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| **Select Polysaccharide Metabolism**  **Gene/Protein Name** | **Source Organism** | **E-value** | **Fold of Increase** | **Comments on Function** |
| Cullin-4 | Arabidopsis thaliana | 0 | 1.609046072 | Component of the CUL4-RBX1- CDD ( COP10-DBB1a-DET1) E3 ubiquitin-protein ligase complex which mediates the ubiquitination and subsequent proteasomal degradation of target proteins. Participates in the CDD complex to light-mediated control of development. May repress photomorphogensis thorugh enhancing COP1 E3 ubiquitin-protein ligase activity. Acts together with the CUL4-DDB1-COP1-SPA E3 ubiquitin-protein ligase complexes in the repression of photomorphogenesis and flowering time. Component ot the CUL4-RBX1-DDB1-PRL1 E3 ubiquitin-protein ligase complex which mediates ubiquitination and subsequent degradtion of AKIN10. Component of the CUL4-RBX1-DDB1-DWA1/DWA2 E3 ubiquitin-protein ligase complex that acts as negative regulator in abscisic acid (ABA) signaling and may target ABI5 for degradation. <http://www.ncbi.nlm.nih.gov/protein/Q8LGH4> |
| Glycylpeptide N-tetradecanoyltransferase 1 | Arabidopsis thaliana | 3.00E-156 | 1.609046072 | Adds a myristoyl group to the N-terminal glycine residue of certain cellular proteins. Can also use decanoyl-CoA and lauroyl-CoA as substrates. <http://www.ncbi.nlm.nih.gov/protein/Q9LTR9> |
| Two-component response regulator ARR10 | Arabidopsis thaliana | 7.00E-15 | 1.609046072 | Transcriptional activator that binds specifically to the DNA sequence 5'-[AG]GATT-3'. Functions as a response regulator involved in His-to-Asp phosphorelay signal transduction system. Phosphorylation of the Asp residue in the receiver domain activates the ability of the protein to promote the transcription of target genes. Could directly activate some type-A response regulators in response to cytokinins. <http://www.ncbi.nlm.nih.gov/protein/O49397> |
| Phospholipid-transporting ATPase 3 | Arabidopsis thaliana | 1.00E-40 | 1.609046072 | Involved in transport of phospholipids. Contributes to transmembrane flipping of lipids. Required for secretory processes during plant development. Requires an interaction with an ALIS protein for activity. Has activity with phosphatidylserine, phosphatidylcholine and phosphatidylethanolamine, but not with lysolipid. <http://www.ncbi.nlm.nih.gov/protein/Q9XIE6> |
| Kinesin-like calmodulin-binding protein | Arabidopsis thaliana | 3.00E-28 | 1.609046072 | Minus-end microtubule-dependent motor protein involved in the regulation of cell division and trichome morphogenesis. Possesses basal and microtubule-stimulated ATPase activities. <http://www.ncbi.nlm.nih.gov/protein/Q9FHN8> |
| DNA topoisomerase 1 | Arabidopsis thaliana | 1.00E-156 | 1.609046072 | Releases the supercoiling and torsional tension of DNA introduced during the DNA replication and transcription by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand break via transesterification at a target site in duplex DNA. The scissile phosphodiester is attacked by the catalytic tyrosine of the enzyme, resulting in the formation of a DNA-(3'-phosphotyrosyl)-enzyme intermediate and the expulsion of a 5'-OH DNA strand. The free DNA strand than undergoes passage around the unbroken strand thus removing DNA supercoils. Finally, in the religation step, the DNA 5'-OH attacks the covalent intermediate to expel the active-site tyrosine and restore the DNA phosphodiester backbone (By similarity). <http://www.ncbi.nlm.nih.gov/protein/P30181> |
| 26S proteasome non-ATPase regulatory subunit RPN12A | Arabidopsis thaliana | 2.00E-43 | 1.609046072 | Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins. May help to control the degradation of one or more factors that repress cytokinin signaling. <http://www.ncbi.nlm.nih.gov/protein/Q9SGW3> |
| Nucleolin 1 | Arabidopsis thaliana | 7.00E-17 | 1.609046072 | Involved in pre-rRNA processing and ribosome assembly. Is associated with intranucleolar chromatin and pre-ribosomal particles and plays a role in controlling activation and repression of a specific subset of rRNA genes located in distinctive nucleolar organizer regions. Binds specifically rDNA chromatin and may be required to maintain rDNA chromatin structure, but is probably not required for the overall histone methylation status of 45S rRNA genes. <http://www.ncbi.nlm.nih.gov/protein/Q9FVQ1> |
| Peptidyl-prolyl cis-trans isomerase FKBP42 | Arabidopsis thaliana | 3.00E-21 | 1.609046072 | PPIases accelerate the folding of proteins. It catalyzes the cis-trans isomerization of proline imidic peptide bonds in oligopeptides (By similarity). Modulates the uptake of MRP substrates into the vacuole; reduces metolachlor-GS (MOC-GS) and enhances 17-beta-estradiol 17-(beta-D-glucuronide) (E(2)17betaG) uptake. Regulates cell elongation and orientation. Functions as a positive regulator of PGP1-mediated auxin transport. Confers drug modulation of PGP1 efflux activity as interaction with NPA or flavonol quercetin prevents its physical and functional interaction with PGP1. Required for the proper localization of auxin-related ABCB transporters. Plays a role in brassinosteroid (BR) signaling pathway. <http://www.ncbi.nlm.nih.gov/protein/Q9LDC0> |
| WD-40 repeat-containing protein MSI4 | Arabidopsis thaliana | 1.00E-75 | 1.609046072 | Core histone-binding subunit that may target chromatinmassembly factors, chromatin remodeling factors and histone deacetylases to their histone substrates in a manner that is regulated by nucleosomal DNA. Component of the flowering autonomous pathway, which positively regulates flowering by promoting transcriptional repression of the flowering repressor FLC. May promote histone deacetylation at the FLC locus leading to the formation of repressive chromatin structures. Also negatively regulates cold-responsive genes. <http://www.ncbi.nlm.nih.gov/protein/O22607> |
| Probable 26S proteasome non-ATPase regulatory subunit 7 | Arabidopsis thaliana | 2.00E-118 | 1.609046072 | Acts as a regulatory subunit of the 26S proteasome which is involved in the ATP-dependent degradation of ubiquitinated proteins (By similarity). <http://www.ncbi.nlm.nih.gov/protein/O24412> |
| Probable adenylate kinase 1 | Arabidopsis thaliana | 1.00E-28 | 1.609046072 | This small ubiquitous enzyme is essential for maintenance and cell growth (By similarity). http://www.ncbi.nlm.nih.gov/protein/  Q9ZUU1 |