SUPPLEMENTAL DATA

Supplemental Table S1. Annotated articles

Authors	Title	Journal	PMID/DOI
Abdulrazzak N, Pollet B, Ehlting J, Larsen K, Asnaghi C, Ronseau S, Proux C, Erhardt M, Seltzer V, Renou JP, Ullmann P, Pauly M, Lapierre C, Werck-Reichhart D	A coumaroyl-ester-3-hydroxylase insertion mutant reveals the existence of nonredundant meta-hydroxylation pathways and essential roles for phenolic precursors in cell expansion and plant growth	Plant Physiol. 2006 Jan;140(1):30-48. Epub 2005 Dec 23. Erratum in: Plant Physiol. 2007 Apr;143(4):1982. Plant Physiol. 2006 Aug;141(4):1708	16377748
Adachi S, Nobusawa T, Umeda M	Quantitative and cell type-specific transcriptional regulation of A-type cyclin-dependent kinase in Arabidopsis thaliana	Dev Biol. 2009 May 15;329(2):306-14. doi: 10.1016/j.ydbio.2009.03.002. Epub 2009 Mar 11	19285489
Aharoni A, Dixit S, Jetter R, Thoenes E, van Arkel G, Pereira A	The SHINE clade of AP2 domain transcription factors activates wax biosynthesis, alters cuticle properties, and confers drought tolerance when overexpressed in Arabidopsis	Plant Cell. 2004 Sep;16(9):2463-80. Epub 2004 Aug 19	15319479
Aloni R, Schwalm K, Langhans M, Ullrich CI	Gradual shifts in sites of free-auxin production during leaf-primordium development and their role in vascular differentiation and leaf morphogenesis in Arabidopsis	Planta. 2003 Mar;216(5):841-53. Epub 2002 Nov 26	12624772
Alonso-Peral MM, Candela H, del Pozo JC, Martínez-Laborda A, Ponce MR, Micol JL	The HVE/CAND1 gene is required for the early patterning of leaf venation in Arabidopsis	Development. 2006 Oct;133(19):3755-66. Epub 2006 Aug 30	16943276
Anastasiou E, Kenz S, Gerstung M, MacLean D, Timmer J, Fleck C, Lenhard M	Control of plant organ size by KLUH/CYP78A5-dependent intercellular signaling	Dev Cell. 2007 Dec;13(6):843-56	18061566
Argyros RD, Mathews DE, Chiang YH, Palmer CM, Thibault DM, Etheridge N, Argyros DA, Mason MG, Kieber JJ, Schaller GE	Type B response regulators of Arabidopsis play key roles in cytokinin signaling and plant development	Plant Cell. 2008 Aug;20(8):2102-16. doi: 10.1105/tpc.108.059584. Epub 2008 Aug 22	18723577
Asano T, Yoshioka Y, Kurei S, Sakamoto W, Machida Y; Sodmergen	A mutation of the CRUMPLED LEAF gene that encodes a protein localized in the outer envelope membrane of plastids affects the pattern of cell division, cell differentiation, and plastid division in Arabidopsis	Plant J. 2004 May;38(3):448-59	15086805
Autran D, Jonak C, Belcram K, Beemster GT, Kronenberger J,	Cell numbers and leaf development in Arabidopsis: a functional analysis of the STRUWWELPETER gene	EMBO J. 2002 Nov 15;21(22):6036-49	12426376

Grandjean O, Inzé D, Traas J			
Azhakanandam S, Nole-Wilson S, Bao F, Franks RG	SEUSS and AINTEGUMENTA mediate patterning and ovule initiation during gynoecium medial domain development	Plant Physiol. 2008 Mar;146(3):1165-81. doi: 10.1104/pp.107.114751. Epub 2008 Jan 9	18184731
Barrero JM, González-Bayón R, del Pozo JC, Ponce MR, Micol JL	INCURVATA2 encodes the catalytic subunit of DNA Polymerase alpha and interacts with genes involved in chromatin-mediated cellular memory in Arabidopsis thaliana	Plant Cell. 2007 Sep;19(9):2822-38. Epub 2007 Sep 14	17873092
Barrero JM, Piqueras P, González-Guzmán M, Serrano R, Rodríguez PL, Ponce MR, Micol JL	A mutational analysis of the ABA1 gene of Arabidopsis thaliana highlights the involvement of ABA in vegetative development	J Exp Bot. 2005 Aug;56(418):2071-83. Epub 2005 Jun 27	15983017
Barrero RA, Umeda M, Yamamura S, Uchimiya H	Arabidopsis CAP regulates the actin cytoskeleton necessary for plant cell elongation and division	Plant Cell. 2002 Jan;14(1):149-63	11826305
Bassil E, Ohto MA, Esumi T, Tajima H, Zhu Z, Cagnac O, Belmonte M, Peleg Z, Yamaguchi T, Blumwald E	The Arabidopsis intracellular Na+/H+ antiporters NHX5 and NHX6 are endosome associated and necessary for plant growth and development	Plant Cell. 2011 Jan;23(1):224-39. doi: 10.1105/tpc.110.079426. Epub 2011 Jan 28	21278129
Beemster GT, Vercruysse S, De Veylder L, Kuiper M, Inzé D	The Arabidopsis leaf as a model system for investigating the role of cell cycle regulation in organ growth	J Plant Res. 2006 Jan;119(1):43-50. Epub 2005 Nov 15	16292465
Bemis SM, Torii KU	Autonomy of cell proliferation and developmental programs during Arabidopsis aboveground organ morphogenesis	Dev Biol. 2007 Apr 1;304(1):367-81. Epub 2006 Dec 29	17258192
Berná G, Robles P, Micol JL	A mutational analysis of leaf morphogenesis in Arabidopsis thaliana	Genetics. 1999 Jun;152(2):729-42	10353913
Bohmert K, Camus I, Bellini C, Bouchez D, Caboche M, Benning C	AGO1 defines a novel locus of Arabidopsis controlling leaf development	EMBO J. 1998 Jan 2;17(1):170-80	9427751
Bollman KM, Aukerman MJ, Park MY, Hunter C, Berardini TZ, Poethig RS	HASTY, the Arabidopsis ortholog of exportin 5/MSN5, regulates phase change and morphogenesis	Development. 2003 Apr;130(8):1493-504	12620976
Bonser SP, Geber MA	Growth form evolution and shifting habitat specialization in annual plants	J Evol Biol. 2005 Jul;18(4):1009-18	16033574
Breeze E, Harrison E, McHattie S, Hughes L, Hickman R, Hill C, Kiddle S, Kim YS, Penfold CA, Jenkins D, Zhang C, Morris K, Jenner C, Jackson S, Thomas B, Tabrett A, Legaie R, Moore JD, Wild DL, Ott S, Rand D, Beynon J, Denby K, Mead A, Buchanan-Wollaston V	High-resolution temporal profiling of transcripts during Arabidopsis leaf senescence reveals a distinct chronology of processes and regulation	Plant Cell. 2011 Mar;23(3):873-94. doi: 10.1105/tpc.111.083345. Epub 2011 Mar 29	21447789
Breuer C, Stacey NJ, West CE, Zhao	BIN4, a novel component of the plant DNA	Plant Cell. 2007 Nov;19(11):3655-68. Epub	18055605

Y, Chory J, Tsukaya H, Azumi Y, Maxwell A, Roberts K, Sugimoto-Shirasu K	topoisomerase VI complex, is required for endoreduplication in Arabidopsis	2007 Nov 30	
Brioudes F, Thierry AM, Chambrier P, Mollereau B, Bendahmane M	Translationally controlled tumor protein is a conserved mitotic growth integrator in animals and plants	Proc Natl Acad Sci U S A. 2010 Sep 14;107(37):16384-9. doi: 10.1073/pnas.1007926107. Epub 2010 Aug 24	20736351
Broun P, Poindexter P, Osborne E, Jiang CZ, Riechmann JL	WIN1, a transcriptional activator of epidermal wax accumulation in Arabidopsis	Proc Natl Acad Sci U S A. 2004 Mar 30;101(13):4706-11. Epub 2004 Mar 22	15070782
Buschmann H, Hauptmann M, Niessing D, Lloyd CW, Schäffner AR	Helical growth of the Arabidopsis mutant tortifolia2 does not depend on cell division patterns but involves handed twisting of isolated cells	Plant Cell. 2009 Jul;21(7):2090-106. doi: 10.1105/tpc.108.061242. Epub 2009 Jul 28	19638477
Byrne ME, Barley R, Curtis M, Arroyo JM, Dunham M, Hudson A, Martienssen RA	Asymmetric leaves1 mediates leaf patterning and stem cell function in Arabidopsis	Nature. 2000 Dec 21-28;408(6815):967-71	11140682
Candela H, Martínez-Laborda A, Micol JL	Venation pattern formation in Arabidopsis thaliana vegetative leaves	Dev Biol. 1999 Jan 1;205(1):205-16	9882508
Catala R, Ouyang J, Abreu IA, Hu Y, Seo H, Zhang X, Chua NH	The Arabidopsis E3 SUMO ligase SIZ1 regulates plant growth and drought responses	Plant Cell. 2007 Sep;19(9):2952-66. Epub 2007 Sep 28	17905899
Chen JH, Jiang HW, Hsieh EJ, Chen HY, Chien CT, Hsieh HL, Lin TP	Drought and salt stress tolerance of an Arabidopsis glutathione S-transferase U17 knockout mutant are attributed to the combined effect of glutathione and abscisic acid	Plant Physiol. 2012 Jan;158(1):340-51. doi: 10.1104/pp.111.181875. Epub 2011 Nov 17	22095046
Chitwood DH, Headland LR, Ranjan A, Martinez CC, Braybrook SA, Koenig DP, Kuhlemeier C, Smith RS, Sinha NR	Leaf asymmetry as a developmental constraint imposed by auxin-dependent phyllotactic patterning	Plant Cell. 2012 Jun;24(6):2318-27. doi: 10.1105/tpc.112.098798. Epub 2012 Jun 21	22722959
Chiu WH, Chandler J, Cnops G, Van Lijsebettens M, Werr W	Mutations in the TORNADO2 gene affect cellular decisions in the peripheral zone of the shoot apical meristem of Arabidopsis thaliana	Plant Mol Biol. 2007 Apr;63(6):731-44. Epub 2007 Feb 16	17351828
Cho HT, Cosgrove DJ	Altered expression of expansin modulates leaf growth and pedicel abscission in Arabidopsis thaliana	Proc Natl Acad Sci U S A. 2000 Aug 15;97(17):9783-8	10931949
Choe S, Fujioka S, Noguchi T, Takatsuto S, Yoshida S, Feldmann KA	Overexpression of DWARF4 in the brassinosteroid biosynthetic pathway results in increased vegetative growth and seed yield in Arabidopsis	Plant J. 2001 Jun;26(6):573-82	11489171
Chua YL, Channelière S, Mott E, Gray JC	The bromodomain protein GTE6 controls leaf development in Arabidopsis by histone acetylation at ASYMMETRIC LEAVES1	Genes Dev. 2005 Sep 15;19(18):2245-54	16166385

Clay NK, Nelson T	Arabidopsis thickvein mutation affects vein thickness and organ vascularization, and resides in a provascular cell-specific spermine synthase involved in vein definition and in polar auxin transport	Plant Physiol. 2005 Jun;138(2):767-77. Epub 2005 May 13	15894745
Clay NK, Nelson T	The recessive epigenetic swellmap mutation affects the expression of two step II splicing factors required for the transcription of the cell proliferation gene STRUWWELPETER and for the timing of cell cycle arrest in the Arabidopsis leaf	Plant Cell. 2005 Jul;17(7):1994-2008. Epub 2005 Jun 3	15937226
Cnops G, Jover-Gil S, Peters JL, Neyt P, De Block S, Robles P, Ponce MR, Gerats T, Micol JL, Van Lijsebettens M	The rotunda2 mutants identify a role for the LEUNIG gene in vegetative leaf morphogenesis	J Exp Bot. 2004 Jul;55(402):1529-39. Epub 2004 Jun 18	15208345
Cnops G, Neyt P, Raes J, Petrarulo M, Nelissen H, Malenica N, Luschnig C, Tietz O, Ditengou F, Palme K, Azmi A, Prinsen E, Van Lijsebettens M	The TORNADO1 and TORNADO2 genes function in several patterning processes during early leaf development in Arabidopsis thaliana	Plant Cell. 2006 Apr;18(4):852-66. Epub 2006 Mar 10	16531491
Coles JP, Phillips AL, Croker SJ, García-Lepe R, Lewis MJ, Hedden P	Modification of gibberellin production and plant development in Arabidopsis by sense and antisense expression of gibberellin 20-oxidase genes	Plant J. 1999 Mar;17(5):547-56	10205907
Coll-Garcia D, Mazuch J, Altmann T, Müssig C	EXORDIUM regulates brassinosteroid-responsive genes	FEBS Lett. 2004 Apr 9;563(1-3):82-6	15063727
Cookson SJ, Radziejwoski A, Granier C	Cell and leaf size plasticity in Arabidopsis: what is the role of endoreduplication? Plant Cell Environ	2006 Jul;29(7):1273-83	17080949
Creff A, Sormani R, Desnos T	The two Arabidopsis RPS6 genes, encoding for cytoplasmic ribosomal proteins S6, are functionally equivalent	Plant Mol Biol. 2010 Jul;73(4-5):533-46. doi: 10.1007/s11103-010-9639-y. Epub 2010 May 1	20437080
Cui YL, Jia QS, Yin QQ, Lin GN, Kong MM, Yang ZN	The GDC1 gene encodes a novel ankyrin domain-containing protein that is essential for grana formation in Arabidopsis	Plant Physiol. 2011 Jan;155(1):130-41. doi: 10.1104/pp.110.165589. Epub 2010 Nov 19	21098677
Danisman S, van der Wal F, Dhondt S, Waites R, de Folter S, Bimbo A, van Dijk AD, Muino JM, Cutri L, Dornelas MC, Angenent GC, Immink RG	Arabidopsis class I and class II TCP transcription factors regulate jasmonic acid metabolism and leaf development antagonistically	Plant Physiol. 2012 Aug;159(4):1511-23. doi: 10.1104/pp.112.200303. Epub 2012 Jun 20	22718775
del Pozo JC, Dharmasiri S, Hellmann H, Walker L, Gray WM, Estelle M	AXR1-ECR1-dependent conjugation of RUB1 to the Arabidopsis Cullin AtCUL1 is required for auxin response	Plant Cell. 2002 Feb;14(2):421-33	11884684
Delessert C, Kazan K, Wilson IW, Van Der Straeten D, Manners J, Dennis ES,	The transcription factor ATAF2 represses the expression of pathogenesis-related genes in	Plant J. 2005 Sep;43(5):745-57	16115070

Dolferus R	Arabidopsis		
Deprost D, Yao L, Sormani R, Moreau M, Leterreux G, Nicolaï M, Bedu M, Robaglia C, Meyer C	The Arabidopsis TOR kinase links plant growth, yield, stress resistance and mRNA translation	EMBO Rep. 2007 Sep;8(9):864-70. Epub 2007 Aug 3	17721444
Desvoyes B, Ramirez-Parra E, Xie Q, Chua NH, Gutierrez C	Cell type-specific role of the retinoblastoma/E2F pathway during Arabidopsis leaf development	Plant Physiol. 2006 Jan;140(1):67-80. Epub 2005 Dec 16	16361519
Dewitte W, Riou-Khamlichi C, Scofield S, Healy JM, Jacqmard A, Kilby NJ, Murray JA	Altered cell cycle distribution, hyperplasia, and inhibited differentiation in Arabidopsis caused by the D-type cyclin CYCD3	Plant Cell. 2003 Jan;15(1):79-92	12509523
Dewitte W, Scofield S, Alcasabas AA, Maughan SC, Menges M, Braun N, Collins C, Nieuwland J, Prinsen E, Sundaresan V, Murray JA	Arabidopsis CYCD3 D-type cyclins link cell proliferation and endocycles and are rate-limiting for cytokinin responses	Proc Natl Acad Sci U S A. 2007 Sep 4;104(36):14537-42. Epub 2007 Aug 28	17726100
DeYoung BJ, Bickle KL, Schrage KJ, Muskett P, Patel K, Clark SE	The CLAVATA1-related BAM1, BAM2 and BAM3 receptor kinase-like proteins are required for meristem function in Arabidopsis	Plant J. 2006 Jan;45(1):1-16	16367950
Dharmasiri N, Dharmasiri S, Weijers D, Karunarathna N, Jurgens G, Estelle M	AXL and AXR1 have redundant functions in RUB conjugation and growth and development in Arabidopsis	Plant J. 2007 Oct;52(1):114-23. Epub 2007 Jul 26	17655650
Dharmasiri S, Dharmasiri N, Hellmann H, Estelle M	The RUB/Nedd8 conjugation pathway is required for early development in Arabidopsis	EMBO J. 2003 Apr 15;22(8):1762-70	12682009
Dhawan R, Luo H, Foerster AM, Abuqamar S, Du HN, Briggs SD, Mittelsten Scheid O, Mengiste T	HISTONE MONOUBIQUITINATION1 interacts with a subunit of the mediator complex and regulates defense against necrotrophic fungal pathogens in Arabidopsis	Plant Cell. 2009 Mar;21(3):1000-19. doi: 10.1105/tpc.108.062364. Epub 2009 Mar 13	19286969
Dinneny JR, Yadegari R, Fischer RL, Yanofsky MF, Weigel D	The role of JAGGED in shaping lateral organs	Development. 2004 Mar;131(5):1101-10	14973282
Disch S, Anastasiou E, Sharma VK, Laux T, Fletcher JC, Lenhard M	The E3 ubiquitin ligase BIG BROTHER controls arabidopsis organ size in a dosage-dependent manner	Curr Biol. 2006 Feb 7;16(3):272-9	16461280
Duguay J, Jamal S, Liu Z, Wang TW, Thompson JE	Leaf-specific suppression of deoxyhypusine synthase in Arabidopsis thaliana enhances growth without negative pleiotropic effects	J Plant Physiol. 2007 Apr;164(4):408-20. Epub 2006 Apr 5	16600425
Elliott RC, Betzner AS, Huttner E, Oakes MP, Tucker WQ, Gerentes D, Perez P, Smyth DR	AINTEGUMENTA, an APETALA2-like gene of Arabidopsis with pleiotropic roles in ovule development and floral organ growth	Plant Cell. 1996 Feb;8(2):155-68	8742707
Ellis CM, Nagpal P, Young JC, Hagen G, Guilfoyle TJ, Reed JW	AUXIN RESPONSE FACTOR1 and AUXIN RESPONSE FACTOR2 regulate senescence and floral organ abscission in Arabidopsis thaliana	Development. 2005 Oct;132(20):4563-74. Epub 2005 Sep 21	16176952
Eloy NB, Gonzalez N, Van Leene J, Maleux K, Vanhaeren H, De Milde L,	SAMBA, a plant-specific anaphase-promoting complex/cyclosome regulator is involved in early	Proc Natl Acad Sci U S A. 2012 Aug 21;109(34):13853-8. doi:	22869741

Dhondt S, Vercruysse L, Witters E, Mercier R, Cromer L, Beemster GT, Remaut H, Van Montagu MC, De Jaeger G, Ferreira PC, Inzé D	development and A-type cyclin stabilization	10.1073/pnas.1211418109. Epub 2012 Aug 6	
Engelhorn J, Reimer JJ, Leuz I, Göbel U, Huettel B, Farrona S, Turck F	Development-related PcG target in the apex 4 controls leaf margin architecture in Arabidopsis thaliana	Development. 2012 Jul;139(14):2566-75. doi: 10.1242/dev.078618. Epub 2012 Jun 6	22675210
Engstrom EM, Andersen CM, Gumulak-Smith J, Hu J, Orlova E, Sozzani R, Bowman JL	Arabidopsis homologs of the petunia hairy meristem gene are required for maintenance of shoot and root indeterminacy	Plant Physiol. 2011 Feb;155(2):735-50. doi: 10.1104/pp.110.168757. Epub 2010 Dec 20	21173022
Eshed Y, Baum SF, Perea JV, Bowman JL	Establishment of polarity in lateral organs of plants	Curr Biol. 2001 Aug 21;11(16):1251-60	11525739
Eshed Y, Izhaki A, Baum SF, Floyd SK, Bowman JL	Asymmetric leaf development and blade expansion in Arabidopsis are mediated by KANADI and YABBY activities	Development. 2004 Jun;131(12):2997-3006	15169760
Exner V, Taranto P, Schönrock N, Gruissem W, Hennig L	Chromatin assembly factor CAF-1 is required for cellular differentiation during plant development	Development. 2006 Nov;133(21):4163-72. Epub 2006 Oct 4	17021044
Eyüboglu B, Pfister K, Haberer G, Chevalier D, Fuchs A, Mayer KF, Schneitz K	Molecular characterisation of the STRUBBELIG-RECEPTOR FAMILY of genes encoding putative leucine-rich repeat receptor-like kinases in Arabidopsis thaliana	BMC Plant Biol. 2007 Mar 30;7:16	17397538
Falkenberg B, Witt I, Zanor MI, Steinhauser D, Mueller-Roeber B, Hesse H, Hoefgen R	Transcription factors relevant to auxin signalling coordinate broad-spectrum metabolic shifts including sulphur metabolism	J Exp Bot. 2008;59(10):2831-46. doi: 10.1093/jxb/ern144	18596113
Feng G, Qin Z, Yan J, Zhang X, Hu Y	Arabidopsis ORGAN SIZE RELATED1 regulates organ growth and final organ size in orchestration with ARGOS and ARL	New Phytol. 2011 Aug;191(3):635-46. doi: 10.1111/j.1469-8137.2011.03710.x. Epub 2011 Apr 1	21457262
Fleury D, Himanen K, Cnops G, Nelissen H, Boccardi TM, Maere S, Beemster GT, Neyt P, Anami S, Robles P, Micol JL, Inzé D, Van Lijsebettens M	The Arabidopsis thaliana homolog of yeast BRE1 has a function in cell cycle regulation during early leaf and root growth	Plant Cell. 2007 Feb;19(2):417-32. Epub 2007 Feb 28	17329565
Folkers U, Kirik V, Schöbinger U, Falk S, Krishnakumar S, Pollock MA, Oppenheimer DG, Day I, Reddy AS, Jürgens G, Hülskamp M	The cell morphogenesis gene ANGUSTIFOLIA encodes a CtBP/BARS-like protein and is involved in the control of the microtubule cytoskeleton	EMBO J. 2002 Mar 15;21(6):1280-8. Erratum in: EMBO J 2002 May 15;21(10):2507. Reddy AR [corrected to Reddy ASN]	11889034
Fujikura U, Horiguchi G, Ponce MR, Micol JL, Tsukaya H	Coordination of cell proliferation and cell expansion mediated by ribosome-related processes in the leaves of Arabidopsis thaliana	Plant J. 2009 Aug;59(3):499-508. doi: 10.1111/j.1365-313X.2009.03886.x. Epub 2009 Apr 6. Erratum in: Plant J. 2009	19392710

