Research</i> , 2014, , 47-90.	0.5	6
77	A Backdrop. <i>Advances in Botanical Research</i> , 2014, 69, 1-11.	0.5	2
78	P-MITE: a database for plant miniature inverted-repeat transposable elements. <i>Nucleic Acids Research</i> , 2014, 42, D1176-D1181.	6.5	121
79	UpSet: Visualization of Intersecting Sets. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2014, 20, 1983-1992.	2.9	1,549

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81	The diversification and activity of hAT transposons in <i>Musa</i> genomes. <i>Chromosome Research</i> , 2014, 22, 559-571.	1.0	14
82	The genome of African yam ( <i>Dioscorea cayenensis</i> rotundata complex) hosts endogenous sequences from four distinct badnavirus species. <i>Molecular Plant Pathology</i> , 2014, 15, 790-801.	2.0	28
83	The X Chromosome Is Necessary for Somatic Development in the Dioecious <i>Silene latifolia</i> : Cytogenetic and Molecular Evidence and Sequencing of a Haploid Genome. <i>Cytogenetic and Genome Research</i> , 2014, 143, 96-103.	0.6	5
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85	Assessment of RNAi-induced silencing in banana ( <i>Musa</i> spp.). <i>BMC Research Notes</i> , 2014, 7, 655.	0.6	9
86	The First Monocot Genome Sequence. <i>Advances in Botanical Research</i> , 2014, , 119-135.	0.5	1
87	Plant genome sequencing – applications for crop improvement. <i>Current Opinion in Biotechnology</i> , 2014, 26, 31-37.	3.3	164
88	The common evolutionary history of badnaviruses and banana. <i>Infection, Genetics and Evolution</i> , 2014, 21, 83-89.	1.0	31
89	Occurrence, prevalence and molecular diversity of banana streak viruses in Cuba. <i>European Journal of Plant Pathology</i> , 2014, 138, 157-166.	0.8	11
90	Genome-wide identification and expression analysis of the mitogen-activated protein kinase gene family from banana suggest involvement of specific members in different stages of fruit ripening. <i>Functional and Integrative Genomics</i> , 2014, 14, 161-175.	1.4	47
91	Plant genome size variation: bloating and purging DNA. <i>Briefings in Functional Genomics</i> , 2014, 13, 308-317.	1.3	137
92	Early History of the Angiosperms. <i>Advances in Botanical Research</i> , 2014, 69, 195-222.	0.5	6
93	Genomic analysis of NAC transcription factors in banana ( <i>Musa acuminata</i> ) and definition of NAC orthologous groups for monocots and dicots. <i>Plant Molecular Biology</i> , 2014, 85, 63-80.	2.0	91
94	Isolation, classification and transcription profiles of the AP2/ERF transcription factor superfamily in citrus. <i>Molecular Biology Reports</i> , 2014, 41, 4261-4271.	1.0	80
95	Transgenic banana plants overexpressing MusabZIP53 display severe growth retardation with enhanced sucrose and polyphenol oxidase activity. <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 116, 387-402.	1.2	29
96	Genetic relationships among a collection of <i>Musa</i> germplasm by fluorescent-labeled SRAP. <i>Tree Genetics and Genomes</i> , 2014, 10, 465-476.	0.6	12
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99	Sample sequencing of vascular plants demonstrates widespread conservation and divergence of microRNAs. <i>Nature Communications</i> , 2014, 5, 3722.	5.8	224
100	The paralogous SPX3 and SPX5 genes redundantly modulate Pi homeostasis in rice. <i>Journal of Experimental Botany</i> , 2014, 65, 859-870.	2.4	88
101	Profiling of extensively diversified plant <i>LINE</i> s reveals distinct plant-specific subclades. <i>Plant Journal</i> , 2014, 79, 385-397.	2.8	35
102	Plant defense response against <i>Fusarium oxysporum</i> and strategies to develop tolerant genotypes in banana. <i>Planta</i> , 2014, 239, 735-751.	1.6	83
