



Gene Model Search Results

Locus Identifier	Representative Gene Model Name	Gene Description	Gene Model Type	Primary Gene Symbol	All Gene Symbols
AT4G34150	AT4G34150.1	Calcium-dependent lipid-binding (CaLB domain) family protein;(source:Araport11)	protein_coding		
AT5G47690	AT5G47690.3	One of 5 PO76/PDS5 cohesion cofactor orthologs of Arabidopsis.	protein_coding	(PDS5A)	(PDS5) (ATPDS5A) (PDS5A)
AT5G48380	AT5G48380.1	Encodes a BAK1-interacting receptor-like kinase named BIR1. Negatively regulates multiple plant resistance signaling pathways, one of which is the SOBIR1(AT2G31880)-dependent pathway.	protein_coding	BAK1-INTERACTING RECEPTOR-LIKE KINASE 1 (BIR1)	BAK1-INTERACTING RECEPTOR-LIKE KINASE 1 (BIR1)
AT5G65700	AT5G65700.1	Encodes a CLAVATA1-related receptor kinase-like protein required for both shoot and flower meristem function. Very similar to BAM2, with more than 85% a.a. identity. It has a broad expression pattern and is involved in vascular strand development in the leaf, control of leaf shape, size and symmetry, male gametophyte development and ovule specification and function. Anthers of double mutants (bam1bam2) appeared abnormal at a very early stage and lack the endothecium, middle, and tapetum layers. Further analyses revealed that cells interior to the epidermis (in anther tissue) acquire some characteristics of pollen mother cells (PMCs), suggesting defects in cell fate specification. The pollen mother-like cells degenerate before the completion of meiosis, suggesting that these cells are defective. In addition, the BAM1 expression pattern supports both an early role in promoting somatic cell fates and a subsequent function in the PMCs. The mRNA is cell-to-cell mobile.	protein_coding	BARELY ANY MERISTEM 1 (BAM1)	BARELY ANY MERISTEM 1 (BAM1)
AT1G55530	AT1G55530.1	RING/U-box superfamily protein;(source:Araport11)	protein_coding	BCA2A ZINC FINGER ATL 6 (BTL06)	BCA2A ZINC FINGER ATL 6 (BTL06)
AT1G33730	AT1G33730.1	cytochrome P450, family 76, subfamily C, polypeptide 5;(source:Araport11)	protein_coding	CYTOCHROME P450, FAMILY 76, SUBFAMILY C, POLYPEPTIDE 5 (CYP76C5)	CYTOCHROME P450, FAMILY 76, SUBFAMILY C, POLYPEPTIDE 5 (CYP76C5)
AT1G07910	AT1G07910.2	Encodes a tRNA ligase that resembles the yeast Trl1 RNA ligase in structure and function but very different in sequence. Like Trl1, AtRNL consists of two domains, an N-terminal ligase component and a C-terminal 5'-kinase/2',3'-cyclic phosphodiesterase (CPD) component that can function in tRNA splicing in vivo when expressed as separate polypeptides. Requires a 2'-PO4 end for tRNA splicing in vivo.	protein_coding	RNALIGASE (RNL)	ARABIDOPSIS THALIANA RNA LIGASE (ATRNL) RNALIGASE (RNL) (RLG1) ZYGOTE-ARREST 3 (ZYG3) ATRLG1 (AtRLG1)

Last updated on : Fri Sep 29 14:00:07 2023