		Dec;60(5):930	
Galichet A, Gruissem W	Developmentally controlled farnesylation modulates AtNAP1;1 function in cell proliferation and cell expansion during Arabidopsis leaf development	Plant Physiol. 2006 Dec;142(4):1412-26. Epub 2006 Oct 13	17041028
Garcia D, Collier SA, Byrne ME, Martienssen RA	Specification of leaf polarity in Arabidopsis via the trans-acting siRNA pathway	Curr Biol. 2006 May 9;16(9):933-8	16682355
Gardiner J, Donner TJ, Scarpella E	Simultaneous activation of SHR and ATHB8 expression defines switch to preprocambial cell state in Arabidopsis leaf development	Dev Dyn. 2011 Jan;240(1):261-70. doi: 10.1002/dvdy.22516	21128301
Gilkerson J, Perez-Ruiz JM, Chory J, Callis J	The plastid-localized pfkB-type carbohydrate kinases FRUCTOKINASE-LIKE 1 and 2 are essential for growth and development of Arabidopsis thaliana	BMC Plant Biol. 2012 Jul 8;12:102. doi: 10.1186/1471-2229-12-102	22770232
Godge MR, Kumar D, Kumar PP	Arabidopsis HOG1 gene and its petunia homolog PETCBP act as key regulators of yield parameters	Plant Cell Rep. 2008 Sep;27(9):1497-507. doi: 10.1007/s00299-008-0576-z. Epub 2008 Jul 1	18592247
Goh HH, Sloan J, Dorca-Fornell C, Fleming A	Inducible repression of multiple expansin genes leads to growth suppression during leaf development	Plant Physiol. 2012 Aug;159(4):1759-70. doi: 10.1104/pp.112.200881. Epub 2012 Jun 27	22740614
Gonzalez N, De Bodt S, Sulpice R, Jikumaru Y, Chae E, Dhondt S, Van Daele T, De Milde L, Weigel D, Kamiya Y, Stitt M, Beemster GT, Inzé D	Increased leaf size: different means to an end	Plant Physiol. 2010 Jul;153(3):1261-79. doi: 10.1104/pp.110.156018. Epub 2010 May 11	20460583
González-Bayón R, Kinsman EA, Quesada V, Vera A, Robles P, Ponce MR, Pyke KA, Micol JL	Mutations in the RETICULATA gene dramatically alter internal architecture but have little effect on overall organ shape in Arabidopsis leaves	J Exp Bot. 2006;57(12):3019-31. Epub 2006 Jul 26	16873448
Grigg SP, Canales C, Hay A, Tsiantis M	SERRATE coordinates shoot meristem function and leaf axial patterning in Arabidopsis	Nature. 2005 Oct 13;437(7061):1022-6	16222298
Groszmann M, Bylstra Y, Lampugnani ER, Smyth DR	Regulation of tissue-specific expression of SPATULA, a bHLH gene involved in carpel development, seedling germination, and lateral organ growth in Arabidopsis	J Exp Bot. 2010 Mar;61(5):1495-508. doi: 10.1093/jxb/erq015. Epub 2010 Feb 22	20176890
Guan H, Kang D, Fan M, Chen Z, Qu LJ	Overexpression of a new putative membrane protein gene AtMRB1 results in organ size enlargement in Arabidopsis	J Integr Plant Biol. 2009 Feb;51(2):130-9. doi: 10.1111/j.1744-7909.2008.00795.x	19200151
Guenot B, Bayer E, Kierzkowski D, Smith RS, Mandel T, Žádníková P, Benková E, Kuhlemeier C	Pin1-independent leaf initiation in Arabidopsis	Plant Physiol. 2012 Aug;159(4):1501-10. doi: 10.1104/pp.112.200402. Epub 2012 Jun 21	22723086
Guo H, Li L, Ye H, Yu X, Algreen A, Yin Y	Three related receptor-like kinases are required for optimal cell elongation in Arabidopsis thaliana	Proc Natl Acad Sci U S A. 2009 May 5;106(18):7648-53. doi:	19383785

		10.1073/pnas.0812346106. Epub 2009 Apr 21	
Guo H, Ye H, Li L, Yin Y	A family of receptor-like kinases are regulated by BES1 and involved in plant growth in Arabidopsis thaliana	Plant Signal Behav. 2009 Aug;4(8):784-6. doi: 10.1073/pnas.0812346106. Epub 2009 Aug 8	19820315
Ha CM, Jun JH, Fletcher JC	Control of Arabidopsis leaf morphogenesis through regulation of the YABBY and KNOX families of transcription factors	Genetics. 2010 Sep;186(1):197-206. doi: 10.1534/genetics.110.118703. Epub 2010 Jul 6	20610407
Ha CM, Jun JH, Nam HG, Fletcher JC	BLADE-ON-PETIOLE1 encodes a BTB/POZ domain protein required for leaf morphogenesis in Arabidopsis thaliana	Plant Cell Physiol. 2004 Oct;45(10):1361-70	15564519
Ha CM, Jun JH, Nam HG, Fletcher JC	BLADE-ON-PETIOLE 1 and 2 control Arabidopsis lateral organ fate through regulation of LOB domain and adaxial-abaxial polarity genes	Plant Cell. 2007 Jun;19(6):1809-25. Epub 2007 Jun 29	17601823
Ha CM, Kim GT, Kim BC, Jun JH, Soh MS, Ueno Y, Machida Y, Tsukaya H, Nam HG	The BLADE-ON-PETIOLE 1 gene controls leaf pattern formation through the modulation of meristematic activity in Arabidopsis	Development. 2003 Jan;130(1):161-72	12441300
Han W, Rhee HI, Cho JW, Ku MS, Song PS, Wang MH	Overexpression of Arabidopsis ACK1 alters leaf morphology and retards growth and development	Biochem Biophys Res Commun. 2005 May 13;330(3):887-90	15809079
Hanson J, Johannesson H, Engström P	Sugar-dependent alterations in cotyledon and leaf development in transgenic plants expressing the HDZhdip gene ATHB13	Plant Mol Biol. 2001 Feb;45(3):247-62	11292072
Hara K, Yokoo T, Kajita R, Onishi T, Yahata S, Peterson KM, Torii KU, Kakimoto T	Epidermal cell density is autoregulated via a secretory peptide, EPIDERMAL PATTERNING FACTOR 2 in Arabidopsis leaves	Plant Cell Physiol. 2009 Jun;50(6):1019-31. doi: 10.1093/pcp/pcp068. Epub 2009 May 12	19435754
Hasson A, Plessis A, Blein T, Adroher B, Grigg S, Tsiantis M, Boudaoud A, Damerval C, Laufs P	Evolution and diverse roles of the CUP-SHAPED COTYLEDON genes in Arabidopsis leaf development	Plant Cell. 2011 Jan;23(1):54-68. doi: 10.1105/tpc.110.081448. Epub 2011 Jan 21	21258003
Hay A, Barkoulas M, Tsiantis M	ASYMMETRIC LEAVES1 and auxin activities converge to repress BREVIPEDICELLUS expression and promote leaf development in Arabidopsis	Development. 2006 Oct;133(20):3955-61. Epub 2006 Sep 13	16971475
He SS, Liu J, Xie Z, O'Neill D, Dotson S	Arabidopsis E2Fa plays a bimodal role in regulating cell division and cell growth	Plant Mol Biol. 2004 Sep;56(2):171-84	15604736
Hectors K, Jacques E, Prinsen E, Guisez Y, Verbelen JP, Jansen MA, Vissenberg K	UV radiation reduces epidermal cell expansion in leaves of Arabidopsis thaliana	J Exp Bot. 2010 Oct;61(15):4339-49. doi: 10.1093/jxb/erq235. Epub 2010 Aug 11	20702567
Hepworth SR, Zhang Y, McKim S, Li X, Haughn GW	BLADE-ON-PETIOLE-dependent signaling controls leaf and floral patterning in Arabidopsis	Plant Cell. 2005 May;17(5):1434-48. Epub 2005 Apr 1	15805484

Holst K, Schmülling T, Werner T	Enhanced cytokinin degradation in leaf primordia of transgenic Arabidopsis plants reduces leaf size and shoot organ primordia formation	J Plant Physiol. 2011 Aug 15;168(12):1328-34. doi: 10.1016/j.jplph.2011.03.003. Epub 2011 Apr 6	21474200
Hong Y, Devaiah SP, Bahn SC, Thamasandra BN, Li M, Welti R, Wang X	Phospholipase D epsilon and phosphatidic acid enhance Arabidopsis nitrogen signaling and growth	Plant J. 2009 May;58(3):376-87. doi: 10.1111/j.1365-313X.2009.03788.x. Epub 2009 Jan 8	19143999
Horiguchi G, Ferjani A, Fujikura U, Tsukaya H	Coordination of cell proliferation and cell expansion in the control of leaf size in Arabidopsis thaliana	J Plant Res. 2006 Jan;119(1):37-42. Epub 2005 Nov 12. Review	16284709
Horiguchi G, Gonzalez N, Beemster GT, Inzé D, Tsukaya H	Impact of segmental chromosomal duplications on leaf size in the grandifolia-D mutants of Arabidopsis thaliana	Plant J. 2009 Oct;60(1):122-33. doi: 10.1111/j.1365-313X.2009.03940.x. Epub 2009 Jun 5	19508432
Horiguchi G, Kim GT, Tsukaya H	The transcription factor AtGRF5 and the transcription coactivator AN3 regulate cell proliferation in leaf primordia of Arabidopsis thaliana	Plant J. 2005 Jul;43(1):68-78	15960617
Horiguchi G, Mollá-Morales A, Pérez-Pérez JM, Kojima K, Robles P, Ponce MR, Micol JL, Tsukaya H	Differential contributions of ribosomal protein genes to Arabidopsis thaliana leaf development	Plant J. 2011 Mar;65(5):724-36. doi: 10.1111/j.1365-313X.2010.04457.x. Epub 2011 Jan 19	21251100
Horváth BM, Magyar Z, Zhang Y, Hamburger AW, Bakó L, Visser RG, Bachem CW, Bögre L	EBP1 regulates organ size through cell growth and proliferation in plants	EMBO J. 2006 Oct 18;25(20):4909-20. Epub 2006 Oct 5	17024182
Hricová A, Quesada V, Micol JL	The SCABRA3 nuclear gene encodes the plastid RpoTp RNA polymerase, which is required for chloroplast biogenesis and mesophyll cell proliferation in Arabidopsis	Plant Physiol. 2006 Jul;141(3):942-56. Epub 2006 May 12	16698900
Hu W, Ma H	Characterization of a novel putative zinc finger gene MIF1: involvement in multiple hormonal regulation of Arabidopsis development	Plant J. 2006 Feb;45(3):399-422	16412086
Hu Y, Poh HM, Chua NH	The Arabidopsis ARGOS-LIKE gene regulates cell expansion during organ growth	Plant J. 2006 Jul;47(1):1-9. Erratum in: Plant J. 2006 Aug;47(3):490	16824178
Hu Y, Xie Q, Chua NH	The Arabidopsis auxin-inducible gene ARGOS controls lateral organ size	Plant Cell. 2003 Sep;15(9):1951-61	12953103
Hu Z, Qin Z, Wang M, Xu C, Feng G, Liu J, Meng Z, Hu Y	The Arabidopsis SMO2, a homologue of yeast TRM112, modulates progression of cell division during organ growth	Plant J. 2010 Feb;61(4):600-10. doi: 10.1111/j.1365-313X.2009.04085.x. Epub 2009 Nov 19	19929876
Huang S, Raman AS, Ream JE, Fujiwara H, Cerny RE, Brown SM	Overexpression of 20-oxidase confers a gibberellin-overproduction phenotype in Arabidopsis	Plant Physiol. 1998 Nov;118(3):773-81	9808721
Huang X, Zhang X, Yang S	A novel chloroplast-localized protein EMB1303 is	Cell Res. 2009 Oct;19(10):1205-16. doi:	19581937

	required for chloroplast development in Arabidopsis	10.1038/cr.2009.84. Epub 2009 Jul 7. Erratum in: Cell Res. 2009 Oct;19(10):1225	
Hunt L, Gray JE	The signaling peptide EPF2 controls asymmetric cell divisions during stomatal development	Curr Biol. 2009 May 26;19(10):864-9. doi: 10.1016/j.cub.2009.03.069. Epub 2009 Apr 23	19398336
Hunt L, Gray JE	BASL and EPF2 act independently to regulate asymmetric divisions during stomatal development	Plant Signal Behav. 2010 Mar;5(3):278-80. Epub 2010 Mar 18	20220310
Ichihashi Y, Horiguchi G, Gleissberg S, Tsukaya H	The bHLH transcription factor SPATULA controls final leaf size in Arabidopsis thaliana	Plant Cell Physiol. 2010 Feb;51(2):252-61. doi: 10.1093/pcp/pcp184. Epub 2009 Dec 29	20040585
Ikezaki M, Kojima M, Sakakibara H, Kojima S, Ueno Y, Machida C, Machida Y	Genetic networks regulated by ASYMMETRIC LEAVES1 (AS1) and AS2 in leaf development in Arabidopsis thaliana: KNOX genes control five morphological events	Plant J. 2010 Jan;61(1):70-82. doi: 10.1111/j.1365-313X.2009.04033.x. Epub 2009 Sep 26	19891706
Irigoyen S, Karlsson PM, Kuruvilla J, Spetea C, Versaw WK	The sink-specific plastidic phosphate transporter PHT4;2 influences starch accumulation and leaf size in Arabidopsis	Plant Physiol. 2011 Dec;157(4):1765-77. doi: 10.1104/pp.111.181925. Epub 2011 Sep 29	21960139
Iwakawa H, Iwasaki M, Kojima S, Ueno Y, Soma T, Tanaka H, Semiarti E, Machida Y, Machida C	Expression of the ASYMMETRIC LEAVES2 gene in the adaxial domain of Arabidopsis leaves represses cell proliferation in this domain and is critical for the development of properly expanded leaves	Plant J. 2007 Jul;51(2):173-84. Epub 2007 Jun 8	17559509
Jing Y, Cui D, Bao F, Hu Z, Qin Z, Hu Y	Tryptophan deficiency affects organ growth by retarding cell expansion in Arabidopsis	Plant J. 2009 Feb;57(3):511-21. doi: 10.1111/j.1365-313X.2008.03706.x. Epub 2008 Oct 8	18980661
Jonathan Lightner, Douglas W. James Jr., Hugo K. Dooner, John Browse	Altered body morphology is caused by increased stearate levels in a mutant of Arabidopsis	The Plant Journal	10.1046_j. 1365-313X.1994. 06030401.x
Jover-Gil S, Candela H, Robles P, Aguilera V, Barrero JM, Micol JL, Ponce MR	The microRNA pathway genes AGO1, HEN1 and HYL1 participate in leaf proximal-distal, venation and stomatal patterning in Arabidopsis	Plant Cell Physiol. 2012 Jul;53(7):1322-33. doi: 10.1093/pcp/pcs077. Epub 2012 May 22	22623415
Jun JH, Ha CM, Fletcher JC	BLADE-ON-PETIOLE1 coordinates organ determinacy and axial polarity in arabidopsis by directly activating ASYMMETRIC LEAVES2	Plant Cell. 2010 Jan;22(1):62-76. doi: 10.1105/tpc.109.070763. Epub 2010 Jan 29	20118228
Kang J, Mizukami Y, Wang H, Fowke L, Dengler NG	Modification of cell proliferation patterns alters leaf vein architecture in Arabidopsis thaliana	Planta. 2007 Oct;226(5):1207-18. Epub 2007 Jun 15	17569988

Kerstetter RA, Bollman K, Taylor RA, Bomblies K, Poethig RS	KANADI regulates organ polarity in Arabidopsis	Nature. 2001 Jun 7;411(6838):706-9	11395775
Kieffer M, Master V, Waites R, Davies B	TCP14 and TCP15 affect internode length and leaf shape in Arabidopsis	Plant J. 2011 Oct;68(1):147-58. doi: 10.1111/j.1365-313X.2011.04674.x. Epub 2011 Jul 21	21668538
Kim GT, Shoda K, Tsuge T, Cho KH, Uchimiya H, Yokoyama R, Nishitani K, Tsukaya H	The ANGUSTIFOLIA gene of Arabidopsis, a plant CtBP gene, regulates leaf-cell expansion, the arrangement of cortical microtubules in leaf cells and expression of a gene involved in cell-wall formation	EMBO J. 2002 Mar 15;21(6):1267-79	11889033
Kim GT, Tsukaya H, Saito Y, Uchimiya H	Changes in the shapes of leaves and flowers upon overexpression of cytochrome P450 in Arabidopsis	Proc Natl Acad Sci U S A. 1999 Aug 3;96(16):9433-7	10430960
Kim GT, Tsukaya H, Uchimiya H	The ROTUNDIFOLIA3 gene of Arabidopsis thaliana encodes a new member of the cytochrome P-450 family that is required for the regulated polar elongation of leaf cells	Genes Dev. 1998 Aug 1;12(15):2381-91	9694802
Kim GT, Tsukaya H, Uchimiya H	The CURLY LEAF gene controls both division and elongation of cells during the expansion of the leaf blade in Arabidopsis thaliana	Planta. 1998 Oct;206(2):175-83	9736998
Kim HS, Kim SJ, Abbasi N, Bressan RA, Yun DJ, Yoo SD, Kwon SY, Choi SB	The DOF transcription factor Dof5	1 influences leaf axial patterning by promoting Revoluta transcription in Arabidopsis. Plant J. 2010 Nov;64(3):524-35. doi: 10.1111/j.1365-313X.2010.04346.x. Epub 2010 Oct 5	20807212
Kim JH, Choi D, Kende H	The AtGRF family of putative transcription factors is involved in leaf and cotyledon growth in Arabidopsis	Plant J. 2003 Oct;36(1):94-104	12974814
Kim JH, Kende H	A transcriptional coactivator, AtGIF1, is involved in regulating leaf growth and morphology in Arabidopsis	Proc Natl Acad Sci U S A. 2004 Sep 7;101(36):13374-9. Epub 2004 Aug 23	15326298
Kim TH, Kim BH, Yahalom A, Chamovitz DA, von Arnim AG	Translational regulation via 5' mRNA leader sequences revealed by mutational analysis of the Arabidopsis translation initiation factor subunit eIF3h	Plant Cell. 2004 Dec;16(12):3341-56. Epub 2004 Nov 17	15548739
Kirch T, Simon R, Grünewald M, Werr W	The DORNROSCHEN/ENHANCER OF SHOOT REGENERATION1 gene of Arabidopsis acts in the control of meristem ccll fate and lateral organ development	Plant Cell. 2003 Mar;15(3):694-705	12615942
Kirik V, Schrader A, Uhrig JF, Hulskamp M	MIDGET unravels functions of the Arabidopsis topoisomerase VI complex in DNA endoreduplication, chromatin condensation, and transcriptional silencing	Plant Cell. 2007 Oct;19(10):3100-10. Epub 2007 Oct 19	17951446
Klucher KM, Chow H, Reiser L, Fischer	The AINTEGUMENTA gene of Arabidopsis required for	Plant Cell. 1996 Feb;8(2):137-53	8742706

RL	ovule and female gametophyte development is related to the floral homeotic gene APETALA2		
Koiwa H, Barb AW, Xiong L, Li F, McCully MG, Lee BH, Sokolchik I, Zhu J, Gong Z, Reddy M, Sharkhuu A, Manabe Y, Yokoi S, Zhu JK, Bressan RA, Hasegawa PM	C-terminal domain phosphatase-like family members (AtCPLs) differentially regulate Arabidopsis thaliana abiotic stress signaling, growth, and development	Proc Natl Acad Sci U S A. 2002 Aug 6;99(16):10893-8. Epub 2002 Jul 29	12149434
Köllmer I, Werner T, Schmülling T	Ectopic expression of different cytokinin-regulated transcription factor genes of Arabidopsis thaliana alters plant growth and development	J Plant Physiol. 2011 Aug 15;168(12):1320-7. doi: 10.1016/j.jplph.2011.02.006. Epub 2011 Mar 31	21453984
Kozuka T, Horiguchi G, Kim GT, Ohgishi M, Sakai T, Tsukaya H	The different growth responses of the Arabidopsis thaliana leaf blade and the petiole during shade avoidance are regulated by photoreceptors and sugar	Plant Cell Physiol. 2005 Jan;46(1):213-23. Epub 2005 Jan 19	15659441
Krizek B	AINTEGUMENTA and AINTEGUMENTA-LIKE6 act redundantly to regulate Arabidopsis floral growth and patterning	Plant Physiol. 2009 Aug;150(4):1916-29. doi: 10.1104/pp.109.141119. Epub 2009 Jun 19	19542297
Krizek BA	AINTEGUMENTA utilizes a mode of DNA recognition distinct from that used by proteins containing a single AP2 domain	Nucleic Acids Res. 2003 Apr 1;31(7):1859-68	12655002
Krizek BA	Aintegumenta and Aintegumenta-Like6 regulate auxin-mediated flower development in Arabidopsis	BMC Res Notes. 2011 Jun 7;4:176. doi: 10.1186/1756-0500-4-176	21645408
Krizek BA, Sulli C	Mapping sequences required for nuclear localization and the transcriptional activation function of the Arabidopsis protein AINTEGUMENTA	Planta. 2006 Aug;224(3):612-21. Epub 2006 Mar 8	16523347
Kumaran MK, Bowman JL, Sundaresan V	YABBY polarity genes mediate the repression of KNOX homeobox genes in Arabidopsis	Plant Cell. 2002 Nov;14(11):2761-70	12417699
Kurdyukov S, Faust A, Nawrath C, Bär S, Voisin D, Efremova N, Franke R, Schreiber L, Saedler H, Métraux JP, Yephremov A	The epidermis-specific extracellular BODYGUARD controls cuticle development and morphogenesis in Arabidopsis	Plant Cell. 2006 Feb;18(2):321-39. Epub 2006 Jan 13	16415209
Kurepa J, Wang S, Li Y, Zaitlin D, Pierce AJ, Smalle JA	Loss of 26S proteasome function leads to increased cell size and decreased cell number in Arabidopsis shoot organs	Plant Physiol. 2009 May;150(1):178-89. doi: 10.1104/pp.109.135970. Epub 2009 Mar 25	19321709
Kwon YR, Lee HJ, Kim KH, Hong SW, Lee SJ, Lee H	Ectopic expression of Expansin3 or Expansinbeta1 causes enhanced hormone and salt stress sensitivity in Arabidopsis	Biotechnol Lett. 2008 Jul;30(7):1281-8. doi: 10.1007/s10529-008-9678-5. Epub 2008 Mar 4	18317696
Larson-Rabin Z, Li Z, Masson PH, Day	FZR2/CCS52A1 expression is a determinant of	Plant Physiol. 2009 Feb;149(2):874-84.	19074624

