

Small auxin upregulated RNA (*SAUR*) gene family
and its phylogenetic comparison with *Arabidopsis*

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Genome-wide and molecular evolution analysis of the subtilase gene family in <i>Vitis vinifera</i> . <i>BMC Genomics</i> , 2014, 15, 1116.	1.2	28
2	Comparative genomic analysis of the Sm gene family in rice and maize. <i>Gene</i> , 2014, 539, 238-249.	1.0	14
3	Comparative analysis of the phytocyanin gene family in 10 plant species: a focus on <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2015, 6, 515.	1.7	36
4	Genome-wide identification, expression analysis of auxin-responsive GH3 family genes in maize (<i>Zea mays</i> L.) under abiotic stresses. <i>Journal of Integrative Plant Biology</i> , 2015, 57, 783-795.	4.1	104
5	SAUR Proteins as Effectors of Hormonal and Environmental Signals in Plant Growth. <i>Molecular Plant</i> , 2015, 8, 1153-1164.	3.9	386
6	Comprehensive analysis of SAUR gene family in citrus and its transcriptional correlation with fruitlet drop from abscission zone A. <i>Functional and Integrative Genomics</i> , 2015, 15, 729-740.	1.4	27
7	Identification and Analysis of <i>Medicago truncatula</i> Auxin Transporter Gene Families Uncover their Roles in Responses to <i>Sinorhizobium meliloti</i> Infection. <i>Plant and Cell Physiology</i> , 2015, 56, 1930-1943.	1.5	23
8	Identification and phylogenetic analysis of late embryogenesis abundant proteins family in tomato (<i>Solanum lycopersicum</i>). <i>Planta</i> , 2015, 241, 757-772.	1.6	93
9	Comparative Analysis of Dof Transcription Factor Family in Maize. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 1245-1258.	1.0	27
10	Analysis of the Prefoldin Gene Family in 14 Plant Species. <i>Frontiers in Plant Science</i> , 2016, 7, 317.	1.7	20
11	The papaya CpAUX1/LAX and CpPIN genes: structure, phylogeny and expression analysis related to root formation on in vitro plantlets. <i>Plant Cell, Tissue and Organ Culture</i> , 2016, 126, 187-204.	1.2	12
12	Identification of small auxin-up RNA (SAUR) genes in Urticales plants: mulberry (<i>Morus notabilis</i>), hemp (<i>Cannabis sativa</i>) and ramie (<i>Boehmeria nivea</i>). <i>Journal of Genetics</i> , 2016, 95, 119-129.	0.4	20
13	Genomewide analysis of MATE-type gene family in maize reveals microsynteny and their expression patterns under aluminum treatment. <i>Journal of Genetics</i> , 2016, 95, 691-704.	0.4	37
14	Evolutionary analysis of the jacalin-related lectin family genes in 11 fishes. <i>Fish and Shellfish Immunology</i> , 2016, 56, 543-553.	1.6	11
15	Non-syntenic genes drive RTCS-dependent regulation of the embryo transcriptome during formation of seminal root primordia in maize (<i>Zea mays</i> L.). <i>Journal of Experimental Botany</i> , 2017, 68, erw422.	2.4	11
16	Expansion and evolution of thaumatin-like protein (TLP) gene family in six plants. <i>Plant Growth Regulation</i> , 2016, 79, 299-307.	1.8	39
17	Transcript profiling analysis reveals crucial genes regulating main metabolism during adventitious root formation in cuttings of <i>Morus alba</i> L.. <i>Plant Growth Regulation</i> , 2016, 79, 251-262.	1.8	11
18	Late Embryogenesis Abundant (LEA) Gene Family in Maize: Identification, Evolution, and Expression Profiles. <i>Plant Molecular Biology Reporter</i> , 2016, 34, 15-28.	1.0	42