103	Detecting and Locating Whole Genome Duplications on a Phylogeny: A Probabilistic Approach. <i>Molecular Biology and Evolution</i> , 2014, 31, 750-762.	3.5	73
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105	Phenalenone-type phytoalexins mediate resistance of banana plants ( <i>Musa</i> spp.) to the burrowing nematode <i>Radopholus similis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 105-110.	3.3	130
106	Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , 2014, 46, 270-278.	9.4	867
107	Two Evolutionarily Distinct Classes of Paleopolyploidy. <i>Molecular Biology and Evolution</i> , 2014, 31, 448-454.	3.5	159
108	Templated Biomineralization on Self-Assembled Protein Nanofibers Buried in Calcium Oxalate Raphides of <i>Musa</i> spp.. <i>Chemistry of Materials</i> , 2014, 26, 3862-3869.	3.2	17
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111	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	13.7	725
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113	Expansion of banana ( <i>Musa acuminata</i> ) gene families involved in ethylene biosynthesis and signalling after lineage-specific whole-genome duplications. <i>New Phytologist</i> , 2014, 202, 986-1000.	3.5	47
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117	Doubling down on genomes: Polyploidy and crop plants. <i>American Journal of Botany</i> , 2014, 101, 1711-1725.	0.8	336
118	SeqControl: process control for DNA sequencing. <i>Nature Methods</i> , 2014, 11, 1071-1075.	9.0	10
119	Polyploidy-associated genome modifications during land plant evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130355.	1.8	90
120	Genome-wide identification, classification and expression analysis of the heat shock transcription factor family in Chinese cabbage. <i>Molecular Genetics and Genomics</i> , 2014, 289, 541-551.	1.0	59
121	The Banana MaLBD (LATERAL ORGAN BOUNDARIES DOMAIN) Transcription Factors Regulate EXPANSIN Expression and Are Involved in Fruit Ripening. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 1103-1113.	1.0	34
122	Transgenic banana plants expressing a <i>Stellaria media</i> defensin gene (Sm-AMP-D1) demonstrate improved resistance to <i>Fusarium oxysporum</i> . <i>Plant Cell, Tissue and Organ Culture</i> , 2014, 119, 247-255.	1.2	39
123	Comparative transcriptome analysis of eggplant ( <i>Solanum melongena</i> L.) and turkey berry ( <i>Solanum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	86
124	Impact of recurrent gene duplication on adaptation of plant genomes. <i>BMC Plant Biology</i> , 2014, 14, 151.	1.6	32
125	Genomics: A potential panacea for the perennial problem. <i>American Journal of Botany</i> , 2014, 101, 1780-1790.	0.8	49
126	Dissection of the Octoploid Strawberry Genome by Deep Sequencing of the Genomes of <i>Fragaria</i> Species. <i>DNA Research</i> , 2014, 21, 169-181.	1.5	201
127	Evasion of Short Interfering RNA-Directed Antiviral Silencing in <i>Musa acuminata</i> Persistently Infected with Six Distinct Banana Streak Pararetroviruses. <i>Journal of Virology</i> , 2014, 88, 11516-11528.	1.5	27
128	Single nucleotide polymorphisms in partial sequences of the gene encoding the large sub-units of ADP-glucose pyrophosphorylase within a representative collection of 10 <i>Musa</i> genotypes. <i>Electronic Journal of Biotechnology</i> , 2014, 17, 137-147.	1.2	1
129	A possible scenario for the evolution of Banana streak virus in banana. <i>Virus Research</i> , 2014, 186, 155-162.	1.1	29
130	The bright side of transposons in crop evolution. <i>Briefings in Functional Genomics</i> , 2014, 13, 276-295.	1.3	106
131	Engineering Complex Metabolic Pathways in Plants. <i>Annual Review of Plant Biology</i> , 2014, 65, 187-223.	8.6	117