CD	endoreduplication and cell expansion in Arabidopsis	doi: 10.1104/pp.108.132449. Epub 2008 Dec 12	
Lease KA, Wen J, Li J, Doke JT, Liscum E, Walker JC	A mutant Arabidopsis heterotrimeric G-protein beta subunit affects leaf, flower, and fruit development	Plant Cell. 2001 Dec;13(12):2631-41	11752377
Leasure CD, Fiume E, Fletcher JC	The essential gene EMB1611 maintains shoot apical meristem function during Arabidopsis development	Plant J. 2009 Feb;57(4):579-92. doi: 10.1111/j.1365-313X.2008.03708.x. Epub 2008 Oct 8	18980659
Lechner E, Xie D, Grava S, Pigaglio E, Planchais S, Murray JA, Parmentier Y, Mutterer J, Dubreucq B, Shen WH, Genschik P	The AtRbx1 protein is part of plant SCF complexes, and its down-regulation causes severe growth and developmental defects	J Biol Chem. 2002 Dec 20;277(51):50069-80. Epub 2002 Oct 14	12381738
Lee BH, Ko JH, Lee S, Lee Y, Pak JH, Kim JH	The Arabidopsis GRF-INTERACTING FACTOR gene family performs an overlapping function in determining organ size as well as multiple developmental properties	Plant Physiol. 2009 Oct;151(2):655-68. doi: 10.1104/pp.109.141838. Epub 2009 Jul 31	19648231
Lee LY, Hou X, Fang L, Fan S, Kumar PP, Yu H	STUNTED mediates the control of cell proliferation by GA in Arabidopsis	Development. 2012 May;139(9):1568-76. doi: 10.1242/dev.079426	22492352
Lee YK, Kim GT, Kim IJ, Park J, Kwak SS, Choi G, Chung WI	LONGIFOLIA1 and LONGIFOLIA2, two homologous genes, regulate longitudinal cell elongation in Arabidopsis	Development. 2006 Nov;133(21):4305-14	17038516
Li E, Wang S, Liu Y, Chen JG, Douglas CJ	OVATE FAMILY PROTEIN4 (OFP4) interaction with KNAT7 regulates secondary cell wall formation in Arabidopsis thaliana	Plant J. 2011 Jul;67(2):328-41. doi: 10.1111/j.1365-313X.2011.04595.x. Epub 2011 May 12	21457372
Li H, Johnson P, Stepanova A, Alonso JM, Ecker JR	Convergence of signaling pathways in the control of differential cell growth in Arabidopsis	Dev Cell. 2004 Aug;7(2):193-204	15296716
Li S, van Os GM, Ren S, Yu D, Ketelaar T, Emons AM, Liu CM	Expression and functional analyses of EXO70 genes in Arabidopsis implicate their roles in regulating cell type-specific exocytosis	Plant Physiol. 2010 Dec;154(4):1819-30. doi: 10.1104/pp.110.164178. Epub 2010 Oct 13	20943851
Li Y, Zheng L, Corke F, Smith C, Bevan MW	Control of final seed and organ size by the DA1 gene family in Arabidopsis thaliana	Genes Dev. 2008 May 15;22(10):1331-6. doi: 10.1101/gad.463608	18483219
Li Z, Li B, Shen WH, Huang H, Dong A	TCP transcription factors interact with AS2 in the repression of class-I KNOX genes in Arabidopsis thaliana	Plant J. 2012 Jul;71(1):99-107. doi: 10.1111/j.1365-313X.2012.04973.x. Epub 2012 Apr 26	22380849
Lim PO, Lee IC, Kim J, Kim HJ, Ryu JS, Woo HR, Nam HG	Auxin response factor 2 (ARF2) plays a major role in regulating auxin-mediated leaf longevity	J Exp Bot. 2010 Mar;61(5):1419-30. doi: 10.1093/jxb/erq010. Epub 2010 Feb 17	20164142
Lin WC, Shuai B, Springer PS	The Arabidopsis LATERAL ORGAN BOUNDARIES-domain gene ASYMMETRIC LEAVES2 functions in the repression of KNOX gene expression and in adaxial-abaxial patterning	Plant Cell. 2003 Oct;15(10):2241-52. Epub 2003 Sep 24	14508003

Lincoln C, Britton JH, Estelle M	Growth and development of the axr1 mutants of Arabidopsis	Plant Cell. 1990 Nov;2(11):1071-80	1983791
Liu D, Song Y, Chen Z, Yu D	Ectopic expression of miR396 suppresses GRF target gene expression and alters leaf growth in Arabidopsis	Physiol Plant. 2009 Jun;136(2):223-36. doi: 10.1111/j.1399-3054.2009.01229.x. Epub 2009 Feb 2	19453503
Liu Y, Wang F, Zhang H, He H, Ma L, Deng XW	Functional characterization of the Arabidopsis ubiquitin-specific protease gene family reveals specific role and redundancy of individual members in development	Plant J. 2008 Sep;55(5):844-56. doi: 10.1111/j.1365-313X.2008.03557.x. Epub 2008 May 14	18485060
Lolas IB, Himanen K, Grønlund JT, Lynggaard C, Houben A, Melzer M, Van Lijsebettens M, Grasser KD	The transcript elongation factor FACT affects Arabidopsis vegetative and reproductive development and genetically interacts with HUB1/2	Plant J. 2010 Feb;61(4):686-97. doi: 10.1111/j.1365-313X.2009.04096.x. Epub 2009 Nov 27	19947984
Lynn K, Fernandez A, Aida M, Sedbrook J, Tasaka M, Masson P, Barton MK	The PINHEAD/ZWILLE gene acts pleiotropically in Arabidopsis development and has overlapping functions with the ARGONAUTE1 gene	Development. 1999 Feb;126(3):469-81	9876176
MacAlister CA, Ohashi-Ito K, Bergmann DC	Transcription factor control of asymmetric cell divisions that establish the stomatal lineage	Nature. 2007 Feb 1;445(7127):537-40. Epub 2006 Dec 20	17183265
Magyar Z, Horváth B, Khan S, Mohammed B, Henriques R, De Veylder L, Bakó L, Scheres B, Bögre L	Arabidopsis E2FA stimulates proliferation and endocycle separately through RBR-bound and RBR-free complexes	EMBO J. 2012 Mar 21;31(6):1480-93. doi: 10.1038/emboj.2012.13. Epub 2012 Feb 3	22307083
Marsch-Martinez N, Greco R, Becker JD, Dixit S, Bergervoet JH, Karaba A, de Folter S, Pereira A	BOLITA, an Arabidopsis AP2/ERF-like transcription factor that affects cell expansion and proliferation/differentiation pathways	Plant Mol Biol. 2006 Dec;62(6):825-43. Epub 2006 Oct 12	17096212
Masuda HP, Cabral LM, De Veylder L, Tanurdzic M, de Almeida Engler J, Geelen D, Inzé D, Martienssen RA, Ferreira PC, Hemerly AS	ABAP1 is a novel plant Armadillo BTB protein involved in DNA replication and transcription	EMBO J. 2008 Oct 22;27(20):2746-56. doi: 10.1038/emboj.2008.191. Epub 2008 Sep 25	18818695
McConnell JR, Barton MK	Leaf polarity and meristem formation in Arabidopsis	Development. 1998 Aug;125(15):2935-42	9655815
McConnell JR, Emery J, Eshed Y, Bao N, Bowman J, Barton MK	Role of PHABULOSA and PHAVOLUTA in determining radial patterning in shoots	Nature. 2001 Jun 7;411(6838):709-13	11395776
Mizukami Y, Fischer RL	Plant organ size control: AINTEGUMENTA regulates growth and cell numbers during organogenesis	Proc Natl Acad Sci U S A. 2000 Jan 18;97(2):942-7	10639184
Mollá-Morales A, Sarmiento-Mañús R, Robles P, Quesada V, Pérez-Pérez JM, González-Bayón R, Hannah MA, Willmitzer L, Ponce MR, Micol JL	Analysis of ven3 and ven6 reticulate mutants reveals the importance of arginine biosynthesis in Arabidopsis leaf development	Plant J. 2011 Feb;65(3):335-45. doi: 10.1111/j.1365-313X.2010.04425.x. Epub 2010 Dec 13	21265888
Nakata M, Matsumoto N, Tsugeki R, Rikirsch E, Laux T, Okada K	Roles of the middle domain-specific WUSCHEL-RELATED HOMEOBOX genes in early development of leaves in Arabidopsis	Plant Cell. 2012 Feb;24(2):519-35. doi: 10.1105/tpc.111.092858. Epub 2012 Feb 28	22374393

Nakaya M, Tsukaya H, Murakami N, Kato M	Brassinosteroids control the proliferation of leaf cells of Arabidopsis thaliana	Plant Cell Physiol. 2002 Feb;43(2):239-44	11867704
Nam KH, Li J	The Arabidopsis transthyretin-like protein is a potential substrate of BRASSINOSTEROID-INSENSITIVE 1	Plant Cell. 2004 Sep;16(9):2406-17. Epub 2004 Aug 19	15319482
Narita NN, Moore S, Horiguchi G, Kubo M, Demura T, Fukuda H, Goodrich J, Tsukaya H	Overexpression of a novel small peptide ROTUNDIFOLIA4 decreases cell proliferation and alters leaf shape in Arabidopsis thaliana	Plant J. 2004 May;38(4):699-713	15125775
Nelissen H, Clarke JH, De Block M, De Block S, Vanderhaeghen R, Zielinski RE, Dyer T, Lust S, Inzé D, Van Lijsebettens M	DRL1, a homolog of the yeast TOT4/KTI12 protein, has a function in meristem activity and organ growth in plants	Plant Cell. 2003 Mar;15(3):639-54	12615938
Nelissen H, Fleury D, Bruno L, Robles P, De Veylder L, Traas J, Micol JL, Van Montagu M, Inzé D, Van Lijsebettens M	The elongata mutants identify a functional Elongator complex in plants with a role in cell proliferation during organ growth	Proc Natl Acad Sci U S A. 2005 May 24;102(21):7754-9. Epub 2005 May 13	15894610
Newman KL, Fernandez AG, Barton MK	Regulation of axis determinacy by the Arabidopsis PINHEAD gene	Plant Cell. 2002 Dec;14(12):3029-42	12468725
Nikovics K, Blein T, Peaucelle A, Ishida T, Morin H, Aida M, Laufs P	The balance between the MIR164A and CUC2 genes controls leaf margin serration in Arabidopsis	Plant Cell. 2006 Nov;18(11):2929-45. Epub 2006 Nov 10	17098808
Nishimura C, Ohashi Y, Sato S, Kato T, Tabata S, Ueguchi C	Histidine kinase homologs that act as cytokinin receptors possess overlapping functions in the regulation of shoot and root growth in Arabidopsis	Plant Cell. 2004 Jun;16(6):1365-77. Epub 2004 May 21	15155880
Nole-Wilson S, Krizek BA	DNA binding properties of the Arabidopsis floral development protein AINTEGUMENTA	Nucleic Acids Res. 2000 Nov 1;28(21):4076-82. Erratum in: Nucleic Acids Res 2001 Mar 1;29(5):1261	11058102
Nole-Wilson S, Krizek BA	AINTEGUMENTA contributes to organ polarity and regulates growth of lateral organs in combination with YABBY genes	Plant Physiol. 2006 Jul;141(3):977-87. Epub 2006 May 19	16714408
Nole-Wilson S, Tranby TL, Krizek BA	AINTEGUMENTA-like (AIL) genes are expressed in young tissues and may specify meristematic or division-competent states	Plant Mol Biol. 2005 Mar;57(5):613-28	15988559
Norberg M, Holmlund M, Nilsson O	The BLADE ON PETIOLE genes act redundantly to control the growth and development of lateral organs	Development. 2005 May;132(9):2203-13. Epub 2005 Mar 30	15800002
Ochando I, Jover-Gil S, Ripoll JJ, Candela H, Vera A, Ponce MR, Martínez-Laborda A, Micol JL	Mutations in the microRNA complementarity site of the INCURVATA4 gene perturb meristem function and adaxialize lateral organs in arabidopsis	Plant Physiol. 2006 Jun;141(2):607-19. Epub 2006 Apr 14	16617092
Ohno CK, Reddy GV, Heisler MG, Meyerowitz EM	The Arabidopsis JAGGED gene encodes a zinc finger protein that promotes leaf tissue development	Development. 2004 Mar;131(5):1111-22	14973281

Ojangu EL, Tanner K, Pata P, Järve K, Holweg CL, Truve E, Paves H	Myosins XI-K, XI-1, and XI-2 are required for development of pavement cells, trichomes, and stigmatic papillae in Arabidopsis	BMC Plant Biol. 2012 Jun 6;12:81. doi: 10.1186/1471-2229-12-81	22672737
Okushima Y, Mitina I, Quach HL, Theologis A	AUXIN RESPONSE FACTOR 2 (ARF2): a pleiotropic developmental regulator	Plant J. 2005 Jul;43(1):29-46	15960614
Ori N, Eshed Y, Chuck G, Bowman JL, Hake S	Mechanisms that control knox gene expression in the Arabidopsis shoot	Development. 2000 Dec;127(24):5523-32	11076771
Palatnik JF, Allen E, Wu X, Schommer C, Schwab R, Carrington JC, Weigel D	Control of leaf morphogenesis by microRNAs	Nature. 2003 Sep 18;425(6955):257-63. Epub 2003 Aug 20	12931144
Pauwels L, Barbero GF, Geerinck J, Tilleman S, Grunewald W, Pérez AC, Chico JM, Bossche RV, Sewell J, Gil E, García-Casado G, Witters E, Inzé D, Long JA, De Jaeger G, Solano R, Goossens A	NINJA connects the co-repressor TOPLESS to jasmonate signalling	Nature. 2010 Apr 1;464(7289):788-91. doi: 10.1038/nature08854	20360743
Pei Y, Niu L, Lu F, Liu C, Zhai J, Kong X, Cao X	Mutations in the Type II protein arginine methyltransferase AtPRMT5 result in pleiotropic developmental defects in Arabidopsis	Plant Physiol. 2007 Aug;144(4):1913-23. Epub 2007 Jun 15	17573539
Peragine A, Yoshikawa M, Wu G, Albrecht HL, Poethig RS	SGS3 and SGS2/SDE1/RDR6 are required for juvenile development and the production of trans-acting siRNAs in Arabidopsis	Genes Dev. 2004 Oct 1;18(19):2368-79	15466488
Pérez-Pérez JM, Candela H, Robles P, López-Torrejón G, del Pozo JC, Micol JL	A role for AUXIN RESISTANT3 in the coordination of leaf growth	Plant Cell Physiol. 2010 Oct;51(10):1661-73. doi: 10.1093/pcp/pcq123. Epub 2010 Aug 24	20739302
Pérez-Pérez JM, Ponce MR, Micol JL	The UCU1 Arabidopsis gene encodes a SHAGGY/GSK3-like kinase required for cell expansion along the proximodistal axis	Dev Biol. 2002 Feb 15;242(2):161-73	11820813
Pérez-Pérez JM, Ponce MR, Micol JL	The ULTRACURVATA2 gene of Arabidopsis encodes an FK506-binding protein involved in auxin and brassinosteroid signaling	Plant Physiol. 2004 Jan;134(1):101-17	14730066
Pérez-Pérez JM, Serrano-Cartagena J, Micol JL	Genetic analysis of natural variations in the architecture of Arabidopsis thaliana vegetative leaves	Genetics. 2002 Oct;162(2):893-915	12399398
Petricka JJ, Clay NK, Nelson TM	Vein patterning screens and the defectively organized tributaries mutants in Arabidopsis thaliana	Plant J. 2008 Oct;56(2):251-63. doi: 10.1111/j.1365-313X.2008.03595.x. Epub 2008 Jul 4	18643975
Petricka JJ, Nelson TM	Arabidopsis nucleolin affects plant development and patterning	Plant Physiol. 2007 May;144(1):173-86. Epub 2007 Mar 16	17369435
Pillitteri LJ, Sloan DB, Bogenschutz	Termination of asymmetric cell division and	Nature. 2007 Feb 1;445(7127):501-5.	17183267

NL, Torii KU	differentiation of stomata	Epub 2006 Dec 20	
Qiu JL, Jilk R, Marks MD, Szymanski DB	The Arabidopsis SPIKE1 gene is required for normal cell shape control and tissue development	Plant Cell. 2002 Jan;14(1):101-18	11826302
Quesada V, Sarmiento-Mañús R, González-Bayón R, Hricová A, Pérez-Marcos R, Graciá-Martínez E, Medina-Ruiz L, Leyva-Díaz E, Ponce MR, Micol JL	Arabidopsis RUGOSA2 encodes an mTERF family member required for mitochondrion, chloroplast and leaf development	Plant J. 2011 Nov;68(4):738-53. doi: 10.1111/j.1365-313X.2011.04726.x. Epub 2011 Sep 13	21790815
Ranjan A, Fiene G, Fackendahl P, Hoecker U	The Arabidopsis repressor of light signaling SPA1 acts in the phloem to regulate seedling de-etiolation, leaf expansion and flowering time	Development. 2011 May;138(9):1851-62. doi: 10.1242/dev.061036. Epub 2011 Mar 29	21447551
Reinhardt B, Hänggi E, Müller S, Bauch M, Wyrzykowska J, Kerstetter R, Poethig S, Fleming AJ	Restoration of DWF4 expression to the leaf margin of a dwf4 mutant is sufficient to restore leaf shape but not size: the role of the margin in leaf development	Plant J. 2007 Dec;52(6):1094-104. Epub 2007 Oct 1	17908154
Riefler M, Novak O, Strnad M, Schmülling T	Arabidopsis cytokinin receptor mutants reveal functions in shoot growth, leaf senescence, seed size, germination, root development, and cytokinin metabolism	Plant Cell. 2006 Jan;18(1):40-54. Epub 2005 Dec 16	16361392
Robles P, Fleury D, Candela H, Cnops G, Alonso-Peral MM, Anami S, Falcone A, Caldana C, Willmitzer L, Ponce MR, Van Lijsebettens M, Micol JL	The RON1/FRY1/SAL1 gene is required for leaf morphogenesis and venation patterning in Arabidopsis	Plant Physiol. 2010 Mar;152(3):1357-72. doi: 10.1104/pp.109.149369. Epub 2009 Dec 31	20044451
Robles P, Micol JL, Quesada V	Arabidopsis MDA1, a nuclear-encoded protein, functions in chloroplast development and abiotic stress responses	PLoS One. 2012;7(8):e42924. doi: 10.1371/journal.pone.0042924. Epub 2012 Aug 8	22905186
Rodriguez RE, Mecchia MA, Debernardi JM, Schommer C, Weigel D, Palatnik JF	Control of cell proliferation in Arabidopsis thaliana by microRNA miR396	Development. 2010 Jan;137(1):103-12. doi: 10.1242/dev.043067	20023165
Rubio S, Whitehead L, Larson TR, Graham IA, Rodriguez PL	The coenzyme a biosynthetic enzyme phosphopantetheine adenylyltransferase plays a crucial role in plant growth, salt/osmotic stress resistance, and seed lipid storage	Plant Physiol. 2008 Sep;148(1):546-56. doi: 10.1104/pp.108.124057. Epub 2008 Jul 11	18621975
Rubio-Díaz S, Pérez-Pérez JM, González-Bayón R, Muñoz-Viana R, Borrega N, Mouille G, Hernández-Romero D, Robles P, Höfte H, Ponce MR, Micol JL	Cell expansion-mediated organ growth is affected by mutations in three EXIGUA genes	PLoS One. 2012;7(5):e36500. doi: 10.1371/journal.pone.0036500. Epub 2012 May 4	22586475
Saedler R, Jakoby M, Marin B,	The cell morphogenesis gene SPIRRIG in Arabidopsis	Plant J. 2009 Aug;59(4):612-21. doi:	19392685

Galiana-Jaime E, Hülskamp M	encodes a WD/BEACH domain protein	10.1111/j.1365-313X.2009.03900.x. Epub 2009 Apr 25. Erratum in: Plant J. 2009 Nov;60(4):755	
SARAH J. COOKSON1, MIEKE VAN LIJSEBETTENS, CHRISTINE GRANIER,	Correlation between leaf growth variables suggest intrinsic and early controls of leaf size in Arabidopsis thaliana	Plant, Cell & Environment	10.1111_j. 1365-3040.2005. 01368
Sarojam R, Sappl PG, Goldshmidt A, Efroni I, Floyd SK, Eshed Y, Bowman JL	Differentiating Arabidopsis shoots from leaves by combined YABBY activities	Plant Cell. 2010 Jul;22(7):2113-30. doi: 10.1105/tpc.110.075853. Epub 2010 Jul 13	20628155
Sarvepalli K, Nath U	Hyper-activation of the TCP4 transcription factor in Arabidopsis thaliana accelerates multiple aspects of plant maturation	Plant J. 2011 Aug;67(4):595-607. doi: 10.1111/j.1365-313X.2011.04616.x. Epub 2011 Jul 4	21518050
Schommer C, Palatnik JF, Aggarwal P, Chételat A, Cubas P, Farmer EE, Nath U, Weigel D	Control of jasmonate biosynthesis and senescence by miR319 targets	PLoS Biol. 2008 Sep 23;6(9):e230. doi: 10.1371/journal.pbio.0060230	18816164
Schröder F, Lisso J, Lange P, Müssig C	The extracellular EXO protein mediates cell expansion in Arabidopsis leaves	BMC Plant Biol. 2009 Feb 13;9:20. doi: 10.1186/1471-2229-9-20	19216774
Schruff MC, Spielman M, Tiwari S, Adams S, Fenby N, Scott RJ	The AUXIN RESPONSE FACTOR 2 gene of Arabidopsis links auxin signalling, cell division, and the size of seeds and other organs	Development. 2006 Jan;133(2):251-61. Epub 2005 Dec 8	16339187
Schwager KM, Calderon-Villalobos LI, Dohmann EM, Willige BC, Knierer S, Nill C, Schwechheimer C	Characterization of the VIER F-BOX PROTEINE genes from Arabidopsis reveals their importance for plant growth and development	Plant Cell. 2007 Apr;19(4):1163-78. Epub 2007 Apr 13	17435085
Semiarti E, Ueno Y, Tsukaya H, Iwakawa H, Machida C, Machida Y	The ASYMMETRIC LEAVES2 gene of Arabidopsis thaliana regulates formation of a symmetric lamina, establishment of venation and repression of meristem-related homeobox genes in leaves	Development. 2001 May;128(10):1771-83	11311158
Serrano-Cartagena J, Candela H, Robles P, Ponce MR, Pérez-Pérez JM, Piqueras P, Micol JL	Genetic analysis of incurvata mutants reveals three independent genetic operations at work in Arabidopsis leaf morphogenesis	Genetics. 2000 Nov;156(3):1363-77	11063708
Serrano-Cartagena J, Robles P, Ponce MR, Micol JL	Genetic analysis of leaf form mutants from the Arabidopsis Information Service collection	Mol Gen Genet. 1999 Jun;261(4-5):725-39	10394910
Siegfried KR, Eshed Y, Baum SF, Otsuga D, Drews GN, Bowman JL	Members of the YABBY gene family specify abaxial cell fate in Arabidopsis	Development. 1999 Sep;126(18):4117-28	10457020
Skirycz A, Reichelt M, Burow M, Birkemeyer C, Rolcik J, Kopka J, Zanor MI, Gershenzon J, Strnad M, Szopa J,	DOF transcription factor AtDof1	1 (OBP2) is part of a regulatory network controlling glucosinolate biosynthesis in Arabidopsis. Plant J. 2006 Jul;47(1):10-24.	16740150