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19	Genome-wide analysis and expression characteristics of small auxin-up RNA (<i>SAUR</i>) genes in moso bamboo (<i>Phyllostachys edulis</i>). <i>Genome</i> , 2017, 60, 325-336.	0.9	22
20	Genome-wide identification of SAUR genes in watermelon (<i>Citrullus lanatus</i>). <i>Physiology and Molecular Biology of Plants</i> , 2017, 23, 619-628.	1.4	29
21	Candidate regulators of Early Leaf Development in Maize Perturb Hormone Signalling and Secondary Cell Wall Formation When Constitutively Expressed in Rice. <i>Scientific Reports</i> , 2017, 7, 4535.	1.6	18
22	Dynamic Regulation of Auxin Response during Rice Development Revealed by Newly Established Hormone Biosensor Markers. <i>Frontiers in Plant Science</i> , 2017, 8, 256.	1.7	41
23	The TOR Pathway Is Involved in Adventitious Root Formation in Arabidopsis and Potato. <i>Frontiers in Plant Science</i> , 2017, 8, 784.	1.7	49
24	A genome-wide analysis of the small auxin-up RNA (SAUR) gene family in cotton. <i>BMC Genomics</i> , 2017, 18, 815.	1.2	47
25	Transcriptional and Hormonal Regulation of Weeping Trait in <i>Salix matsudana</i> . <i>Genes</i> , 2017, 8, 359.	1.0	12
26	A <i>Vitis vinifera</i> basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass and reproductive yield. <i>Plant Biotechnology Journal</i> , 2018, 16, 1595-1615.	4.1	39
27	Differential expression of hormone related genes between extreme segregants of a <i>Saccharum</i> interspecific F2 population. <i>Euphytica</i> , 2018, 214, 1.	0.6	2
28	Function of the auxin-responsive gene TaSAUR75 under salt and drought stress. <i>Crop Journal</i> , 2018, 6, 181-190.	2.3	83
29	Association Mapping of Flowering and Height Traits in Germplasm Enhancement of Maize Doubled Haploid (GEMâ€œDH) Lines. <i>Plant Genome</i> , 2018, 11, 170083.	1.6	33
30	SMALL AUXIN UP RNA62/75 Are Required for the Translation of Transcripts Essential for Pollen Tube Growth. <i>Plant Physiology</i> , 2018, 178, 626-640.	2.3	21
31	Genome-wide analysis of poplar SAUR gene family and expression profiles under cold, polyethylene glycol and indole-3-acetic acid treatments. <i>Plant Physiology and Biochemistry</i> , 2018, 128, 50-65.	2.8	31
32	Comparative analysis of the tetraspanin gene family in six teleost fishes. <i>Fish and Shellfish Immunology</i> , 2018, 82, 432-441.	1.6	9
33	Gene Characterization and Expression Analysis Reveal the Importance of Auxin Signaling in Bud Dormancy Regulation in Tea Plant. <i>Journal of Plant Growth Regulation</i> , 2019, 38, 225-240.	2.8	13
34	Uncovering the molecular signature underlying the light intensity-dependent root development in <i>Arabidopsis thaliana</i> . <i>BMC Genomics</i> , 2019, 20, 596.	1.2	17
35	Identification and Expression of SAUR Genes in the CAM Plant Agave. <i>Genes</i> , 2019, 10, 555.	1.0	11
36	Genome-wide identification and characterization of <i>Gretchen Hagen3</i> (<i>GH3</i>) family genes in <i>Brassica napus</i>. <i>Genome</i> , 2019, 62, 597-608.	0.9	7

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37	Genome-Wide Analysis of Cotton Auxin Early Response Gene Families and Their Roles in Somatic Embryogenesis. <i>Genes</i> , 2019, 10, 730.	1.0	18
38	The <i>SAUR</i> gene family: the plant's toolbox for adaptation of growth and development. <i>Journal of Experimental Botany</i> , 2019, 70, 17-27.	2.4	182
39	Genome-scale identification, classification, and tissue specific expression analysis of late embryogenesis abundant (LEA) genes under abiotic stress conditions in <i>Sorghum bicolor</i> L.. <i>PLoS ONE</i> , 2019, 14, e0209980.	1.1	59
40	Structural genome analysis in cultivated potato taxa. <i>Theoretical and Applied Genetics</i> , 2020, 133, 951-966.	1.8	32
41	Transcriptional and physiological analyses of reduced density in apple provide insight into the regulation involved in photosynthesis. <i>PLoS ONE</i> , 2020, 15, e0239737.	1.1	4
42	Genome-wide identification, characterization analysis and expression profiling of auxin-responsive GH3 family genes in wheat (<i>Triticum aestivum</i> L.). <i>Molecular Biology Reports</i> , 2020, 47, 3885-3907.	1.0	23
43	Rapid Auxin-Mediated Cell Expansion. <i>Annual Review of Plant Biology</i> , 2020, 71, 379-402.	8.6	128
44	Interaction of SAUR53 and Its Close Homologs with Calmodulin May Play a Role in Early Development in Arabidopsis. <i>Plant Molecular Biology Reporter</i> , 2020, 38, 343-351.	1.0	6
45	Plant tissue succulence engineering improves water-use efficiency, water-deficit stress attenuation and salinity tolerance in Arabidopsis. <i>Plant Journal</i> , 2020, 103, 1049-1072.	2.8	36
46	Identification and expression analysis of the small auxin-up RNA (SAUR) gene family in apple by inducing of auxin. <i>Gene</i> , 2020, 750, 144725.	1.0	20
47	Genome-wide identification and expression analyses of Sm genes reveal their involvement in early somatic embryogenesis in <i>Dimocarpus longan</i> Lour. <i>PLoS ONE</i> , 2020, 15, e0230795.	1.1	5
48	Genome-wide identification and analysis of <i>Medicago truncatula</i> Small auxin upregulated RNA (SAUR) gene family uncover their roles in nodule formation. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2021, 30, 126-137.	0.9	3
49	Genome-wide identification and characterization of small auxin-up RNA (SAUR) gene family in plants: evolution and expression profiles during normal growth and stress response. <i>BMC Plant Biology</i> , 2021, 21, 4.	1.6	28
50	The Rice Small Auxin-Up RNA Gene OsSAUR33 Regulates Seed Vigor via Sugar Pathway during Early Seed Germination. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1562.	1.8	25
51	Genome-wide identification, characterization, and expression profiles of auxin responsive GH3 gene family in <i>Salvia miltiorrhiza</i> involved in MeJA treatment. <i>Journal of Plant Biochemistry and Biotechnology</i> , 0, , 1.	0.9	2
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53	Synthesis and regulation of auxin and abscisic acid in maize. <i>Plant Signaling and Behavior</i> , 2021, 16, 1891756.	1.2	10
54	Melatonin influences the early growth stage in <i>Zoysia japonica</i> Steud. by regulating plant oxidation and genes of hormones. <i>Scientific Reports</i> , 2021, 11, 12381.	1.6	8