132	Understanding development and ripening of fruit crops in an "omics" era. <i>Horticulture Research</i> , 2014, 1, 14034.	2.9	53
133	Gene families as soft cliques with backbones: Amborella contrasted with other flowering plants. <i>BMC Genomics</i> , 2014, 15, S8.	1.2	1



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134	Computational prediction, identification, and expression profiling of microRNAs in banana ( <i>Musa</i> spp.) during soil moisture deficit stress. <i>Journal of Horticultural Science and Biotechnology</i> , 2014, 89, 208-214.	0.9	15
135	Insights into <i>Musa balbisiana</i> and <i>Musa acuminata</i> species divergence and development of genic microsatellites by transcriptomics approach. <i>Plant Gene</i> , 2015, 4, 78-82.	1.4	26
136	Paralogue Interference Affects the Dynamics after Gene Duplication. <i>Trends in Plant Science</i> , 2015, 20, 814-821.	4.3	31
138	An integrated database of wood-formation related genes in plants. <i>Scientific Reports</i> , 2015, 5, 11422.	1.6	3
139	Sequencing of plant genomes – a review. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 361-376.	0.8	20
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142	InteractiVenn: a web-based tool for the analysis of sets through Venn diagrams. <i>BMC Bioinformatics</i> , 2015, 16, 169.	1.2	1,609
143	Identification of miRNAs involved in fruit ripening in Cavendish bananas by deep sequencing. <i>BMC Genomics</i> , 2015, 16, 776.	1.2	61
144	Genome-wide identification and characterization of the superoxide dismutase gene family in <i>Musa acuminata</i> cv. Tianbaojiao (AAA group). <i>BMC Genomics</i> , 2015, 16, 823.	1.2	74
145	Molecular cloning and expression analysis of KIN10 and cold-acclimation related genes in wild banana ‘Huanxi’ (Musa itinerans). <i>SpringerPlus</i> , 2015, 4, 829.	1.2	7
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147	Analysis of the giant genomes of <i>Fritillaria</i> ( <i>Liliaceae</i> ) indicates that a lack of DNA removal characterizes extreme expansions in genome size. <i>New Phytologist</i> , 2015, 208, 596-607.	3.5	122
148	Genetic Diversity in Bananas and Plantains ( <i>Musa</i> spp.). , 0, , .		6
149	Transcriptome analysis of banana ( <i>Musa balbisiana</i> ) based on next-generation sequencing technology. <i>Turk Tarim Ve Ormancilik Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2015, 39, 705-717.	0.8	13
150	Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. <i>Frontiers in Plant Science</i> , 2015, 6, 563.	1.7	243
151	Genome-Wide Identification and Expression Analyses of Aquaporin Gene Family during Development and Abiotic Stress in Banana. <i>International Journal of Molecular Sciences</i> , 2015, 16, 19728-19751.	1.8	69
152	Banana Ovate Family Protein MaOFP1 and MADS-Box Protein MuMADS1 Antagonistically Regulated Banana Fruit Ripening. <i>PLoS ONE</i> , 2015, 10, e0123870.	1.1	24
153	Small RNA Profiling of Two Important Cultivars of Banana and Overexpression of miRNA156 in Transgenic Banana Plants. <i>PLoS ONE</i> , 2015, 10, e0127179.	1.1	19

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155	Comprehensive Evolutionary and Expression Analysis of FCS-Like Zinc finger Gene Family Yields Insights into Their Origin, Expansion and Divergence. PLoS ONE, 2015, 10, e0134328.	1.1	22
156	Worse Comes to Worst: Bananas and Panama Disease“When Plant and Pathogen Clones Meet. PLoS Pathogens, 2015, 11, e1005197.	2.1	167
157	The auxin response factor gene family in banana: genome-wide identification and expression analyses during development, ripening, and abiotic stress. Frontiers in Plant Science, 2015, 6, 742.	1.7	131
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