Mueller-Roeber B, Witt I		Epub 2006 Jun 1	
Solheim C, Li L, Hatzopoulos P, Millar AH	Loss of Lon1 in Arabidopsis changes the mitochondrial proteome leading to altered metabolite profiles and growth retardation without an accumulation of oxidative damage	Plant Physiol. 2012 Nov;160(3):1187-203. doi: 10.1104/pp.112.203711. Epub 2012 Sep 11	22968828
Song JB, Huang SQ, Dalmay T, Yang ZM	Regulation of Leaf Morphology by MicroRNA394 and Its Target LEAF CURLING RESPONSIVENESS	Plant Cell Physiol. 2012 Aug 3	22864450
Sonoda Y, Sako K, Maki Y, Yamazaki N, Yamamoto H, Ikeda A, Yamaguchi J	Regulation of leaf organ size by the Arabidopsis RPT2a 19S proteasome subunit	Plant J. 2009 Oct;60(1):68-78. doi: 10.1111/j.1365-313X.2009.03932.x. Epub 2009 May 23	19500299
Spartz AK, Lee SH, Wenger JP, Gonzalez N, Itoh H, Inzé D, Peer WA, Murphy AS, Overvoorde PJ, Gray WM	The SAUR19 subfamily of SMALL AUXIN UP RNA genes promote cell expansion	Plant J. 2012 Jun;70(6):978-90. doi: 10.1111/j.1365-313X.2012.04946.x. Epub 2012 Mar 31	22348445
Strabala TJ, O'donnell PJ, Smit AM, Ampomah-Dwamena C, Martin EJ, Netzler N, Nieuwenhuizen NJ, Quinn BD, Foote HC, Hudson KR	Gain-of-function phenotypes of many CLAVATA3/ESR genes, including four new family members, correlate with tandem variations in the conserved CLAVATA3/ESR domain	Plant Physiol. 2006 Apr;140(4):1331-44. Epub 2006 Feb 17	16489133
Sugimoto-Shirasu K, Roberts GR, Stacey NJ, McCann MC, Maxwell A, Roberts K	RHL1 is an essential component of the plant DNA topoisomerase VI complex and is required for ploidy-dependent cell growth	Proc Natl Acad Sci U S A. 2005 Dec 20;102(51):18736-41. Epub 2005 Dec 8	16339310
Sugimoto-Shirasu K, Stacey NJ, Corsar J, Roberts K, McCann MC	DNA topoisomerase VI is essential for endoreduplication in Arabidopsis	Curr Biol. 2002 Oct 15;12(20):1782-6	12401175
Sun Y, Zhou Q, Zhang W, Fu Y, Huang H	ASYMMETRIC LEAVES1, an Arabidopsis gene that is involved in the control of cell differentiation in leaves	Planta. 2002 Mar;214(5):694-702. Epub 2001 Nov 10	11882937
Szakonyi D, Byrne ME	Ribosomal protein L27a is required for growth and patterning in Arabidopsis thaliana	Plant J. 2011 Jan;65(2):269-81. doi: 10.1111/j.1365-313X.2010.04422.x. Epub 2010 Dec 1	21223391
Takahashi N, Nakazawa M, Shibata K, Yokota T, Ishikawa A, Suzuki K, Kawashima M, Ichikawa T, Shimada H, Matsui M	shk1-D, a dwarf Arabidopsis mutant caused by activation of the CYP72C1 gene, has altered brassinosteroid levels	Plant J. 2005 Apr;42(1):13-22	15773850
Talbert PB, Adler HT, Parks DW, Comai L	The REVOLUTA gene is necessary for apical meristem development and for limiting cell divisions in the leaves and stems of Arabidopsis thaliana	Development. 1995 Sep;121(9):2723-35	7555701
Tateda C, Watanabe K, Kusano T, Takahashi Y	Molecular and genetic characterization of the gene family encoding the voltage-dependent anion channel in Arabidopsis	J Exp Bot. 2011 Oct;62(14):4773-85. doi: 10.1093/jxb/err113. Epub 2011 Jun 24	21705391
Teper-Bamnolker P, Samach A	The flowering integrator FT regulates SEPALLATA3 and	Plant Cell. 2005 Oct;17(10):2661-75. Epub	16155177

	FRUITFULL accumulation in Arabidopsis leaves	2005 Sep 9	
Tsukaya H, Kozuka T, Kim GT	Genetic control of petiole length in Arabidopsis thaliana	Plant Cell Physiol. 2002 Oct;43(10):1221-8	12407202
Tsukaya H, Uchimiya H	Genetic analyses of the formation of the serrated margin of leaf blades in Arabidopsis: combination of a mutational analysis of leaf morphogenesis with the characterization of a specific marker gene expressed in hydathodes and stipules	Mol Gen Genet. 1997 Oct;256(3):231-8	9393447
Turlapati PV, Kim KW, Davin LB, Lewis NG	The laccase multigene family in Arabidopsis thaliana: towards addressing the mystery of their gene function(s)	Planta. 2011 Mar;233(3):439-70. doi: 10.1007/s00425-010-1298-3. Epub 2010 Nov 10	21063888
Ueda A, Li P, Feng Y, Vikram M, Kim S, Kang CH, Kang JS, Bahk JD, Lee SY, Fukuhara T, Staswick PE, Pepper AE, Koiwa H	The Arabidopsis thaliana carboxyl-terminal domain phosphatase-like 2 regulates plant growth, stress and auxin responses	Plant Mol Biol. 2008 Aug;67(6):683-97. doi: 10.1007/s11103-008-9348-y. Epub 2008 May 28	18506580
Ueda M, Matsui K, Ishiguro S, Sano R, Wada T, Paponov I, Palme K, Okada K	The HALTED ROOT gene encoding the 26S proteasome subunit RPT2a is essential for the maintenance of Arabidopsis meristems	Development. 2004 May;131(9):2101-11. Epub 2004 Apr 8	15073153
Ullah H, Chen JG, Temple B, Boyes DC, Alonso JM, Davis KR, Ecker JR, Jones AM	The beta-subunit of the Arabidopsis G protein negatively regulates auxin-induced cell division and affects multiple developmental processes	Plant Cell. 2003 Feb;15(2):393-409	12566580
Ullah H, Chen JG, Young JC, Im KH, Sussman MR, Jones AM	Modulation of cell proliferation by heterotrimeric G protein in Arabidopsis	Science. 2001 Jun 15;292(5524):2066-9	11408654
van der Graaff E, Dulk-Ras AD, Hooykaas PJ, Keller B	Activation tagging of the LEAFY PETIOLE gene affects leaf petiole development in Arabidopsis thaliana	Development. 2000 Nov;127(22):4971-80	11044410
Van Minnebruggen A, Neyt P, De Groeve S, Coussens G, Ponce MR, Micol JL, Van Lijsebettens M	The ang3 mutation identified the ribosomal protein gene RPL5B with a role in cell expansion during organ growth	Physiol Plant. 2010 Jan;138(1):91-101. doi: 10.1111/j.1399-3054.2009.01301.x. Epub 2009 Oct 6	19878482
Vandenbussche M, Horstman A, Zethof J, Koes R, Rijpkema AS, Gerats T	Differential recruitment of WOX transcription factors for lateral development and organ fusion in Petunia and Arabidopsis	Plant Cell. 2009 Aug;21(8):2269-83. doi: 10.1105/tpc.109.065862. Epub 2009 Aug 28	19717616
Vert G, Walcher CL, Chory J, Nemhauser JL	Integration of auxin and brassinosteroid pathways by Auxin Response Factor 2	Proc Natl Acad Sci U S A. 2008 Jul 15;105(28):9829-34. doi: 10.1073/pnas.0803996105. Epub 2008 Jul 3	18599455
Von Groll U, Berger D, Altmann T	The subtilisin-like serine protease SDD1 mediates cell-to-cell signaling during Arabidopsis stomatal development	Plant Cell. 2002 Jul;14(7):1527-39	12119372
Wang H, Zhou Y, Gilmer S, Whitwill S,	Expression of the plant cyclin-dependent kinase inhibitor	Plant J. 2000 Dec;24(5):613-23	11123800

Fowke LC	ICK1 affects cell division, plant growth and morphology		
Wang HX, Weerasinghe RR, Perdue TD, Cakmakci NG, Taylor JP, Marzluff WF, Jones AM	A Golgi-localized hexose transporter is involved in heterotrimeric G protein-mediated early development in Arabidopsis	Mol Biol Cell. 2006 Oct;17(10):4257-69. Epub 2006 Jul 19	16855027
Wang JW, Schwab R, Czech B, Mica E, Weigel D	Dual effects of miR156-targeted SPL genes and CYP78A5/KLUH on plastochron length and organ size in Arabidopsis thaliana	Plant Cell. 2008 May;20(5):1231-43. doi: 10.1105/tpc.108.058180. Epub 2008 May 20	18492871
Wang L, Gu X, Xu D, Wang W, Wang H, Zeng M, Chang Z, Huang H, Cui X	miR396-targeted AtGRF transcription factors are required for coordination of cell division and differentiation during leaf development in Arabidopsis	J Exp Bot. 2011 Jan;62(2):761-73. doi: 10.1093/jxb/erq307. Epub 2010 Oct 29	21036927
Wang L, Hua D, He J, Duan Y, Chen Z, Hong X, Gong Z	Auxin Response Factor2 (ARF2) and its regulated homeodomain gene HB33 mediate abscisic acid response in Arabidopsis	PLoS Genet. 2011 Jul;7(7):e1002172. doi: 10.1371/journal.pgen.1002172. Epub 2011 Jul 14	21779177
Wang S, Chang Y, Guo J, Chen JG	Arabidopsis Ovate Family Protein 1 is a transcriptional repressor that suppresses cell elongation	Plant J. 2007 Jun;50(5):858-72. Epub 2007 Apr 25	17461792
Wang S, Chang Y, Guo J, Zeng Q, Ellis BE, Chen JG	Arabidopsis ovate family proteins, a novel transcriptional repressor family, control multiple aspects of plant growth and development	PLoS One. 2011;6(8):e23896. doi: 10.1371/journal.pone.0023896. Epub 2011 Aug 23	21886836
Wang TW, Lu L, Zhang CG, Taylor C, Thompson JE	Pleiotropic effects of suppressing deoxyhypusine synthase expression in Arabidopsis thaliana	Plant Mol Biol. 2003 Aug;52(6):1223-35	14682621
Wang W, Chen X	HUA ENHANCER3 reveals a role for a cyclin-dependent protein kinase in the specification of floral organ identity in Arabidopsis	Development. 2004 Jul;131(13):3147-56. Epub 2004 Jun 2	15175247
Wang W, Xu B, Wang H, Li J, Huang H, Xu L	YUCCA genes are expressed in response to leaf adaxial-abaxial juxtaposition and are required for leaf margin development	Plant Physiol. 2011 Dec;157(4):1805-19. doi: 10.1104/pp.111.186395. Epub 2011 Oct 14	22003085
Wang X, Zhang Y, Ma Q, Zhang Z, Xue Y, Bao S, Chong K	SKB1-mediated symmetric dimethylation of histone H4R3 controls flowering time in Arabidopsis	EMBO J. 2007 Apr 4;26(7):1934-41. Epub 2007 Mar 15	17363895
Wang Y, Henriksson E, Söderman E, Henriksson KN, Sundberg E, Engström P	The Arabidopsis homeobox gene, ATHB16, regulates leaf development and the sensitivity to photoperiod in Arabidopsis	Dev Biol. 2003 Dec 1;264(1):228-39	14623244
Wang ZY, Seto H, Fujioka S, Yoshida S, Chory J	BRI1 is a critical component of a plasma-membrane receptor for plant steroids	Nature. 2001 Mar 15;410(6826):380-3. Erratum in: Nature 2001 May 10;411(6834):219	11268216
Wargent JJ, Gegas VC, Jenkins GI, Doonan JH, Paul ND	UVR8 in Arabidopsis thaliana regulates multiple aspects of cellular differentiation during leaf development in response to ultraviolet B radiation	New Phytol. 2009;183(2):315-26. doi: 10.1111/j.1469-8137.2009.02855.x. Epub 2009 Apr 27	19402876
Werner T, Motyka V, Laucou V, Smets	Cytokinin-deficient transgenic Arabidopsis plants show	Plant Cell. 2003 Nov;15(11):2532-50. Epub	14555694

R, Van Onckelen H, Schmülling T	multiple developmental alterations indicating opposite functions of cytokinins in the regulation of shoot and root meristem activity	2003 Oct 10	
White DW	PEAPOD regulates lamina size and curvature in Arabidopsis	Proc Natl Acad Sci U S A. 2006 Aug 29;103(35):13238-43. Epub 2006 Aug 17	16916932
Williams L, Carles CC, Osmont KS, Fletcher JC	A database analysis method identifies an endogenous trans-acting short-interfering RNA that targets the Arabidopsis ARF2, ARF3, and ARF4 genes	Proc Natl Acad Sci U S A. 2005 Jul 5;102(27):9703-8. Epub 2005 Jun 24	15980147
Woo HR, Kim JH, Kim J, Kim J, Lee U, Song IJ, Kim JH, Lee HY, Nam HG, Lim PO	The RAV1 transcription factor positively regulates leaf senescence in Arabidopsis	J Exp Bot. 2010 Sep;61(14):3947-57. doi: 10.1093/jxb/erq206	20826506
Wu G, Lin WC, Huang T, Poethig RS, Springer PS, Kerstetter RA	KANADI1 regulates adaxial-abaxial polarity in Arabidopsis by directly repressing the transcription of ASYMMETRIC LEAVES2	Proc Natl Acad Sci U S A. 2008 Oct 21;105(42):16392-7. doi: 10.1073/pnas.0803997105. Epub 2008 Oct 10	18849474
Xiao Y, Savchenko T, Baidoo EE, Chehab WE, Hayden DM, Tolstikov V, Corwin JA, Kliebenstein DJ, Keasling JD, Dehesh K	Retrograde signaling by the plastidial metabolite MEcPP regulates expression of nuclear stress-response genes	Cell. 2012 Jun 22;149(7):1525-35. doi: 10.1016/j.cell.2012.04.038	22726439
Xie Q, Frugis G, Colgan D, Chua NH	Arabidopsis NAC1 transduces auxin signal downstream of TIR1 to promote lateral root development	Genes Dev. 2000 Dec 1;14(23):3024-36	11114891
Xu D, Huang W, Li Y, Wang H, Huang H, Cui X	Elongator complex is critical for cell cycle progression and leaf patterning in Arabidopsis	Plant J. 2012 Mar;69(5):792-808. doi: 10.1111/j.1365-313X.2011.04831.x. Epub 2011 Nov 23	22026817
Xu L, Xu Y, Dong A, Sun Y, Pi L, Xu Y, Huang H	Novel as1 and as2 defects in leaf adaxial-abaxial polarity reveal the requirement for ASYMMETRIC LEAVES1 and 2 and ERECTA functions in specifying leaf adaxial identity	Development. 2003 Sep;130(17):4097-107	12874130
Xu L, Yang L, Pi L, Liu Q, Ling Q, Wang H, Poethig RS, Huang H	Genetic interaction between the AS1-AS2 and RDR6-SGS3-AGO7 pathways for leaf morphogenesis	Plant Cell Physiol. 2006 Jul;47(7):853-63. Epub 2006 May 13	16699177
Xu R, Li Y	Control of final organ size by Mediator complex subunit 25 in Arabidopsis thaliana	Development. 2011 Oct;138(20):4545-54. doi: 10.1242/dev.071423. Epub 2011 Sep 8	21903673
Yan Z, Zhao J, Peng P, Chihara RK, Li J	BIN2 functions redundantly with other Arabidopsis GSK3-like kinases to regulate brassinosteroid signaling	Plant Physiol. 2009 Jun;150(2):710-21. doi: 10.1104/pp.109.138099. Epub 2009 Apr 24	19395409
Yang Y, Karlson D	Effects of mutations in the Arabidopsis Cold Shock Domain Protein 3 (AtCSP3) gene on leaf cell expansion	J Exp Bot. 2012 Aug;63(13):4861-73. doi: 10.1093/jxb/ers160. Epub 2012 Aug 9	22888122

Yoo CY, Hasegawa PM, Mickelbart MV	Regulation of stomatal density by the GTL1 transcription factor for improving water use efficiency	Plant Signal Behav. 2011 Jul;6(7):1069-71	21691149
Yuan T, Fujioka S, Takatsuto S, Matsumoto S, Gou X, He K, Russell SD, Li J	BEN1, a gene encoding a dihydroflavonol 4-reductase (DFR)-like protein, regulates the levels of brassinosteroids in Arabidopsis thaliana	Plant J. 2007 Jul;51(2):220-33. Epub 2007 May 23	17521414
Yuan Z, Luo D, Li G, Yao X, Wang H, Zeng M, Huang H, Cui X	Characterization of the AE7 gene in Arabidopsis suggests that normal cell proliferation is essential for leaf polarity establishment	Plant J. 2010 Oct;64(2):331-42. doi: 10.1111/j.1365-313X.2010.04326.x. Epub 2010 Sep 7	21070412
Zgurski JM, Sharma R, Bolokoski DA, Schultz EA	Asymmetric auxin response precedes asymmetric growth and differentiation of asymmetric leaf1 and asymmetric leaf2 Arabidopsis leaves	Plant Cell. 2005 Jan;17(1):77-91. Epub 2004 Dec 17	15608337
Zhang B, Chen HW, Mu RL, Zhang WK, Zhao MY, Wei W, Wang F, Yu H, Lei G, Zou HF, Ma B, Chen SY, Zhang JS	NIMA-related kinase NEK6 affects plant growth and stress response in Arabidopsis	Plant J. 2011 Dec;68(5):830-43. doi: 10.1111/j.1365-313X.2011.04733.x. Epub 2011 Sep 14	21801253
Zhao D, Yang M, Solava J, Ma H	The ASK1 gene regulates development and interacts with the UFO gene to control floral organ identity in Arabidopsis	Dev Genet. 1999 Sep;25(3):209-23	10528262

Supplemental Table S2. Ontologies included in KnownLeaf relations

Ontology	Acronym	Version	URL	Reference
BRENDA tissue / enzyme source	BTO	11/02/2010	http://www.brenda-enzymes.info	Gremse *et al.* 2011
Gene Ontology	GO	1.1049 (11/08/2010)	http://www.geneontology.org/	Ashburner *et al.* 2000
Molecular Interaction	MI	1.52 (07/28/2008)	http://psidev.sf.net http://psidev.sourceforge.net/molecular_interactions/xml/doc/user/index.html	Hermjakob *et al.* 2004
Phenotype, Attribute and Trait Ontology	PATO	1.260 (09/08/2010)	http://obofoundry.org/wiki/index.php/PATO:Main_Page	http://obofoundry.org/wiki/index.php/PATO:Main_Page
Plant environmental conditions	EO	1.6 (02/16/2010)	http://www.gramene.org/plant_ontology/ontology_browse.html#eo	Liang *et al.* 2008
Plant Ontology	PO	Release #0409 (#12) (04/2009)	http://www.plantontology.org/	Jaiswal *et al.* 2005
The Arabidopsis Information Resource	TAIR	TAIR10 (17/11/2010)	http://arabidopsis.org/	Lamesch *et al.* 2012

Supplemental Table S3. Structure of the relation statements

Phenotype: The rot3-2 allele causes enlarged leaf blades

Information type	Slot	Slot type	Required	Example	
				Annotated text	**Entry**
Genotype	Genotype	Ontology	Yes	rot3-2	mutated gene_MI:0804
	Gene	Ontology	Yes[#]	rot3	ROT3_AT4G36380
	Genotype Zygosity	Ontology	Yes[†]		homozygous diploid _APO:0000229
	Mutant LOF_GOF	Ontology	Yes[†]		loss of function_APO:0000011
	Mutant type‡	Free text	No		
Phenotype	Plant part	Ontology	Yes	leaf blades	leaf lamina_PO:0020039
	Localisation	Ontology	No		
	Property	Ontology	(Yes)*		size_PATO:0000117
	Process	Ontology	(Yes)*		
	Value	Ontology	Yes	enlarged	increased size_PATO:0000586
	Factuality	Ontology	No		
	Developmental stage	Ontology	No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		

(Yes)[#]: If the Genotype is not Wild type_SO:0000817

(Yes)[†]: If the Genotype is mutated gene_MI:0804

(Yes)*: A Phenotype relation requires at least either a Process or a Property entry

‡: In the case of transgenic genetic background, the free text entry slot is called Construct description.

Gene Expression: ROT3P::GUS ... we observed ... in leaves

Information type	Slot	Slot type	Required	Example	
				Annotated text	**Entry**
Genotype	Genotype	Ontology	Yes		Wild type_SO:0000817
	Gene	Ontology	Yes[#]		
	Genotype Zygosity	Ontology	Yes[†]		
	Mutant LOF_GOF	Ontology	Yes[†]		
	Mutant type‡	Free text	No		
	Gene studied	Ontology	Yes	ROT3	ROT3_AT4G36380
Expression	Plant part	Ontology	Yes	leaves	leaf_PO:0025034
	Localisation	Ontology	No		
	Property	Ontology	Yes		spatial pattern_PATO:0000060
	Gene expression	Ontology	Yes	observed	present_PATO:0000467
	Factuality	Ontology	No		
	Developmental stage	Ontology	No		
	Growth condition	Ontology	No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		GUS staining

(Yes)[#]: If the Genotype is not Wild type_SO:0000817

(Yes)[†]: If the Genotype is mutated gene_MI:0804

‡: In the case of transgenic genetic background, the free text entry slot is called Construct description.

Feature: SWP protein ... two putative nuclear localization signals

Information type	Slot	Slot type	Required	Example	
				Annotated text	**Entry**
Genotype	Protein	Ontology	Yes	SWP	SWP MED14 ATMED14_AT3G04740
Feature	Molecular feature	Free text	No		two putative nuclear localization signals
	Factuality	Ontology	No	Putative	speculation

Genetic interaction: hyl1 ... appeared to suppress the as2 phenotypes

Information type	**Slot**	**Slot type**	**Required?**	**Example**	
				Annotated text	**Entry**
Genotype	Genotype	Ontology	Yes	hyl1	mutated gene_MI:0804
	Gene	Ontology	No	hyl1	HYL1 DRB1_AT1G09700
	Genotype Zygosity	Ontology	No		homozygous diploid _APO:0000229
	Mutant LOF_GOF	Ontology	No		loss of function_APO:0000011
	Mutant type‡	Free text	No	as2	mutated gene_MI:0804
	Genetic interactor	Ontology	Yes	as2	AS2_AT1G65620
	Gene	Ontology	No		
	Genotype Zygosity	Ontology	No		homozygous diploid _APO:0000229
	Mutant LOF_GOF	Ontology	No		loss of function_APO:0000011
	Mutant type‡	Free text	No		
Interaction	Plant part	Ontology	No		
	Property	Ontology	No		
	Process	Ontology	No		
	Interaction type	Ontology	Yes	suppress	suppressive genetic interaction defined by inequality_MI:0796
	Factuality	Ontology	No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		

‡: In the case of transgenic genetic background, the free text entry slot is called Construct description.