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55	Plant Hormones and Volatiles Response to Temperature Stress in Sweet Corn (<i>Zea mays</i> L.) Seedlings. <i>Journal of Agricultural and Food Chemistry</i> , 2021, 69, 6779-6790.	2.4	20
56	Mapping of QTL for agronomic traits using high-density SNPs with an RIL population in maize. <i>Genes and Genomics</i> , 2021, 43, 1403-1411.	0.5	7
57	Identification and Analysis of <i>Aux/IAA</i> Family in <i>Acer rubrum</i> . <i>Evolutionary Bioinformatics</i> , 2021, 17, 117693432199412.	0.6	3
58	Evolutionary Analysis of GH3 Genes in Six <i>Oryza</i> Species/Subspecies and Their Expression under Salinity Stress in <i>Oryza sativa</i> ssp. <i>japonica</i> . <i>Plants</i> , 2019, 8, 30.	1.6	46
59	Recent research progress on the functional roles and regulatory mechanisms of <i>SMALL AUXIN UP RNA</i> gene family. <i>Journal of Plant Biotechnology</i> , 2018, 45, 183-189.	0.1	0
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62	Morphological Characterization and Transcriptome Analysis of New Dwarf and Narrow-Leaf (<i>dnl2</i>) Mutant in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 795.	1.8	8
63	Identification of the soybean small auxin upregulated RNA (SAUR) gene family and specific haplotype for drought tolerance. <i>Biologia (Poland)</i> , 2022, 77, 1197-1217.	0.8	4
64	Genome-wide identification and expression of SAUR gene family in peanut (<i>Arachis hypogaea</i> L.) and functional identification of <i>AhSAUR3</i> in drought tolerance. <i>BMC Plant Biology</i> , 2022, 22, 178.	1.6	5
65	Local and Systemic Response to Heterogeneous Sulfate Resupply after Sulfur Deficiency in Rice. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6203.	1.8	3
66	<i>SAUR8</i> , a small auxin-up RNA gene in poplar, confers drought tolerance to transgenic <i>Arabidopsis</i> plants. <i>Gene</i> , 2022, 837, 146692.	1.0	2
67	Genome-Wide Identification of <i>TaSAUR</i> Gene Family Members in Hexaploid Wheat and Functional Characterization of <i>TaSAUR66-5B</i> in Improving Nitrogen Use Efficiency. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7574.	1.8	2
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69	A Long Noncoding RNA Derived from <i>lncRNA</i> mRNA Networks Modulates Seed Vigor. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9472.	1.8	3
70	Genome-wide identification and analysis of SAUR gene family in strawberry (<i>Fragaria vesca</i> L.) reveal its potential functions in different developmental stages. <i>Acta Botanica Brasilica</i> , 0, 36, .	0.8	1
71	Comparative transcriptome profiling and weighted gene co-expression network analysis to identify core genes in maize (<i>Zea mays</i> L.) silks infected by multiple fungi. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
72	Comparative Biochemical and Transcriptomic Analyses Provide New Insights into Phytoplasma Infection Responses in Cucumber. <i>Genes</i> , 2022, 13, 1903.	1.0	1

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73	Genome-Wide Analysis of SAUR Gene Family Identifies a Candidate Associated with Fruit Size in Loquat (<i>Eriobotrya japonica</i> Lindl.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 13271.	1.8	3
74	Molecular characterization of the GH3 family in alfalfa under abiotic stress. <i>Gene</i> , 2023, 851, 146982.	1.0	3
75	Genome-Wide Identification of the SAUR Gene Family in Wax Gourd (<i>Benincasa hispida</i>) and Functional Characterization of BhSAUR60 during Fruit Development. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14021.	1.8	3
76	Analysis of the Small Auxin-Up RNA (SAUR) Genes Regulating Root Growth Angle (RGA) in Apple. <i>Genes</i> , 2022, 13, 2121.	1.0	2
77	Genome-wide identification of the bHLH transcription factor family and analysis of bHLH genes related to puerarin biosynthesis in <i>Pueraria lobata</i> var. <i>thomsonii</i> (Benth.). <i>Plant Gene</i> , 2023, 33, 100390.	1.4	1
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80	An EMS-induced allele of the <i>brachytic2</i> gene can reduce plant height in maize. <i>Plant Cell Reports</i> , 2023, 42, 749-761.	2.8	1
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82	Genome-Wide Identification and Functional Analysis of the Roles of SAUR Gene Family Members in the Promotion of Cucumber Root Expansion. <i>International Journal of Molecular Sciences</i> , 2023, 24, 5940.	1.8	2
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