Protein-protein interaction: molecular interaction of AN and ZWI ... using the ... yeast two-hybrid system

Information type	Slot	Slot type	Required?	Example	
				Annotated text	**Entry**
Gene	Protein studied	Ontology	Yes	AN	AN_AT1G01510
	Interactor protein	Ontology	Yes	ZWI	ZWI_AT5G65930
Interaction					
	Interaction type	Ontology	Yes	interaction	direct interaction_MI:0407
	Factuality	Ontology	No		
Experiment	Methodology	Free text	No		

DNA-protein interaction: Using double-stranded oligonucleotides covering the potential TCP binding sites in the context of the LOX2 promoter, we performed EMSAs. The in vitro studies confirmed that TCP4 can bind strongly to at least two of the consensus motifs

Information type	Slot	Slot type	Required?	Example	
				Annotated text	Entry
Gene	Protein	Ontology	Yes	TCP4	TCP4_AT3G15030
	DNA target	Ontology	Yes	LOX2	LOX2 ATLOX2_AT3G45140
	DNA target sequence	Free text	No		
Interaction					
	Regulation	Ontology	Yes	bind	direct interaction_MI:0407
	Plant part	Ontology	No		
	Factuality	Ontology	No		
Experiment	Methodology	Free text	No		mobility shift assay

Process: These results indicate that ATHB16 affects rosette leaf growth

Information type	Slot	Slot type	Required?	Example	
				Annotated text	**Entry**
Gene	Gene studied	Ontology	Yes	ATHB16	ATHB16 ATHB-16 HB16_AT4G40060
Phenotype	Plant part	Ontology	No	rosette leaf	rosette leaf_PO:0000014
	Localisation	Ontology	No		
	Property	Ontology	No		
	Process	Ontology	No	growth	growth_GO:0040007
	Value	Ontology	No		
	Factuality	Ontology	No	Indicate	Speculation
	Developmental stage	Ontology	No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		

Regulation of gene expression: TCP4 ... positively regulate LOX2 promoter activity

Information type	**Slot**	**Slot type**	**Required?**	**Example**	
				Annotated text	**Entry**
Gene	Gene studied	Ontology	Yes	TCP4	TCP4_AT3G15030
Regulation	Plant part	Ontology	No		
	Regulation	Ontology	Yes	positively regulate	positive regulation of gene expression_GO:0010628
	Gene target	Ontology	Yes	LOX2	LOX2 ATLOX2_AT3G45140
	Factuality	Ontology	No		
	Developmental stage	Ontology	No		
Experiment	Methodology	Free text	No		

Regulation of process: KLU gene is ... promoting growth

Information type	Slot	Slot type	Required?	Example	
				Annotated text	Entry
Gene	Gene studied	Ontology	Yes	KLU	CYP78A5 KLU_AT1G13710
Regulation	Regulation	Ontology	No	promoting	positive regulation of biological process_GO:0048518
	Plant part	Ontology	No		
	Localisation	Ontology	No		
	Property	Ontology	No		
	Process	Ontology	Yes	growth	growth_GO:0040007
	Value	Ontology	No		
	Factuality	Ontology	No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		

Regulation of phenotype: PHABULOSA ... influence leaf shape

Information type	Slot	Slot type	Required?	Example	
				Annotated text	Entry
Genotype	Gene studied	Ontology	Yes	PHABULOSA	PHB ATHB14 ATHB-14 PHB-1D_AT2G34710
Regulation	Regulation	Ontology	No	influence	regulation of developmental process_GO:0050793
	Plant part	Ontology	Yes	leaf	leaf_PO:0025034
	Localisation	Ontology	No		
	Property	Ontology	Yes	shape	shape_PATO:0000052
		Ontology	No		
	Factuality	Ontology	No		
			No		
Environment	Growth condition	Ontology	No		
Experiment	Methodology	Free text	No		

Supplemental Table S4. KnownLeaf Ontology terms

Slot	Ontology	Ontology term	Number of annotations with term
developmental_stage	BTO	seedling_BTO:0001228	62
developmental_stage	PO	3 leaf fully expanded stage_PO:0001053	167
developmental_stage	PO	leaf development stages_PO:0001050	166
developmental_stage	PO	2 leaf expansion stage_PO:0001052	137
developmental_stage	PO	1 leaf initiation stage_PO:0001051	46
developmental_stage	PO	D bilateral stage_PO:0004507	29
developmental_stage	PO	C globular stage_PO:0001185	20
developmental_stage	PO	4 leaf senescence stage_PO:0001054	13
developmental_stage	PO	juvenile leaf_PO:0006339	10
developmental_stage	PO	E expanded cotyledon stage_PO:0001078	7
developmental_stage	PO	embryo development stages_PO:0007631	7
developmental_stage	PO	F mature embryo stage_PO:0001081	5
developmental_stage	PO	B proembryo stage_PO:0001180	2
genetic_interactor	MI	mutated gene_MI:0804	294
genetic_interactor	MI	over expressed level_MI:0506	14
gene_expression	MI	over expressed level_MI:0506	713
gene_expression	MI	under expressed level_MI:0223	505
gene_expression	PATO	present_PATO:0000467	1194
gene_expression	PATO	normal_PATO:0000461	372
gene_expression	PATO	absent_PATO:0000462	189
gene_expression	PATO	mislocalised_PATO:0000628	105
gene_expression	PATO	abnormal_PATO:0000460	12
gene_expression	PATO	delayed_PATO:0000502	2

gene_expression	PATO	variant_PATO:0001227	1
gene_expression	PATO	patchy_PATO:0001608	1
gene_expression	PATO	irregular spatial pattern_PATO:0000330	1
gene_expression	PATO	decreased susceptibility toward_PATO:0001670	1
gene_expression	PATO	regular spatial pattern_PATO:0000440	1
gene_expression	PATO	diffuse_PATO:0001513	1
genotype	MI	mutated gene_MI:0804	5106
genotype	MI	over expressed level_MI:0506	1285
genotype	MI	knock down_MI:0789	163
genotype	SO	Wild type_SO:0000817	1497
genotype	SO	Transgenic_SO:0000781	52
growth_condition	EO	brassinosteroid_EO:0007409	56
growth_condition	EO	continuous dark no light regimen_EO:0007270	45
growth_condition	EO	UV light regimen_EO:0007222	42
growth_condition	EO	chemical regimen_EO:0007189	40
growth_condition	EO	UV-B light regimen_EO:0007001	25
growth_condition	EO	auxin regimen_EO:0007074	23
growth_condition	EO	light regimen_EO:0007196	17
growth_condition	EO	salt regimen_EO:0007185	17
growth_condition	EO	blue light regimen_EO:0007218	16
growth_condition	EO	soil environment_EO:0007049	16
growth_condition	EO	gibberellic acid regimen_EO:0007069	16
growth_condition	EO	short day length regimen_EO:0007200	15
growth_condition	EO	red light regimen_EO:0007207	15
growth_condition	EO	ethylene regimen_EO:0007068	14
growth_condition	EO	tissue culture growth media_EO:0007266	14
growth_condition	EO	abscisic acid regimen_EO:0007105	13

growth_condition	EO	low light intensity regimen_EO:0007271	12
growth_condition	EO	continuous light regimen_EO:0007162	11
growth_condition	EO	warm/hot temperature regimen_EO:0007173	11
growth_condition	EO	drought environment_EO:0007404	11
growth_condition	EO	cytokinin regimen_EO:0007066	10
growth_condition	EO	mechanical damage_EO:0007373	9
growth_condition	EO	benzyladenine regimen_EO:0007291	8
growth_condition	EO	sodium chloride regimen_EO:0007048	8
growth_condition	EO	2,4-dichlorophenoxyacetic acid_EO:0007180	8
growth_condition	EO	long day length regimen_EO:0007199	8
growth_condition	EO	visible light regimen_EO:0007221	8
growth_condition	EO	1-naphthaleneacetic acid_EO:0007204	7
growth_condition	EO	liquid growth media_EO:0007265	6
growth_condition	EO	pest/pathogen/animal/plant environment_EO:0007124	6
growth_condition	EO	solid growth media_EO:0007262	6
growth_condition	EO	carbon nutrient regimen_EO:0007303	6
growth_condition	EO	far red light regimen_EO:0007203	6
growth_condition	EO	cold temperature regimen_EO:0007174	5
growth_condition	EO	humidity regimen_EO:0007197	5
growth_condition	EO	nitrate regimen_EO:0007406	5
growth_condition	EO	indole acetic acid regimen_EO:0007070	5
growth_condition	EO	high light intensity regimen_EO:0007075	5
growth_condition	EO	methyl jasmonate_EO:0007407	4
growth_condition	EO	jasmonic acid regimen_EO:0007080	3
growth_condition	EO	non-mineral nutrient regimen_EO:0007043	2
growth_condition	EO	1,6-dimethylsulfonoxy D-mannitol_EO:0007509	2
growth_condition	EO	fertilizer regimen_EO:0007085	2

growth_condition	EO	nutrient regimen_EO:0007241	2
growth_condition	EO	herbicide regimen_EO:0007183	1
growth_condition	EO	fungicide regimen_EO:0007268	1
growth_condition	EO	methyl methanesulfonate_EO:0007550	1
growth_condition	EO	salicylic acid regimen_EO:0007187	1
growth_condition	EO	growth media_EO:0007147	1
growth_condition	EO	light intensity regimen_EO:0007224	1
growth_condition	EO	natural fertilizer regimen_EO:0007087	1
growth_condition	EO	hydroponic plant culture media_EO:0007067	1
growth_condition	EO	plant environment ontology_EO:0007359	1
interaction_type	GO	protein farnesylation_GO:0018343	1
interaction_type	MI	direct interaction_MI:0407	128
interaction_type	MI	suppressive genetic interaction defined by inequality_MI:0796	73
interaction_type	MI	negative genetic interaction_MI:0933	71
interaction_type	MI	additive genetic interaction defined by inequality_MI:0799	65
interaction_type	MI	epistatic genetic interaction_MI:0930	29
interaction_type	MI	epistatic genetic interaction defined by inequality_MI:0797	27
interaction_type	MI	synthetic genetic interaction defined by inequality_MI:0794	23
interaction_type	MI	association_MI:0914	20
interaction_type	MI	physical association_MI:0915	16
interaction_type	MI	genetic interaction_MI:0208	8
interaction_type	MI	phosphorylation reaction_MI:0217	7
interaction_type	MI	positive genetic interaction_MI:0935	7
interaction_type	MI	noninteractive genetic interaction defined by inequality_MI:0932	3
interaction_type	MI	dephosphorylation reaction_MI:0203	2
interaction_type	MI	enzymatic reaction_MI:0414	1
interaction_type	MI	methylation reaction_MI:0213	1

localisation	BTO	seedling_BTO:0001228	2
localisation	EFO	basal_EFO:0001654	14
localisation	GO	chloroplast_GO:0009507	6
localisation	GO	nucleus_GO:0005634	4
localisation	GO	cell_GO:0005623	2
localisation	GO	plasma membrane_GO:0005886	1
localisation	PATO	abaxial to_PATO:0002046	21
localisation	PATO	distal to_PATO:0001234	19
localisation	PATO	proximal to_PATO:0001195	18
localisation	PATO	adaxial to_PATO:0002047	10
localisation	PATO	surrounding_PATO:0001772	3
localisation	PATO	peripheral_PATO:0002107	3
localisation	PATO	medial to_PATO:0001191	2
localisation	PATO	located in_PATO:0002261	1
localisation	PATO	asymmetrical_PATO:0000616	1
localisation	PATO	lateral to_PATO:0001193	1
localisation	PATO	relational spatial quality_PATO:0001631	1
localisation	PO	leaf_PO:0025034	80
localisation	PO	rosette leaf_PO:0000014	73
localisation	PO	juvenile leaf_PO:0006339	47
localisation	PO	leaf epidermis_PO:0006016	28
localisation	PO	cotyledon_PO:0020030	27
localisation	PO	epidermis_PO:0005679	20
localisation	PO	leaf primordium_PO:0000017	20
localisation	PO	leaf margin_PO:0020128	18
localisation	PO	trichome_PO:0000282	16
localisation	PO	petiole_PO:0020038	15

localisation	PO	shoot apical meristem_PO:0020148	15
localisation	PO	leaf adaxial epidermis_PO:0006018	15
localisation	PO	leaf abaxial epidermis_PO:0006019	12
localisation	PO	mesophyll cell_PO:0004006	12
localisation	PO	leaf lamina adaxial epidermis_PO:0000050	12
localisation	PO	palisade mesophyll cell_PO:0006206	12
localisation	PO	embryo_PO:0009009	11
localisation	PO	long cell_PO:0004717	11
localisation	PO	leaf lamina_PO:0020039	10
localisation	PO	leaf lamina vascular system_PO:0000048	9
localisation	PO	midvein_PO:0020139	6
localisation	PO	epidermal cell_PO:0004013	6
localisation	PO	portion of vascular tissue_PO:0009015	6
localisation	PO	whole plant_PO:0000003	5
localisation	PO	lamina_PO:0025060	5
localisation	PO	palisade mesophyll_PO:0005648	4
localisation	PO	leaf lamina margin_PO:0025009	4
localisation	PO	vascular bundle_PO:0005020	3
localisation	PO	pavement cell_PO:0000332	3
localisation	PO	leaf apex_PO:0020137	3
localisation	PO	adult leaf_PO:0006340	3
localisation	PO	cauline leaf_PO:0000013	3
localisation	PO	leaf base_PO:0020040	3
localisation	PO	bract_PO:0009055	2
localisation	PO	shoot system_PO:0009006	2
localisation	PO	cotyledon epidermis_PO:0006056	2
localisation	PO	petiole proximal end_PO:0008024	2

localisation	PO	leaf vascular system_PO:0000036	2
localisation	PO	stomatal complex_PO:0002000	2
localisation	PO	mesophyll_PO:0006070	2
localisation	PO	phloem_PO:0005417	2
localisation	PO	short cell_PO:0004718	2
localisation	PO	vascular leaf_PO:0009025	2
localisation	PO	petiole epidermis_PO:0000051	2
localisation	PO	hydathode_PO:0005660	2
localisation	PO	leaf trichome_PO:0006504	2
localisation	PO	anther_PO:0009066	1
localisation	PO	tapetum_PO:0025313	1
localisation	PO	guard mother cell_PO:0000351	1
localisation	PO	plant ovule_PO:0020003	1
localisation	PO	spongy mesophyll cell_PO:0006205	1
localisation	PO	axillary bud meristem_PO:0000232	1
localisation	PO	lateral meristem_PO:0020145	1
localisation	PO	meristemoid_PO:0000070	1
localisation	PO	inflorescence meristem_PO:0000230	1
localisation	PO	flower_PO:0009046	1
localisation	PO	apical hook_PO:0000012	1
localisation	PO	embryonic shoot apical meristem_PO:0006362	1
localisation	PO	shoot apex_PO:0000037	1
localisation	PO	trichome branch_PO:0008031	1
localisation	PO	adaxial side of leaf primordium_PO:0004726	1
localisation	PO	cotyledon vascular system_PO:0000035	1
localisation	PO	pollen_PO:0025281	1
localisation	PO	stem_PO:0009047	1

plant_part	BTO	seedling_BTO:0001228	550
plant_part	BTO	flower stalk_BTO:0002244	3
plant_part	BTO	internode_BTO:0000636	2
plant_part	GO	nucleus_GO:0005634	47
plant_part	GO	cell_GO:0005623	42
plant_part	GO	chloroplast_GO:0009507	36
plant_part	GO	plant-type cell wall_GO:0009505	13
plant_part	GO	plasma membrane_GO:0005886	12
plant_part	GO	cytoplasm_GO:0005737	11
plant_part	GO	chloroplast thylakoid membrane_GO:0009535	8
plant_part	GO	endoplasmic reticulum_GO:0005783	7
plant_part	GO	microtubule_GO:0005874	7
plant_part	GO	vacuole_GO:0005773	6
plant_part	GO	intracellular_GO:0005622	5
plant_part	GO	cortical microtubule_GO:0055028	5
plant_part	GO	plastid_GO:0009536	5
plant_part	GO	granum_GO:0009542	3
plant_part	GO	pollen tube_GO:0090406	3
plant_part	GO	polysome_GO:0005844	3
plant_part	GO	cytosol_GO:0005829	3
plant_part	GO	starch grain_GO:0043036	3
plant_part	GO	mitochondrion_GO:0005739	2
plant_part	GO	proplastid_GO:0009537	2
plant_part	GO	chloroplast inner membrane_GO:0009706	2
plant_part	GO	actin filament_GO:0005884	2
plant_part	GO	cyanelle thylakoid membrane_GO:0033115	1
plant_part	GO	nuclear speck_GO:0016607	1

plant_part	GO	apoplast_GO:0048046	1
plant_part	GO	chloroplast thylakoid_GO:0009534	1
plant_part	GO	cytoskeleton_GO:0005856	1
plant_part	GO	Golgi apparatus_GO:0005794	1
plant_part	GO	nuclear membrane_GO:0031965	1
plant_part	GO	plastoglobule_GO:0010287	1
plant_part	GO	endoplasmic reticulum lumen_GO:0005788	1
plant_part	GO	heterochromatin_GO:0000792	1
plant_part	GO	nucleolus_GO:0005730	1
plant_part	GO	etioplast_GO:0009513	1
plant_part	GO	nuclear chromatin_GO:0000790	1
plant_part	GO	actin cytoskeleton_GO:0015629	1
plant_part	GO	microtubule plus end_GO:0035371	1
plant_part	GO	phragmoplast_GO:0009524	1
plant_part	GO	chloroplast outer membrane_GO:0009707	1
plant_part	MI	deoxyribonucleic acid_MI:0319	2
plant_part	MI	ribosomal rna_MI:0608	1
plant_part	PO	leaf_PO:0025034	2339
plant_part	PO	rosette leaf_PO:0000014	500
plant_part	PO	whole plant_PO:0000003	397
plant_part	PO	leaf lamina_PO:0020039	339
plant_part	PO	petiole_PO:0020038	294
plant_part	PO	cotyledon_PO:0020030	293
plant_part	PO	shoot system_PO:0009006	241
plant_part	PO	leaf primordium_PO:0000017	229
plant_part	PO	palisade mesophyll cell_PO:0006206	167
plant_part	PO	leaf margin_PO:0020128	167

plant_part	PO	shoot apical meristem_PO:0020148	160
plant_part	PO	leaf vascular system_PO:0000036	119
plant_part	PO	leaf epidermis_PO:0006016	114
plant_part	PO	shoot apex_PO:0000037	111
plant_part	PO	trichome_PO:0000282	105
plant_part	PO	leaf adaxial epidermis_PO:0006018	79
plant_part	PO	stomatal complex_PO:0002000	78
plant_part	PO	mesophyll cell_PO:0004006	64
plant_part	PO	epidermal cell_PO:0004013	62
plant_part	PO	pavement cell_PO:0000332	50
plant_part	PO	embryo_PO:0009009	48
plant_part	PO	juvenile leaf_PO:0006339	45
plant_part	PO	shoot meristem_PO:0006079	43
plant_part	PO	leaf abaxial epidermis_PO:0006019	41
plant_part	PO	vascular bundle_PO:0005020	40
plant_part	PO	abaxial side of leaf primordium_PO:0004725	39
plant_part	PO	cotyledon vascular system_PO:0000035	38
plant_part	PO	adaxial side of leaf primordium_PO:0004726	35
plant_part	PO	midvein_PO:0020139	33
plant_part	PO	guard cell_PO:0000293	31
plant_part	PO	leaf lamina margin_PO:0025009	29
plant_part	PO	flower_PO:0009046	29
plant_part	PO	hydathode_PO:0005660	29
plant_part	PO	epidermis_PO:0005679	29
plant_part	PO	cotyledon primordium_PO:0000015	28
plant_part	PO	trichome branch_PO:0008031	27
plant_part	PO	cauline leaf_PO:0000013	26

plant_part	PO	leaf vein_PO:0020138	24
plant_part	PO	hypocotyl_PO:0020100	23
plant_part	PO	secondary vein_PO:0020140	22
plant_part	PO	leaf lamina vascular system_PO:0000048	22
plant_part	PO	meristem_PO:0009013	22
plant_part	PO	palisade mesophyll_PO:0005648	21
plant_part	PO	meristemoid_PO:0000070	20
plant_part	PO	mesophyll_PO:0006070	20
plant_part	PO	leaf base_PO:0020040	19
plant_part	PO	leaf trichome_PO:0006504	17
plant_part	PO	cotyledon epidermis_PO:0006056	16
plant_part	PO	lamina_PO:0025060	15
plant_part	PO	leaf lamina adaxial epidermis_PO:0000050	15
plant_part	PO	vascular system_PO:0000034	15
plant_part	PO	petiole vascular system_PO:0000052	15
plant_part	PO	meristem L1_PO:0009020	14
plant_part	PO	cotyledon adaxial epidermis_PO:0006058	14
plant_part	PO	cultured cell_PO:0000005	14
plant_part	PO	intercellular space_PO:0025379	13
plant_part	PO	stipule_PO:0020041	13
plant_part	PO	phloem_PO:0005417	12
plant_part	PO	spongy mesophyll cell_PO:0006205	12
plant_part	PO	vegetative shoot apical meristem_PO:0008016	12
plant_part	PO	embryonic shoot apical meristem_PO:0006362	12
plant_part	PO	leaf lamina epidermis_PO:0000047	11
plant_part	PO	peripheral zone_PO:0000225	10
plant_part	PO	meristematic cell_PO:0004010	10

plant_part	PO	leaf lamina abaxial epidermis_PO:0000049	10
plant_part	PO	stem_PO:0009047	9
plant_part	PO	guard mother cell_PO:0000351	9
plant_part	PO	leaf apex_PO:0020137	9
plant_part	PO	higher order vein_PO:0008023	9
plant_part	PO	petiole proximal end_PO:0008024	9
plant_part	PO	spongy mesophyll_PO:0005647	8
plant_part	PO	fruit_PO:0009001	8
plant_part	PO	vascular leaf_PO:0009025	8
plant_part	PO	leaf mesophyll_PO:0005645	8
plant_part	PO	xylem_PO:0005352	8
plant_part	PO	tertiary vein_PO:0008021	7
plant_part	PO	collective phyllome structure_PO:0025023	7
plant_part	PO	pollen_PO:0025281	6
plant_part	PO	socket cell_PO:0000115	6
plant_part	PO	leaf lamina base_PO:0008019	6
plant_part	PO	apical hook_PO:0000012	5
plant_part	PO	central zone_PO:0000224	5
plant_part	PO	inflorescence meristem_PO:0000230	5
plant_part	PO	adult leaf_PO:0006340	5
plant_part	PO	portion of plant tissue_PO:0009007	4
plant_part	PO	stomatal pore_PO:0008032	4
plant_part	PO	petiole adaxial epidermis_PO:0008027	4
plant_part	PO	cotyledon abaxial epidermis_PO:0006057	4
plant_part	PO	petiole margin_PO:0025010	4
plant_part	PO	procambium_PO:0006074	4
plant_part	PO	xylem element_PO:0000273	4

plant_part	PO	petal_PO:0009032	4
plant_part	PO	parenchyma_PO:0005421	4
plant_part	PO	petiole epidermis_PO:0000051	3
plant_part	PO	cuticle_PO:0000022	3
plant_part	PO	xylem fiber_PO:0000274	3
plant_part	PO	leaflet_PO:0020049	3
plant_part	PO	sepal_PO:0009031	3
plant_part	PO	axillary bud meristem_PO:0000232	3
plant_part	PO	shoot lateral meristem_PO:0006344	2
plant_part	PO	meristem L3_PO:0009022	2
plant_part	PO	cambial initial_PO:0000295	2
plant_part	PO	cotyledon margin_PO:0025012	2
plant_part	PO	axillary shoot system_PO:0006343	2
plant_part	PO	meristem L2_PO:0009021	2
plant_part	PO	stamen_PO:0009029	2
plant_part	PO	branch_PO:0025073	2
plant_part	PO	quaternary vein_PO:0008022	2
plant_part	PO	bract_PO:0009055	1
plant_part	PO	tracheary element_PO:0000290	1
plant_part	PO	hypocotyl epidermis_PO:0005013	1
plant_part	PO	protoderm_PO:0006210	1
plant_part	PO	shoot axis epidermis_PO:0000112	1
plant_part	PO	embryo vascular system_PO:0008011	1
plant_part	PO	cultured protoplast_PO:0000006	1
plant_part	PO	rib zone_PO:0000226	1
plant_part	PO	anther_PO:0009066	1
plant_part	PO	embryo proper_PO:0000001	1

plant_part	PO	plant ovule_PO:0020003	1
plant_part	PO	tapetum_PO:0025313	1
plant_part	PO	carpel_PO:0009030	1
plant_part	PO	true leaf formation_PO:0001095	1
plant_part	PO	lateral meristem_PO:0020145	1
process	GO	growth_GO:0040007	288
process	GO	cell division_GO:0051301	129
process	GO	cell growth_GO:0016049	57
process	GO	leaf formation_GO:0010338	48
process	GO	DNA endoreduplication_GO:0042023	45
process	GO	leaf development_GO:0048366	34
process	GO	leaf vascular tissue pattern formation_GO:0010305	34
process	GO	leaf senescence_GO:0010150	26
process	GO	adaxial/abaxial axis specification_GO:0009943	25
process	GO	organ growth_GO:0035265	24
process	GO	cell proliferation_GO:0008283	21
process	GO	cell differentiation_GO:0030154	21
process	GO	vegetative phase change_GO:0010050	21
process	GO	organ formation_GO:0048645	17
process	GO	adaxial/abaxial pattern formation_GO:0009955	16
process	GO	developmental process_GO:0032502	15
process	GO	stomatal complex patterning_GO:0010375	14
process	GO	stomatal complex development_GO:0010374	14
process	GO	determination of dorsal identity_GO:0048263	14
process	GO	polarity specification of adaxial/abaxial axis_GO:0009944	12
process	GO	asymmetric cell division_GO:0008356	12
process	GO	trichome branching_GO:0010091	11

process	GO	bipolar cell growth_GO:0042815	9
process	GO	leaf morphogenesis_GO:0009965	8
process	GO	cell cycle_GO:0007049	8
process	GO	brassinosteroid mediated signaling pathway_GO:0009742	7
process	GO	vasculature development_GO:0001944	7
process	GO	specification of organ identity_GO:0010092	7
process	GO	cell cycle arrest_GO:0007050	7
process	GO	unidimensional cell growth_GO:0009826	6
process	GO	positive regulation of transcription_GO:0045941	6
process	GO	meristem determinacy_GO:0010022	6
process	GO	determination of ventral identity_GO:0048264	6
process	GO	specification of organ number_GO:0048832	6
process	GO	transcription repressor activity_GO:0016564	6
process	GO	regulation of adaxial/abaxial pattern formation_GO:2000011	6
process	GO	response to ethylene stimulus_GO:0009723	6
process	GO	organ development_GO:0048513	5
process	GO	stomatal complex formation_GO:0010376	5
process	GO	response to auxin stimulus_GO:0009733	5
process	GO	epidermal cell division_GO:0010481	5
process	GO	organ senescence_GO:0010260	5
process	GO	regulation of timing of transition from vegetative to reproductive phase_GO:0048510	5
process	GO	DNA replication_GO:0006260	5
process	GO	gametophyte development_GO:0048229	4
process	GO	meristem maintenance_GO:0010073	4
process	GO	mitotic cell cycle G1/S transition checkpoint_GO:0031575	4
process	GO	leaflet formation_GO:0090014	4
process	GO	auxin mediated signaling pathway_GO:0009734	4

process	GO	trichome differentiation_GO:0010026	4
process	GO	kinase activity_GO:0016301	4
process	GO	abaxial cell fate specification_GO:0010158	4
process	GO	phyllotactic patterning_GO:0060771	4
process	GO	translation_GO:0006412	4
process	GO	establishment of tissue polarity_GO:0007164	4
process	GO	embryo development_GO:0009790	3
process	GO	dedifferentiation_GO:0043696	3
process	GO	acquisition of reproductive competence_GO:0010049	3
process	GO	proteasomal protein catabolic process_GO:0010498	3
process	GO	developmental growth_GO:0048589	3
process	GO	seedling development_GO:0090351	3
process	GO	G1 phase_GO:0051318	3
process	GO	cellulose synthase activity_GO:0016759	3
process	GO	ethylene biosynthetic process_GO:0009693	3
process	GO	pattern specification process_GO:0007389	3
process	GO	pollen development_GO:0009555	3
process	GO	cytokinin mediated signaling pathway_GO:0009736	3
process	GO	shoot development_GO:0048367	3
process	GO	water transport_GO:0006833	3
process	GO	production of ta-siRNAs involved in RNA interference_GO:0010267	3
process	GO	cell wall modification_GO:0042545	3
process	GO	developmental growth involved in morphogenesis_GO:0060560	3
process	GO	post-embryonic development_GO:0009791	3
process	GO	tissue development_GO:0009888	3
process	GO	guard cell development_GO:0010441	3
process	GO	regulation of vegetative phase change_GO:0010321	3

process	GO	chlorophyll biosynthetic process_GO:0015995	2
process	GO	rRNA processing_GO:0006364	2
process	GO	phosphatase activity_GO:0016791	2
process	GO	specification of organ axis polarity_GO:0010084	2
process	GO	trichome morphogenesis_GO:0010090	2
process	GO	cell-cell adhesion_GO:0016337	2
process	GO	transpiration_GO:0010148	2
process	GO	mitotic cell cycle_GO:0000278	2
process	GO	production of miRNAs involved in gene silencing by miRNA_GO:0035196	2
process	GO	dorsal/ventral pattern formation_GO:0009953	2
process	GO	negative regulation of transcription_GO:0016481	2
process	GO	cell maturation_GO:0048469	2
process	GO	regulation of leaf formation_GO:2000025	2
process	GO	ubiquitin-dependent protein catabolic process_GO:0006511	2
process	GO	meristem development_GO:0048507	2
process	GO	nitrogen fixation_GO:0009399	2
process	GO	polarity specification of proximal/distal axis_GO:0010085	2
process	GO	proteasomal ubiquitin-dependent protein catabolic process_GO:0043161	2
process	GO	stomatal complex morphogenesis_GO:0010103	2
process	GO	photosynthesis_GO:0015979	2
process	GO	protein autoubiquitination_GO:0051865	1
process	GO	regulation of stomatal complex development_GO:2000038	1
process	GO	developmental cell growth_GO:0048588	1
process	GO	stem cell differentiation_GO:0048863	1
process	GO	exit from mitosis_GO:0010458	1
process	GO	translation initiation factor activity_GO:0003743	1
process	GO	inorganic phosphate transmembrane transporter activity_GO:0005315	1

process	GO	autophagy_GO:0006914	1
process	GO	regulation of leaf development_GO:2000024	1
process	GO	response to brassinosteroid stimulus_GO:0009741	1
process	GO	epidermis development_GO:0008544	1
process	GO	SUMO ligase activity_GO:0019789	1
process	GO	G2 phase_GO:0051319	1
process	GO	wax biosynthetic process_GO:0010025	1
process	GO	mitochondrial ATP synthesis coupled proton transport_GO:0042776	1
process	GO	nitrite reductase NADPH activity_GO:0008942	1
process	GO	anthocyanin metabolic process_GO:0046283	1
process	GO	oxylipin metabolic process_GO:0031407	1
process	GO	axis elongation_GO:0003401	1
process	GO	cell development_GO:0048468	1
process	GO	protein ubiquitination_GO:0016567	1
process	GO	cotyledon vascular tissue pattern formation_GO:0010588	1
process	GO	regulation of transcription, DNA-dependent_GO:0006355	1
process	GO	endomitotic cell cycle_GO:0007113	1
process	GO	glutamate dehydrogenase activity_GO:0004352	1
process	GO	vegetative cell differentiation_GO:0022620	1
process	GO	isotropic cell growth_GO:0051210	1
process	GO	methyltransferase activity_GO:0008168	1
process	GO	adenylyltransferase activity_GO:0070566	1
process	GO	photomorphogenesis_GO:0009640	1
process	GO	carbohydrate transmembrane transporter activity_GO:0015144	1
process	GO	regulation of secondary shoot formation_GO:2000032	1
process	GO	response to hormone stimulus_GO:0009725	1
process	GO	G2/M transition of mitotic cell cycle_GO:0000086	1

process	GO	ubiquitin-ubiquitin ligase activity_GO:0034450	1
process	GO	histone methylation_GO:0016571	1
process	GO	meristem initiation_GO:0010014	1
process	GO	mitotic cell cycle checkpoint_GO:0007093	1
process	GO	acylglycerol metabolic process_GO:0006639	1
process	GO	nucleocytoplasmic transport_GO:0006913	1
process	GO	brassinosteroid biosynthetic process_GO:0016132	1
process	GO	protein autophosphorylation_GO:0046777	1
process	GO	DNA catabolic process_GO:0006308	1
process	GO	G2 phase of mitotic cell cycle_GO:0000085	1
process	GO	glutamine biosynthetic process_GO:0006542	1
process	GO	lipoxygenase activity_GO:0016165	1
process	GO	microtubule polymerization_GO:0046785	1
process	GO	anthocyanin biosynthetic process_GO:0009718	1
process	GO	auxin transport_GO:0060918	1
process	GO	protein deubiquitination_GO:0016579	1
process	GO	chromosome segregation_GO:0007059	1
process	GO	secondary cell wall biogenesis_GO:0009834	1
process	GO	embryonic pattern specification_GO:0009880	1
process	GO	G1 phase of mitotic cell cycle_GO:0000080	1
process	GO	gibberellin metabolic process_GO:0009685	1
process	GO	intracellular transport_GO:0046907	1
process	GO	meristem structural organization_GO:0009933	1
process	GO	mitotic cell cycle G2/M transition checkpoint_GO:0071780	1
process	GO	auxin biosynthetic process_GO:0009851	1
process	GO	phosphatidic acid biosynthetic process_GO:0006654	1
process	GO	carbohydrate metabolic process_GO:0005975	1

process	GO	G2/M transition checkpoint_GO:0031576	1
process	GO	mitotic cell cycle arrest_GO:0071850	1
process	GO	acyl-acyl-carrier-protein desaturase activity_GO:0045300	1
process	GO	arginine biosynthetic process_GO:0006526	1
process	GO	pattern orientation_GO:0007633	1
process	GO	cellular response to jasmonic acid stimulus_GO:0071395	1
process	GO	proximal/distal pattern formation_GO:0009954	1
process	GO	cuticle development_GO:0042335	1
process	GO	segmentation_GO:0035282	1
process	GO	epidermal cell differentiation_GO:0009913	1
process	GO	G1/S transition of mitotic cell cycle_GO:0000082	1
process	GO	glutamate-ammonia ligase activity_GO:0004356	1
process	GO	jasmonic acid biosynthetic process_GO:0009695	1
process	GO	lignin biosynthetic process_GO:0009809	1
process	GO	microtubule depolymerization_GO:0007019	1
process	GO	mRNA cleavage involved in gene silencing by miRNA_GO:0035279	1
process	GO	anatomical structure arrangement_GO:0048532	1
process	GO	organ morphogenesis_GO:0009887	1
process	GO	auxin polar transport_GO:0009926	1
process	GO	production of siRNA involved in RNA interference_GO:0030422	1
process	GO	cell wall macromolecule metabolic process_GO:0044036	1
property	ECO	transcript expression level evidence_ECO:0000048	1632
property	ECO	protein expression level evidence_ECO:0000046	124
property	GO	granal stacked thylakoid_GO:0009515	4
property	GO	localization_GO:0051179	3
property	GO	vacuole_GO:0005773	2
property	GO	tricarboxylic acid cycle enzyme complex_GO:0045239	2

property	GO	chloroplast_GO:0009507	2
property	GO	actin cytoskeleton_GO:0015629	1
property	GO	plant-type vacuole_GO:0000325	1
property	GO	chloroplast starch grain_GO:0009569	1
property	GO	nucleus_GO:0005634	1
property	GO	chloroplast photosystem II_GO:0030095	1
property	GO	nuclear chromosome_GO:0000228	1
property	MESH	cell size_MESH:68048429	327
property	MESH	cell count_MESH:68002452	313
property	PATO	spatial pattern_PATO:0000060	1224
property	PATO	shape_PATO:0000052	691
property	PATO	size_PATO:0000117	624
property	PATO	length_PATO:0000122	321
property	PATO	morphology_PATO:0000051	258
property	PATO	width_PATO:0000921	210
property	PATO	count_PATO:0000070	169
property	PATO	area_PATO:0001323	151
property	PATO	color_PATO:0000014	131
property	PATO	dorsal-ventral polarity_PATO:0001775	76
property	PATO	ploidy_PATO:0001374	54
property	PATO	rate_PATO:0000161	52
property	PATO	thickness_PATO:0000915	43
property	PATO	surface feature shape_PATO:0001925	39
property	PATO	duration quality of a process_PATO:0001309	38
property	PATO	structure_PATO:0000141	32
property	PATO	complexity_PATO:0001502	25
property	PATO	organization quality_PATO:0002264	22

property	PATO	branchiness_PATO:0002009	20
property	PATO	height_PATO:0000119	18
property	PATO	diameter_PATO:0001334	13
property	PATO	symmetry_PATO:0000965	11
property	PATO	growth rate_PATO:0001492	11
property	PATO	curvature_PATO:0001591	7
property	PATO	3-D shape_PATO:0002266	6
property	PATO	position_PATO:0000140	6
property	PATO	closure_PATO:0000136	5
property	PATO	positional polarity_PATO:0001769	5
property	PATO	present_PATO:0000467	4
property	PATO	concavity_PATO:0002005	4
property	PATO	orientation_PATO:0000133	4
property	PATO	volume_PATO:0000918	4
property	PATO	bilateral symmetry_PATO:0001324	3
property	PATO	sensitivity toward_PATO:0000085	3
property	PATO	aggregated_PATO:0001629	3
property	PATO	mass_PATO:0000125	3
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property	PATO	decreased height_PATO:0000569	1
property	PATO	variability of rate_PATO:0001586	1
property	PATO	apical-basal polarity_PATO:0002023	1
property	PATO	concentration of_PATO:0000033	1
property	PATO	flexibility_PATO:0001543	1
property	PATO	perimeter_PATO:0001711	1
property	PATO	alignment_PATO:0001652	1
property	PATO	direction_PATO:0000039	1

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property	PATO	anterior-posterior polarity_PATO:0002024	1
property	PATO	sharpness_PATO:0000944	1
property	PATO	phase_PATO:0000083	1
property	PO	portion of plant tissue_PO:0009007	23
property	PO	shoot meristem_PO:0006079	15
property	PO	leaf abaxial epidermis_PO:0006019	13
property	PO	stipule_PO:0020041	9
property	PO	leaf lamina_PO:0020039	7
property	PO	leaf margin_PO:0020128	6
property	PO	leaflet_PO:0020049	6
property	PO	leaf vein_PO:0020138	5
property	PO	petiole_PO:0020038	5
property	PO	leaf primordium_PO:0000017	5
property	PO	cotyledon_PO:0020030	4
property	PO	cotyledon vascular system_PO:0000035	4
property	PO	leaf_PO:0025034	4
property	PO	inflorescence meristem_PO:0000230	3
property	PO	shoot apical meristem_PO:0020148	3
property	PO	stomatal complex_PO:0002000	3
property	PO	vascular system_PO:0000034	2
property	PO	leaf adaxial epidermis_PO:0006018	2
property	PO	higher order vein_PO:0008023	2
property	PO	adaxial side of leaf primordium_PO:0004726	2
property	PO	meristematic cell_PO:0004010	2
property	PO	carpel_PO:0009030	1
property	PO	petiole vascular system_PO:0000052	1

property	PO	stem internode_PO:0020142	1
property	PO	epidermal cell_PO:0004013	1
property	PO	palisade mesophyll_PO:0005648	1
property	PO	pith_PO:0006109	1
property	PO	callus_PO:0005052	1
property	PO	leaf vascular system_PO:0000036	1
property	PO	petiole adaxial epidermis_PO:0008027	1
property	PO	shoot system_PO:0009006	1
property	PO	embryonic shoot apical meristem_PO:0006362	1
property	PO	meristemoid_PO:0000070	1
property	PO	rosette leaf_PO:0000014	1
property	PO	vascular bundle_PO:0005020	1
property	PO	flower_PO:0009046	1
property	PO	pavement cell_PO:0000332	1
property	PO	vegetative shoot apical meristem_PO:0008016	1
property	PO	leaf epidermis_PO:0006016	1
property	PO	trichome_PO:0000282	1
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property	TO	leaf length to width ratio_TO:0000542	29
property	TO	chlorophyll content_TO:0000495	27
property	TO	plant fresh weight_TO:0000442	24
property	TO	plastochron_TO:0000735	21
property	TO	phyllotaxy_TO:0006014	13
property	TO	abscisic acid content_TO:0002667	10
property	TO	anthocyanin content_TO:0000071	10
property	TO	biomass yield_TO:0000327	7
property	TO	fat and essential oil composition related trait_TO:0000491	7

property	TO	plant dry weight_TO:0000352	5
property	TO	leaf weight_TO:0000505	5
property	TO	auxin content_TO:0002672	5
property	TO	total biomass yield_TO:0000457	4
property	TO	carotenoid content_TO:0000496	4
property	TO	cytokinin content_TO:0002660	4
property	TO	chlorophyll-b content_TO:0000295	3
property	TO	osmotic response sensitivity_TO:0000095	3
property	TO	leaf dry weight_TO:0001014	3
property	TO	brassinosteroid sensitivity_TO:0002677	3
property	TO	jasmonic acid content_TO:0002668	3
property	TO	shoot dry weight_TO:0000552	3
property	TO	auxin sensitivity_TO:0000163	2
property	TO	shoot fresh weight_TO:0000571	2
property	TO	starch content_TO:0000696	2
property	TO	chlorophyll ratio_TO:0000298	2
property	TO	carbohydrate content_TO:0000291	1
property	TO	flavonoid content_TO:0000290	1
property	TO	total fat content_TO:0000602	1
property	TO	soluble protein content_TO:0000325	1
property	TO	rubisco content_TO:0000319	1
property	TO	chlorophyll-a content_TO:0000293	1
property	TO	abscisic acid sensitivity_TO:0000615	1
property	TO	total soluble sugar content_TO:0000340	1
property	TO	brassinosteroid content_TO:0002676	1
regulation	GO	positive regulation of biological process_GO:0048518	85
regulation	GO	negative regulation of gene expression_GO:0010629	72

regulation	GO	regulation of developmental process_GO:0050793	50
regulation	GO	negative regulation of biological process_GO:0048519	48
regulation	GO	positive regulation of gene expression_GO:0010628	17
regulation	GO	positive regulation of organ growth_GO:0046622	5
regulation	GO	proteasomal protein catabolic process_GO:0010498	2
regulation	MI	direct interaction_MI:0407	29
regulation	MI	acetylation reaction_MI:0192	14
regulation	MI	colocalization_MI:0403	1
regulation	MI	physical association_MI:0915	1
regulation	PATO	necessary occurrent_PATO:0001638	3
regulation	PATO	unnecessary occurrent_PATO:0001639	1
value	PATO	normal_PATO:0000461	682
value	PATO	decreased size_PATO:0000587	503
value	PATO	abnormal_PATO:0000460	398
value	PATO	present in fewer numbers in organism_PATO:0001997	373
value	PATO	increased size_PATO:0000586	227
value	PATO	present in greater numbers in organism_PATO:0000470	216
value	PATO	decreased length_PATO:0000574	184
value	PATO	decreased width_PATO:0000599	154
value	PATO	increased length_PATO:0000573	122
value	PATO	mislocalised_PATO:0000628	111
value	PATO	decreased area_PATO:0002058	104
value	PATO	absent_PATO:0000462	99
value	PATO	serrated_PATO:0001206	82
value	PATO	arrested_PATO:0000297	69
value	PATO	paedomorphic growth_PATO:0001749	68
value	PATO	involute_PATO:0001962	63

value	PATO	decreased rate_PATO:0000911	57
value	PATO	dark green_PATO:0001249	53
value	PATO	increased area_PATO:0002057	52
value	PATO	delayed_PATO:0000502	52
value	PATO	curled_PATO:0000405	50
value	PATO	increased width_PATO:0000600	46
value	PATO	lobed_PATO:0001979	45
value	PATO	round_PATO:0000411	44
value	PATO	dorsalized_PATO:0000620	38
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value	PATO	decreased concentration_PATO:0001163	31
value	PATO	increased concentration_PATO:0001162	31
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value	PATO	peramorphic growth_PATO:0001752	26
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value	PATO	increased duration_PATO:0000498	24
value	PATO	revolute_PATO:0001963	24
value	PATO	increased rate_PATO:0000912	23
value	PATO	disrupted_PATO:0001507	23
value	PATO	simple_PATO:0001503	22
value	PATO	light green_PATO:0001250	21
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value	PATO	increased thickness_PATO:0000591	20
value	PATO	dentated_PATO:0001205	19
value	PATO	kinked_PATO:0001798	19

value	PATO	asymmetrical_PATO:0000616	18
value	PATO	decreased thickness_PATO:0000592	18
value	PATO	accelerated growth_PATO:0001753	18
value	PATO	increased weight_PATO:0000582	18
value	PATO	present in normal numbers in organism_PATO:0002050	17
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value	PATO	decreased height_PATO:0000569	15
value	PATO	netted_PATO:0001947	15
value	PATO	punctiform_PATO:0001366	14
value	PATO	invariant_PATO:0000438	13
value	PATO	variant_PATO:0001227	12
value	PATO	fused with_PATO:0000642	12
value	PATO	flat_PATO:0000407	11
value	PATO	increased accumulation_PATO:0002270	11
value	PATO	decreased diameter_PATO:0001715	10
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value	PATO	high saturation_PATO:0001229	8
value	PATO	multi-colored_PATO:0001533	7
value	PATO	elongated_PATO:0001154	7
value	PATO	protruding_PATO:0001598	7
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value	PATO	increased resistance to_PATO:0001650	6
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value	PATO	decreased occurrence_PATO:0002052	6
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value	PATO	purple_PATO:0000951	6
value	PATO	inconspicuous_PATO:0000464	6
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value	PATO	dwarf-like_PATO:0000969	5
value	PATO	increased depth_PATO:0001596	5
value	PATO	heart shaped_PATO:0000948	5
value	PATO	yellow green_PATO:0001941	5
value	PATO	reniform_PATO:0001871	5
value	PATO	aggregated_PATO:0001629	5
value	PATO	radial symmetry_PATO:0001325	5
value	PATO	deformed_PATO:0001617	5
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value	PATO	circinate_PATO:0001964	4
value	PATO	lanceolate_PATO:0001877	4
value	PATO	complex_PATO:0001504	4
value	PATO	decreased speed_PATO:0000304	4
value	PATO	smooth_PATO:0000701	4
value	PATO	decreased duration_PATO:0000499	4
value	PATO	organized_PATO:0000938	4
value	PATO	yellow_PATO:0000324	4
value	PATO	neotenous growth_PATO:0001491	4
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value	PATO	curved_PATO:0000406	3
value	PATO	decreased fluorescence_PATO:0001927	3

value	PATO	straight_PATO:0002180	3
value	PATO	increased curvature_PATO:0001592	3
value	PATO	domed_PATO:0001789	3
value	PATO	unserrated_PATO:0001975	3
value	PATO	increased frequency_PATO:0000380	3
value	PATO	increased volume_PATO:0000595	3
value	PATO	collapsed_PATO:0001478	3
value	PATO	sterile_PATO:0000956	3
value	PATO	increased mass_PATO:0001563	3
value	PATO	rectangular_PATO:0001867	3
value	PATO	increased variability_PATO:0001584	2
value	PATO	repetitive_PATO:0000441	2
value	PATO	linear_PATO:0001199	2
value	PATO	convolute_PATO:0001966	2
value	PATO	decreased sensitivity toward_PATO:0001550	2
value	PATO	ruffled_PATO:0001799	2
value	PATO	bent_PATO:0000617	2
value	PATO	unbranched_PATO:0000414	2
value	PATO	hypotrophic_PATO:0000585	2
value	PATO	increased variability of size_PATO:0001958	2
value	PATO	low saturation_PATO:0000328	2
value	PATO	ovate_PATO:0001891	2
value	PATO	duplicated_PATO:0001473	2
value	PATO	filamentous_PATO:0001360	2
value	PATO	asynchronous_PATO:0000688	2
value	PATO	mulitple_PATO:0002118	2
value	PATO	cyan_PATO:0000319	2

value	PATO	triangular_PATO:0001875	2
value	PATO	flattened_PATO:0002254	2
value	PATO	amorphous_PATO:0001332	2
value	PATO	closed_PATO:0000608	2
value	PATO	rugose_PATO:0001359	2
value	PATO	drooping_PATO:0002165	2
value	PATO	fasciated_PATO:0000949	2
value	PATO	increased sensitivity of a process_PATO:0001551	2
value	PATO	subulate_PATO:0001954	2
value	PATO	white_PATO:0000323	2
value	PATO	increased pigmentation_PATO:0002250	1
value	PATO	abolished_PATO:0001508	1
value	PATO	irregular spatial pattern_PATO:0000330	1
value	PATO	disfunctional_PATO:0001641	1
value	PATO	spoon-shaped_PATO:0002208	1
value	PATO	transparent_PATO:0000964	1
value	PATO	variant shape_PATO:0001930	1
value	PATO	hyperplastic_PATO:0000644	1
value	PATO	altered number of_PATO:0002083	1
value	PATO	random pattern_PATO:0002401	1
value	PATO	degenerate_PATO:0000639	1
value	PATO	spherical_PATO:0001499	1
value	PATO	teardrop-shaped_PATO:0002240	1
value	PATO	fan-shaped_PATO:0002219	1
value	PATO	unstructured_PATO:0001412	1
value	PATO	decreased efficiency_PATO:0001675	1
value	PATO	decreased pigmentation_PATO:0002251	1

value	PATO	rotated_PATO:0001599	1
value	PATO	displaced_PATO:0002181	1
value	PATO	functional_PATO:0001510	1
value	PATO	closure incomplete_PATO:0000609	1
value	PATO	sensitive toward_PATO:0000516	1
value	PATO	split_PATO:0001786	1
value	PATO	translucent_PATO:0001354	1
value	PATO	V-shaped_PATO:0002224	1
value	PATO	hypermorphic growth_PATO:0001755	1
value	PATO	increased sensitivity toward_PATO:0001549	1
value	PATO	insensitive toward_PATO:0000513	1
value	PATO	broken_PATO:0001444	1
value	PATO	conspicuous_PATO:0000463	1
value	PATO	decreased fluid flow_PATO:0001838	1
value	PATO	decreased sensitivity of a process_PATO:0001552	1
value	PATO	swollen_PATO:0001851	1
value	PATO	erect_PATO:0000622	1
value	PATO	grey_PATO:0000950	1
value	PATO	decreased volume_PATO:0000596	1
value	PATO	severe_PATO:0000396	1
value	PATO	elliptic_PATO:0000947	1
value	PATO	hyporesponsive to_PATO:0001194	1
value	PATO	increased diameter_PATO:0001714	1
value	PATO	inverted_PATO:0000625	1
value	PATO	decreased functionality_PATO:0001624	1
value	PATO	splayed_PATO:0001785	1
value	PATO	temporally extended_PATO:0001333	1

value	PATO	upturned_PATO:0002031	1
value	PATO	concave_PATO:0001857	1
value	PATO	damaged_PATO:0001167	1
value	PATO	decreased flexibility_PATO:0001777	1
value	PATO	slender_PATO:0002212	1
value	PATO	increased fluid flow_PATO:0001839	1
value	PM	cell non-autonomous_PM:0000013	1
value	PM	cell autonomous_PM:0000012	1
value	PM	dominant_PM:0000003	1

Supplemental Table S5. Lists of genes seeding the LeafNet network

AGI	Distinct symbols	Distinct descriptions	Source
AT1G01040	DCL1, CAF, SUS1, SIN1, ASU1, EMB76, EMB60, ATDCL1 | DCL1	dicer-like 1	Knowtator curated
AT1G01060	LHY, LHY1 | LHY	Homeodomain-like superfamily protein	Knowtator curated
AT1G01100	NULL	60S acidic ribosomal protein family	regulated protein Baerenfaller et al. (2012)
AT1G01120	KCS1	3-ketoacyl-CoA synthase 1	Knowtator curated
AT1G01160	GIF2	GRF1-interacting factor 2	Knowtator curated
AT1G01480	ACS2, AT-ACC2	1-amino-cyclopropane-1-carboxylate synthase 2	Knowtator curated
AT1G01510	AN	NAD(P)-binding Rossmann-fold superfamily protein	Knowtator curated
AT1G01720	ATAF1, ANAC002	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Knowtator curated
AT1G02090	FUS5, CSN7, COP15, ATCSN7	Proteasome component (PCI) domain protein	Knowtator curated
AT1G02205	CER1	Fatty acid hydroxylase superfamily	Knowtator curated
AT1G02920	ATGSTF7, GST11, ATGSTF8, GSTF7, ATGST11	glutathione S-transferase 7	regulated protein Baerenfaller et al. (2012)
AT1G02930	ATGSTF6, GST1, ERD11, ATGSTF3, GSTF6, ATGST1 | GSTF6	glutathione S-transferase 6	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G02970	WEE1, ATWEE1	WEE1 kinase homolog	Knowtator curated
AT1G03060	SPI	Beige/BEACH domain ;WD domain, G-beta repeat protein	Knowtator curated
AT1G04110	SDD1	Subtilase family protein	Knowtator curated
AT1G04240	SHY2, IAA3	AUX/IAA transcriptional regulator family protein	Knowtator curated
AT1G04250	AXR3, IAA17	AUX/IAA transcriptional regulator family protein	Knowtator curated
AT1G04400	CRY2, FHA, AT-PHH1, PHH1, ATCRY2	cryptochrome 2	Knowtator curated
AT1G04550	IAA12, BDL	AUX/IAA transcriptional regulator family protein	Knowtator curated
AT1G04820	TUA4, TOR2	tubulin alpha-4 chain	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G05010	EFE, ACO4, EAT1	ethylene-forming enzyme	Knowtator curated
AT1G05180	AXR1	NAD(P)-binding Rossmann-fold superfamily protein	Knowtator curated

AT1G05420	ATOFP12, OFP12	ovate family protein 12	Knowtator curated
AT1G05460	SDE3	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Knowtator curated
AT1G05470	CVP2	DNAse I-like superfamily protein	Knowtator curated
AT1G05570	CALS1, GSL06, ATGSL6, ATGSL06, GSL6 | CALS1	callose synthase 1	Knowtator curated
AT1G06225	CLE3	CLAVATA3/ESR-RELATED 3	Knowtator curated
AT1G06390	GSK1, ATGSK1, ATSK22, SK22, BIL2, ATSK2-3	GSK3/SHAGGY-like protein kinase 1	Knowtator curated
AT1G06920	ATOFP4, OFP4	ovate family protein 4	Knowtator curated
AT1G07000	ATEXO70B2, EXO70B2	exocyst subunit exo70 family protein B2	Knowtator curated
AT1G07370	PCNA1, ATPCNA1	proliferating cellular nuclear antigen 1	Knowtator curated
AT1G07510	ftsh10	FTSH protease 10	Knowtator curated
AT1G07640	OBP2	Dof-type zinc finger DNA-binding family protein	Knowtator curated
AT1G08260	EMB142, EMB2284, POL2A, TIL1, EMB529, ABO4, ESD7	DNA polymerase epsilon catalytic subunit	Knowtator curated
AT1G08465	YAB2	Plant-specific transcription factor YABBY family protein	Knowtator curated
AT1G08560	SYP111, KN, ATSYP111	syntaxin of plants 111	Knowtator curated
AT1G09210	CRT1b, AtCRT1b	calreticulin 1b	regulated protein Baerenfaller et al. (2012)
AT1G09620	NULL	ATP binding;leucine-tRNA ligases;aminoacyl-tRNA ligases;nucleotide binding;ATP binding;aminoacyl-tRNA ligases	regulated protein Baerenfaller et al. (2012)
AT1G09700	HYL1, DRB1	dsRNA-binding domain-like superfamily protein	Knowtator curated
AT1G10370	GST30, ATGSTU17, GST30B, ERD9	Glutathione S-transferase family protein	Knowtator curated
AT1G10470	ARR4, MEE7, ATRR1, IBC7	response regulator 4	Knowtator curated
AT1G10840	TIF3H1	translation initiation factor 3 subunit H1	Knowtator curated
AT1G10960	ATFD1, FD1	ferredoxin 1	Knowtator curated
AT1G11130	SUB, SCM, SRF9	Leucine-rich repeat protein kinase family protein	Knowtator curated
AT1G12980	ESR1, DRN	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT1G13260	RAV1, EDF4	related to ABI3/VP1 1	Knowtator curated
AT1G13280	AOC4	allene oxide cyclase 4	Knowtator curated

AT1G13290	DOT5, WIP6	C2H2-like zinc finger protein	Knowtator curated
AT1G13400	NUB, JGL	C2H2 and C2HC zinc fingers superfamily protein	Knowtator curated
AT1G13710	CYP78A5, KLU	cytochrome P450, family 78, subfamily A, polypeptide 5	Knowtator curated
AT1G13870	DRL1, AtKTI12	calmodulin binding;purine nucleotide binding	Knowtator curated
AT1G13950	EIF-5A, ELF5A-1, ATELF5A-1, EIF5A	eukaryotic elongation factor 5A-1	Knowtator curated
AT1G14350	FLP, AtMYB124, MYB124 | FLP, MYB124	Duplicated homeodomain-like superfamily protein	Knowtator curated
AT1G14620	DECOY	decoy	Knowtator curated
AT1G14720	XTR2, EXGT-A2, ATXTH28, XTH28	xyloglucan endotransglucosylase/hydrolase 28	Knowtator curated
AT1G14790	RDR1, ATRDRP1	RNA-dependent RNA polymerase 1	Knowtator curated
AT1G14920	GAI, RGA2	GRAS family transcription factor family protein	Knowtator curated
AT1G15360	SHN1, WIN1	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT1G15570	CYCA2;3	CYCLIN A2;3	Knowtator curated
AT1G15580	IAA5, ATAUX2-27, AUX2-27	indole-3-acetic acid inducible 5	Knowtator curated
AT1G15690	AVP1, ATAVP3, AVP-3, AtVHP1;1	Inorganic H pyrophosphatase family protein	Knowtator curated
AT1G15750	WSIP1, TPL	Transducin family protein / WD-40 repeat family protein	Knowtator curated
AT1G15820	LHCB6, CP24	light harvesting complex photosystem II subunit 6	Knowtator curated
AT1G16540	SIR3, LOS5, ABA3, ATABA3, ACI2	molybdenum cofactor sulfurase (LOS5) (ABA3)	Knowtator curated
AT1G16720	HCF173	high chlorophyll fluorescence phenotype 173	Knowtator curated
AT1G17060	CYP72C1, SOB7	cytochrome p450 72c1	Knowtator curated
AT1G17110	UBP15	ubiquitin-specific protease 15	Knowtator curated
AT1G17420	LOX3	lipoxygenase 3	Knowtator curated
AT1G18080	ATARCA, RACK1A_AT, RACK1A	Transducin/WD40 repeat-like superfamily protein	regulated protein Baerenfaller et al. (2012)
AT1G18140	LAC1, ATLAC1	laccase 1	Knowtator curated
AT1G18370	HIK, ATNACK1, NACK1	ATP binding microtubule motor family protein	Knowtator curated
AT1G18400	BEE1	BR enhanced expression 1	Knowtator curated
AT1G19050	ARR7	response regulator 7	Knowtator curated
AT1G19180	JAZ1, TIFY10A | TIFY10A	jasmonate-zim-domain protein 1	Knowtator curated

AT1G19220	ARF19, IAA22, ARF11	auxin response factor 19	Knowtator curated
AT1G19270	DA1	DA1	Knowtator curated
AT1G19350	BES1, BZR2	Brassinosteroid signalling positive regulator (BZR1) family protein	Knowtator curated
AT1G19850	MP, ARF5, IAA24	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	Knowtator curated
AT1G19890	ATMGH3, MGH3	male-gamete-specific histone H3	Knowtator curated
AT1G20190	ATEXPA11, EXP11, ATEXP11, ATHEXP ALPHA 1.14, EXPA11	expansin 11	Knowtator curated
AT1G20330	SMT2, CVP1, FRL1	sterol methyltransferase 2	Knowtator curated
AT1G20440	COR47, RD17, AtCOR47	cold-regulated 47	regulated protein Baerenfaller et al. (2012)
AT1G20450	LTI29, LTI45, ERD10	Dehydrin family protein	regulated protein Baerenfaller et al. (2012)
AT1G20610	CYCB2;3	Cyclin B2;3	Knowtator curated
AT1G21250	WAK1, PRO25	cell wall-associated kinase	Knowtator curated
AT1G22770	GI, FB	gigantea protein (GI)	Knowtator curated
AT1G23080	PIN7, ATPIN7 | PIN7	Auxin efflux carrier family protein	Knowtator curated
AT1G23380	KNAT6, KNAT6L, KNAT6S	KNOTTED1-like homeobox gene 6	Knowtator curated
AT1G24020	MLP423	MLP-like protein 423	regulated protein Baerenfaller et al. (2012)
AT1G24260	SEP3, AGL9 | SEP3	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT1G24590	DRNL, DRN-LIKE, SOB2, ESR2	DORNROSCHEN-like	Knowtator curated
AT1G25425	CLE43	CLAVATA3/ESR-RELATED 43	Knowtator curated
AT1G25540	PFT1	phytochrome and flowering time regulatory protein (PFT1)	Knowtator curated
AT1G25560	TEM1, EDF1	AP2/B3 transcription factor family protein	Knowtator curated
AT1G26310	CAL, CAL1, AGL10	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT1G26600	CLE9	CLAVATA3/ESR-RELATED 9	Knowtator curated
AT1G26670	VTI12, ATVTI12, VTI1B	Vesicle transport v-SNARE family protein	Knowtator curated
AT1G26770	ATEXPA10, AT-EXP10, ATEXP10, ATHEXP ALPHA 1.1,	expansin A10	Knowtator curated

	EXP10, EXPA10		
AT1G27320	AHK3, HK3	histidine kinase 3	Knowtator curated
AT1G27360	SPL11	squamosa promoter-like 11	Knowtator curated
AT1G27370	SPL10	squamosa promoter binding protein-like 10	Knowtator curated
AT1G29250	NULL	Alba DNA/RNA-binding protein	regulated protein Baerenfaller et al. (2012)
AT1G29900	CARB	carbamoyl phosphate synthetase B	Knowtator curated
AT1G29920	CAB2, AB165, LHCB1.1	chlorophyll A/B-binding protein 2	Knowtator curated
AT1G29930	CAB1, AB140, CAB140, LHCB1.3	chlorophyll A/B binding protein 1	Knowtator curated
AT1G30135	JAZ8, TIFY5A	jasmonate-zim-domain protein 8	Knowtator curated
AT1G30210	TCP24, ATTCP24 | TCP24	TEOSINTE BRANCHED 1, cycloidea, and PCF family 24	Knowtator curated
AT1G30330	ARF6	auxin response factor 6	Knowtator curated
AT1G30380	PSAK	photosystem I subunit K	Knowtator curated
AT1G30490	PHV, ATHB9	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	Knowtator curated
AT1G30570	HERK2	hercules receptor kinase 2	Knowtator curated
AT1G30950	UFO	F-box family protein	Knowtator curated
AT1G31800	CYP97A3, LUT5	cytochrome P450, family 97, subfamily A, polypeptide 3	Knowtator curated
AT1G32240	KAN2	Homeodomain-like superfamily protein	Knowtator curated
AT1G32640	ATMYC2, RD22BP1, JAI1, JIN1, MYC2, ZBF1	Basic helix-loop-helix (bHLH) DNA-binding family protein	Knowtator curated
AT1G33140	PGY2	Ribosomal protein L6 family	Knowtator curated
AT1G33240	AT-GTL1, AT-GTL2, GTL1	GT-2-like 1	Knowtator curated
AT1G34245	EPF2	Putative membrane lipoprotein	Knowtator curated
AT1G34410	ARF21	auxin response factor 21	Knowtator curated
AT1G35160	GRF4, 14-3-3PHI, GF14 PHI | GF14 PHI	GF14 protein phi chain	Knowtator curated
AT1G35720	ANNAT1, OXY5, ATOXY5	annexin 1	Knowtator curated
AT1G43850	SEU	SEUSS transcriptional co-regulator	Knowtator curated
AT1G44110	CYCA1;1	Cyclin A1;1	Knowtator curated
AT1G45249	ABF2, AREB1, ATAREB1 | ABF2	abscisic acid responsive elements-binding factor 2	Knowtator curated
AT1G47056	VFB1	VIER F-box proteine 1	Knowtator curated

AT1G47870	E2FC, ATE2F2, ATE2FC | ATE2F2	winged-helix DNA-binding transcription factor family protein	Knowtator curated
AT1G48030	mtLPD1	mitochondrial lipoamide dehydrogenase 1	Knowtator curated
AT1G48240	ATNPSN12, NPSN12	novel plant snare 12	Knowtator curated
AT1G48380	RHL1, HYP7	root hair initiation protein root hairless 1 (RHL1)	Knowtator curated
AT1G48410	AGO1	Stabilizer of iron transporter SufD / Polynucleotidyl transferase	Knowtator curated
AT1G48920	ATNUC-L1, PARL1, NUC-L1	nucleolin like 1	Knowtator curated
AT1G49005	CLE11	CLAVATA3/ESR-RELATED 11	Knowtator curated
AT1G50010	TUA2	tubulin alpha-2 chain	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G50030	TOR	target of rapamycin	Knowtator curated
AT1G50900	GDC1	Ankyrin repeat family protein	Knowtator curated
AT1G51640	ATEXO70G2, EXO70G2	exocyst subunit exo70 family protein G2	Knowtator curated
AT1G52150	ATHB-15, ATHB15, CNA, ICU4	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	Knowtator curated
AT1G52230	PSAH2, PSAH-2, PSI-H	photosystem I subunit H2	regulated protein Baerenfaller et al. (2012)
AT1G52340	ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1	NAD(P)-binding Rossmann-fold superfamily protein	Knowtator curated
AT1G52400	BGL1, BGLU18, ATBG1 | BGLU18	beta glucosidase 18	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G52410	TSA1	TSK-associating protein 1	regulated protein Baerenfaller et al. (2012)
AT1G52827	CDT1, ATCDT1	cadmium tolerance 1	Knowtator curated
AT1G52830	IAA6, SHY1	indole-3-acetic acid 6	Knowtator curated
AT1G52890	ANAC019, NAC019	NAC domain containing protein 19	Knowtator curated
AT1G53160	SPL4	squamosa promoter binding protein-like 4	Knowtator curated
AT1G53230	TCP3	TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 3	Knowtator curated
AT1G53240	mMDH1	Lactate/malate dehydrogenase family protein	Knowtator curated
AT1G53580	GLX2-3, ETHE1, GLY3	glyoxalase II 3	regulated protein Baerenfaller et al. (2012)
AT1G53730	SRF6	STRUBBELIG-receptor family 6	Knowtator curated

AT1G54090	ATEXO70D2, EXO70D2	exocyst subunit exo70 family protein D2	Knowtator curated
AT1G54370	NHX5, ATNHX5	sodium hydrogen exchanger 5	Knowtator curated
AT1G54510	ATNEK1, NEK1 | NEK1	NIMA-related serine/threonine kinase 1	Knowtator curated
AT1G55180	PLDEPSILON, PLDALPHA4	phospholipase D alpha 4	Knowtator curated
AT1G55250	HUB2	histone mono-ubiquitination 2	Knowtator curated
AT1G56010	NAC1, anac021 | NAC1, ANAC022	NAC domain containing protein 1	Knowtator curated
AT1G56200	emb1303	embryo defective 1303	Knowtator curated
AT1G56340	CRT1, CRT1a, AtCRT1a	calreticulin 1a	regulated protein Baerenfaller et al. (2012)
AT1G56580	SVB	Protein of unknown function, DUF538	regulated protein Baerenfaller et al. (2012)
AT1G59750	ARF1	auxin response factor 1	Knowtator curated
AT1G62360	STM, BUM1, SHL, WAM1, BUM, WAM	KNOX/ELK homeobox transcription factor	Knowtator curated
AT1G62380	ACO2, ATACO2	ACC oxidase 2	Knowtator curated
AT1G62830	LDL1, SWP1, ATSWP1, ATLSD1, LSD1	LSD1-like 1	Knowtator curated
AT1G62990	KNAT7, IXR11	KNOTTED-like homeobox of Arabidopsis thaliana 7	Knowtator curated
AT1G63700	EMB71, YDA, MAPKKK4	Protein kinase superfamily protein	Knowtator curated
AT1G63940	MDAR6	monodehydroascorbate reductase 6	Knowtator curated
AT1G63970	ISPF, MECPS	isoprenoid F	Knowtator curated
AT1G64280	NPR1, SAI1, NIM1, ATNPR1	regulatory protein (NPR1)	Knowtator curated
AT1G64520	RPN12a	regulatory particle non-ATPase 12A	Knowtator curated
AT1G64670	BDG1	alpha/beta-Hydrolases superfamily protein	Knowtator curated
AT1G64860	SIGA, SIG1, SIG2, SIGB, RPOD1 | SIGA	sigma factor A	Knowtator curated
AT1G65470	FAS1, NFB2 | FAS1	chromatin assembly factor-1 (FASCIATA1) (FAS1)	Knowtator curated
AT1G65480	FT	PEBP (phosphatidylethanolamine-binding protein) family protein	Knowtator curated
AT1G65620	AS2	Lateral organ boundaries (LOB) domain family protein	Knowtator curated
AT1G65660	SMP1	Pre-mRNA splicing Prp18-interacting factor	Knowtator curated
AT1G66280	BGLU22	Glycosyl hydrolase superfamily protein	regulated protein Baerenfaller et al. (2012)

AT1G66340	ETR1, EIN1, ETR, AtETR1	Signal transduction histidine kinase, hybrid-type, ethylene sensor	Knowtator curated
AT1G66350	RGL1, RGL	RGA-like 1	Knowtator curated
AT1G67090	RBCS1A	ribulose bisphosphate carboxylase small chain 1A	Knowtator curated
AT1G67560	LOX6	PLAT/LH2 domain-containing lipoxygenase family protein	Knowtator curated
AT1G68310	AE7	Protein of unknown function (DUF59)	Knowtator curated
AT1G68480	JAG	C2H2 and C2HC zinc fingers superfamily protein	Knowtator curated
AT1G68560	ATXYL1, XYL1, TRG1	alpha-xylosidase 1	regulated protein Baerenfaller et al. (2012)
AT1G68640	PAN	bZIP transcription factor family protein	Knowtator curated
AT1G68990	MGP3	male gametophyte defective 3	Knowtator curated
AT1G69120	AP1, AGL7	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT1G69180	CRC	Plant-specific transcription factor YABBY family protein	Knowtator curated
AT1G69200	FLN2	fructokinase-like 2	Knowtator curated
AT1G69260	AFP1	ABI five binding protein	Knowtator curated
AT1G69320	CLE10	CLAVATA3/ESR-RELATED 10	Knowtator curated
AT1G69440	AGO7, ZIP	Argonaute family protein	Knowtator curated
AT1G69530	ATEXPA1, EXP1, AT-EXP1, ATEXP1, ATHEXP ALPHA 1.2, EXPA1 | EXPA1	expansin A1	Knowtator curated
AT1G69588	CLE45	CLAVATA3/ESR-RELATED 45	Knowtator curated
AT1G69780	ATHB13	Homeobox-leucine zipper protein family	Knowtator curated
AT1G69970	CLE26	CLAVATA3/ESR-RELATED 26	Knowtator curated
AT1G70510	KNAT2, ATK1	KNOTTED-like from Arabidopsis thaliana 2	Knowtator curated
AT1G70940	PIN3, ATPIN3	Auxin efflux carrier family protein	Knowtator curated
AT1G71230	CSN5B, CSN5, AJH2	COP9-signalosome 5B	Knowtator curated
AT1G72450	JAZ6, TIFY11B	jasmonate-zim-domain protein 6	Knowtator curated
AT1G72520	LOX4	PLAT/LH2 domain-containing lipoxygenase family protein	Knowtator curated
AT1G72770	HAB1	homology to ABI1	Knowtator curated
AT1G73590	PIN1, ATPIN1	Auxin efflux carrier family protein	Knowtator curated

AT1G73965	CLE13	CLAVATA3/ESR-RELATED 13	Knowtator curated
AT1G74660	MIF1	mini zinc finger 1	Knowtator curated
AT1G74710	EDS16, ICS1, SID2, ATICS1 | EDS16, ICS1, SID2	ADC synthase superfamily protein	Knowtator curated
AT1G74890	ARR15	response regulator 15	Knowtator curated
AT1G74950	JAZ2, TIFY10B	TIFY domain/Divergent CCT motif family protein	Knowtator curated
AT1G75040	PR5, PR-5	pathogenesis-related gene 5	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G75240	AtHB33, HB33, ZHD5	homeobox protein 33	Knowtator curated
AT1G75270	DHAR2	dehydroascorbate reductase 2	Knowtator curated
AT1G75450	CKX5, ATCKX5, ATCKX6 | CKX5	cytokinin oxidase 5	Knowtator curated
AT1G75750	GASA1	GAST1 protein homolog 1	regulated protein Baerenfaller et al. (2012)
AT1G75820	CLV1, FAS3, FLO5, ATCLV1	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT1G75950	SKP1, ASK1, ATSKP1, SKP1A, UIP1	S phase kinase-associated protein 1	Knowtator curated
AT1G76180	ERD14	Dehydrin family protein	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT1G76420	CUC3, NAC368, ANAC031	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Knowtator curated
AT1G76490	HMG1, HMGR1, AtHMGR1	hydroxy methylglutaryl CoA reductase 1	Knowtator curated
AT1G76540	CDKB2;1	cyclin-dependent kinase B2;1	Knowtator curated
AT1G77120	ADH1, ADH, ATADH, ATADH1	alcohol dehydrogenase 1	Knowtator curated
AT1G78300	GRF2, 14-3-3OMEGA, GF14 OMEGA	general regulatory factor 2	Knowtator curated
AT1G78770	APC6	anaphase promoting complex 6	Knowtator curated
AT1G78980	SRF5	STRUBBELIG-receptor family 5	Knowtator curated
AT1G79320	AtMC6, MC6	metacaspase 6	Knowtator curated
AT1G79610	ATNHX6, NHX6	Na+/H+ antiporter 6	Knowtator curated
AT1G79820	SGB1	Major facilitator superfamily protein	Knowtator curated
AT1G79840	GL2	HD-ZIP IV family of homeobox-leucine zipper protein with lipid-binding START domain	Knowtator curated
AT1G80080	TMM, AtRLP17	Leucine-rich repeat (LRR) family protein	Knowtator curated
AT1G80600	WIN1	HOPW1-1-interacting 1	Knowtator curated

AT2G01420	PIN4, ATPIN4 | PIN4	Auxin efflux carrier family protein	Knowtator curated
AT2G01570	RGA1, RGA	GRAS family transcription factor family protein	Knowtator curated
AT2G01830	WOL, CRE1, WOL1, AHK4, ATCRE1	CHASE domain containing histidine kinase protein	Knowtator curated
AT2G02500	ISPD, ATMEPCT, MCT	Nucleotide-diphospho-sugar transferases superfamily protein	Knowtator curated
AT2G02560	CAND1, ATCAND1, ETA2, TIP120, HVE	cullin-associated and neddylation dissociated	Knowtator curated
AT2G03050	EMB93, SOLDAT10	Mitochondrial transcription termination factor family protein	Knowtator curated
AT2G03090	ATEXPA15, EXP15, ATEXP15, ATHEXP ALPHA 1.3, EXPA15	expansin A15	Knowtator curated
AT2G04160	AIR3	Subtilisin-like serine endopeptidase family protein	Knowtator curated
AT2G04240	XERICO	RING/U-box superfamily protein	Knowtator curated
AT2G04660	APC2	anaphase-promoting complex/cyclosome 2	Knowtator curated
AT2G05070	LHCB2.2, LHCB2	photosystem II light harvesting complex gene 2.2	Knowtator curated
AT2G05380	GRP3S	glycine-rich protein 3 short isoform	regulated protein Baerenfaller et al. (2012)
AT2G05520	GRP-3, ATGRP-3, GRP3, ATGRP3 | GRP-3, ATGRP-3	glycine-rich protein 3	regulated protein Baerenfaller et al. (2012)
AT2G05620	PGR5	proton gradient regulation 5	Knowtator curated
AT2G06050	OPR3, DDE1 | OPR3	oxophytodienoate-reductase 3	regulated protein Baerenfaller et al. (2012)
AT2G06200	AtGRF6, GRF6	growth-regulating factor 6	Knowtator curated
AT2G06850	EXGT-A1, EXT, XTH4	xyloglucan endotransglucosylase/hydrolase 4	Knowtator curated
AT2G14610	PR1, PR 1, ATPR1	pathogenesis-related gene 1	Knowtator curated
AT2G14960	GH3.1	Auxin-responsive GH3 family protein	Knowtator curated
AT2G15790	SQN, CYP40	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase	Knowtator curated
AT2G17230	EXL5	EXORDIUM like 5	Knowtator curated
AT2G17620	CYCB2;1	Cyclin B2;1	Knowtator curated
AT2G17790	VPS35A, ZIP3	VPS35 homolog A	Knowtator curated
AT2G17870	ATCSP3, CSP3	cold shock domain protein 3	Knowtator curated
AT2G17950	WUS, PGA6, WUS1	Homeodomain-like superfamily protein	Knowtator curated

AT2G18170	ATMPK7, MPK7	MAP kinase 7	Knowtator curated
AT2G18250	ATCOAD, COAD	4-phosphopantetheine adenylyltransferase	Knowtator curated
AT2G18290	APC10	anaphase promoting complex 10	Knowtator curated
AT2G18500	ATOFP7, OFP7	ovate family protein 7	Knowtator curated
AT2G18790	PHYB, HY3, OOP1	phytochrome B	Knowtator curated
AT2G19480	NFA02, NFA2, NAP1;2 | NAP1;2	nucleosome assembly protein 1;2	Knowtator curated
AT2G19500	CKX2, ATCKX2	cytokinin oxidase 2	Knowtator curated
AT2G19720	rps15ab	ribosomal protein S15A B	Knowtator curated
AT2G20000	HBT, CDC27b	CDC27 family protein	Knowtator curated
AT2G20570	GPRI1, GLK1, ATGLK1 | GPRI1	GBF's pro-rich region-interacting factor 1	Knowtator curated
AT2G20750	ATEXPB1, EXPB1, ATHEXP BETA 1.5	expansin B1	Knowtator curated
AT2G20850	SRF1	STRUBBELIG-receptor family 1	Knowtator curated
AT2G20875	EPF1	epidermal patterning factor 1	Knowtator curated
AT2G21660	ATGRP7, CCR2, GR-RBP7, GRP7 | ATGRP7, CCR2	cold, circadian rhythm, and rna binding 2	regulated protein Baerenfaller et al. (2012)
AT2G21790	R1, RNR1, CLS8, ATRNR1	ribonucleotide reductase 1	Knowtator curated
AT2G22330	CYP79B3	cytochrome P450, family 79, subfamily B, polypeptide 3	Knowtator curated
AT2G22490	CYCD2;1, ATCYCD2;1 | CYCD2;1	Cyclin D2;1	Knowtator curated
AT2G22840	AtGRF1, GRF1	growth-regulating factor 1	Knowtator curated
AT2G23380	CLF, ICU1, SDG1, SET1	SET domain-containing protein	Knowtator curated
AT2G23430	ICK1, KRP1	Cyclin-dependent kinase inhibitor family protein	Knowtator curated
AT2G23760	BLH4, SAW2	BEL1-like homeodomain 4	Knowtator curated
AT2G24120	PDE319, SCA3	DNA/RNA polymerases superfamily protein	Knowtator curated
AT2G24765	ARF3, ARL1, ATARL1	ADP-ribosylation factor 3	Knowtator curated
AT2G25060	ENODL14, AtENODL14	early nodulin-like protein 14	regulated protein Baerenfaller et al. (2012)
AT2G25170	PKL, GYM, CHD3, CHR6, SSL2	chromatin remodeling factor CHD3 (PICKLE)	Knowtator curated
AT2G25180	ARR12, RR12	response regulator 12	Knowtator curated
AT2G25450	NULL	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	regulated protein Baerenfaller et al. (2012)
AT2G25510	NULL	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi -	regulated protein Baerenfaller et al. (2012)

		0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42530.1).	
AT2G25620	AtDBP1, DBP1	DNA-binding protein phosphatase 1	Knowtator curated
AT2G25880	AtAUR2, AUR2	ataurora2	Knowtator curated
AT2G26300	GPA1, GP ALPHA 1, ATGPA1	G protein alpha subunit 1	Knowtator curated
AT2G26330	ER, QRP1	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT2G26580	YAB5	plant-specific transcription factor YABBY family protein	Knowtator curated
AT2G26710	BAS1, CYP734A1, CYP72B1	Cytochrome P450 superfamily protein	Knowtator curated
AT2G26760	CYCB1;4	Cyclin B1;4	Knowtator curated
AT2G26930	ATCDPMEK, PDE277, ISPE, CDPMEK	4-(cytidine 5'-phospho)-2-C-methyl-D-erithritol kinase	Knowtator curated
AT2G27050	EIL1, AtEIL1	ETHYLENE-INSENSITIVE3-like 1	Knowtator curated
AT2G27100	SE	C2H2 zinc-finger protein SERRATE (SE)	Knowtator curated
AT2G27250	CLV3	CLAVATA3	Knowtator curated
AT2G27530	PGY1	Ribosomal protein L1p/L10e family	Knowtator curated
AT2G27710	NULL	60S acidic ribosomal protein family	regulated protein Baerenfaller et al. (2012)
AT2G28290	SYD, CHR3	P-loop containing nucleoside triphosphate hydrolases superfamily protein	Knowtator curated
AT2G28610	PRS, WOX3, PRS1	Homeodomain-like superfamily protein	Knowtator curated
AT2G28740	HIS4	histone H4	Knowtator curated
AT2G28950	ATEXPA6, ATEXP6, ATHEXP ALPHA 1.8, EXPA6	expansin A6	Knowtator curated
AT2G29130	LAC2, ATLAC2	laccase 2	Knowtator curated
AT2G29550	TUB7	tubulin beta-7 chain	regulated protein Baerenfaller et al. (2012)
AT2G29570	PCNA2, ATPCNA2	proliferating cell nuclear antigen 2	Knowtator curated
AT2G29680	CDC6, ATCDC6	cell division control 6	Knowtator curated

AT2G30210	LAC3	laccase 3	Knowtator curated
AT2G30400	ATOFP2, OFP2	ovate family protein 2	Knowtator curated
AT2G30490	ATC4H, C4H, CYP73A5, REF3	cinnamate-4-hydroxylase	Knowtator curated
AT2G30520	RPT2	Phototropic-responsive NPH3 family protein	regulated protein Baerenfaller et al. (2012)
AT2G30980	ASKdZeta, ATSK23, BIL1, ATSK2-2, SKdZeta	SHAGGY-related protein kinase dZeta	Knowtator curated
AT2G31070	TCP10	TCP domain protein 10	Knowtator curated
AT2G31081	CLE4	CLAVATA3/ESR-RELATED 4	Knowtator curated
AT2G31082	CLE7	CLAVATA3/ESR-RELATED 7	Knowtator curated
AT2G31083	CLE5	CLAVATA3/ESR-RELATED 5	Knowtator curated
AT2G31085	CLE6	CLAVATA3/ESR-RELATED 6	Knowtator curated
AT2G31270	ATCDT1A, CDT1A, CDT1	homolog of yeast CDT1 A	Knowtator curated
AT2G31320	PARP2, ATPARP2	poly(ADP-ribose) polymerase 2	Knowtator curated
AT2G32060	NULL	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	regulated protein Baerenfaller et al. (2012)
AT2G32100	ATOFP16, OFP16	ovate family protein 16	Knowtator curated
AT2G32410	AXL	AXR1-like	Knowtator curated
AT2G32710	KRP4, ACK2, ICK7	Cyclin-dependent kinase inhibitor family protein	Knowtator curated
AT2G33210	HSP60-2	heat shock protein 60-2	Knowtator curated
AT2G33310	IAA13	auxin-induced protein 13	Knowtator curated
AT2G33410	NULL	RNA-binding (RRM/RBD/RNP motifs) family protein	regulated protein Baerenfaller et al. (2012)
AT2G33540	CPL3, ATCPL3	C-terminal domain phosphatase-like 3	Knowtator curated
AT2G33810	SPL3	squamosa promoter binding protein-like 3	Knowtator curated
AT2G33860	ETT, ARF3	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	Knowtator curated
AT2G33880	WOX9, HB-3, STIP	homeobox-3	Knowtator curated
AT2G34430	LHB1B1, LHCB1.4	light-harvesting chlorophyll-protein complex II subunit B1	Knowtator curated
AT2G34590	NULL	Transketolase family protein	regulated protein Baerenfaller et al. (2012)
AT2G34650	PID, ABR	Protein kinase superfamily protein	Knowtator curated
AT2G34710	PHB, ATHB14, ATHB-14, PHB-1D	Homeobox-leucine zipper family protein / lipid-binding	Knowtator curated

		START domain-containing protein	
AT2G34720	NF-YA4	nuclear factor Y, subunit A4	Knowtator curated
AT2G34780	EMB1611, MEE22 | MEE22	maternal effect embryo arrest 22	Knowtator curated
AT2G34925	CLE42	CLAVATA3/ESR-RELATED 42	Knowtator curated
AT2G35150	EXL1	EXORDIUM like 1	Knowtator curated
AT2G36010	E2F3, ATE2FA	E2F transcription factor 3	Knowtator curated
AT2G36050	ATOFP15, OFP15	ovate family protein 15	Knowtator curated
AT2G36120	DOT1	Glycine-rich protein family	Knowtator curated
AT2G36145	NULL	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast stroma, chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 49 Blast hits to 49 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	regulated protein Baerenfaller et al. (2012)
AT2G36270	ABI5, GIA1	Basic-leucine zipper (bZIP) transcription factor family protein	Knowtator curated
AT2G36400	AtGRF3, GRF3	growth-regulating factor 3	Knowtator curated
AT2G36985	ROT4, DVL16	DVL family protein	Knowtator curated
AT2G37040	PAL1, ATPAL1	PHE ammonia lyase 1	Knowtator curated
AT2G37560	ORC2, ATORC2	origin recognition complex second largest subunit 2	Knowtator curated
AT2G37590	ATDOF2.4, DOF2.4	DNA binding with one finger 2.4	Knowtator curated
AT2G37630	ATPHAN, AS1, ATMYB91, MYB91	myb-like HTH transcriptional regulator family protein	Knowtator curated
AT2G37640	ATEXPA3, ATEXP3, ATHEXP ALPHA 1.9, EXP3	Barwin-like endoglucanases superfamily protein	Knowtator curated
AT2G37760	NULL	NAD(P)-linked oxidoreductase superfamily protein	regulated protein Baerenfaller et al. (2012)
AT2G37860	LCD1	Protein of unknown function (DUF3411)	Knowtator curated
AT2G38050	DET2, DWF6, ATDET2	3-oxo-5-alpha-steroid 4-dehydrogenase family protein	Knowtator curated
AT2G38060	PHT4;2	phosphate transporter 4;2	Knowtator curated
AT2G38080	IRX12, LAC4, ATLMCO4, LMCO4	Laccase/Diphenol oxidase family protein	Knowtator curated

AT2G38120	AUX1, WAV5, PIR1, MAP1	Transmembrane amino acid transporter family protein	Knowtator curated
AT2G38310	PYL4, RCAR10	PYR1-like 4	Knowtator curated
AT2G38540	LP1, LTP1, ATLTP1	lipid transfer protein 1	regulated protein Baerenfaller et al. (2012)
AT2G39090	APC7, AtAPC7	tetratricopeptide repeat (TPR)-containing protein	Knowtator curated
AT2G39380	ATEXO70H2, EXO70H2	exocyst subunit exo70 family protein H2	Knowtator curated
AT2G39700	ATEXPA4, ATEXP4, ATHEXP ALPHA 1.6, EXPA4	expansin A4	Knowtator curated
AT2G40220	ABI4, SUN6, SIS5, ISI3, GIN6, SAN5, ATABI4	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT2G40370	LAC5	laccase 5	Knowtator curated
AT2G40610	ATEXPA8, EXP8, ATEXP8, ATHEXP ALPHA 1.11, EXPA8	expansin A8	Knowtator curated
AT2G40890	CYP98A3	cytochrome P450, family 98, subfamily A, polypeptide 3	Knowtator curated
AT2G40940	ERS1, ERS	ethylene response sensor 1	Knowtator curated
AT2G41100	TCH3, ATCAL4 | TCH3	Calcium-binding EF hand family protein	Knowtator curated
AT2G41370	BOP2	Ankyrin repeat family protein / BTB/POZ domain-containing protein	Knowtator curated
AT2G41510	ATCKX1, CKX1	cytokinin oxidase/dehydrogenase 1	Knowtator curated
AT2G42200	SPL9, AtSPL9	squamosa promoter binding protein-like 9	Knowtator curated
AT2G42260	UVI4, PYM	uv-b-insensitive 4	Knowtator curated
AT2G42520	NULL	P-loop containing nucleoside triphosphate hydrolases superfamily protein	regulated protein Baerenfaller et al. (2012)
AT2G42530	COR15B	cold regulated 15b	Knowtator curated
AT2G42540	COR15A, COR15 | COR15A	cold-regulated 15a	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT2G42590	GRF9, GF14 MU	general regulatory factor 9	Knowtator curated
AT2G42620	MAX2, ORE9, PPS	RNI-like superfamily protein	Knowtator curated
AT2G42840	PDF1	protodermal factor 1	Knowtator curated
AT2G43100	IPMI2, ATLEUD1	isopropylmalate isomerase 2	regulated protein Baerenfaller et al. (2012)
AT2G43570	CHI	chitinase, putative	Knowtator curated
AT2G43710	SSI2, FAB2	Plant stearoyl-acyl-carrier-protein desaturase family	Knowtator curated

		protein	
AT2G44080	ARL	ARGOS-like	Knowtator curated
AT2G44950	RDO4, HUB1	histone mono-ubiquitination 1	Knowtator curated
AT2G44990	CCD7, MAX3, ATCCD7	carotenoid cleavage dioxygenase 7	Knowtator curated
AT2G45160	HAM1, ATHAM1, LOM1	GRAS family transcription factor	Knowtator curated
AT2G45190	AFO, FIL, YAB1	Plant-specific transcription factor YABBY family protein	Knowtator curated
AT2G45280	ATRAD51C, RAD51C | RAD51C	RAS associated with diabetes protein 51C	Knowtator curated
AT2G45400	BEN1	NAD(P)-binding Rossmann-fold superfamily protein	Knowtator curated
AT2G45480	AtGRF9, GRF9	growth-regulating factor 9	Knowtator curated
AT2G45660	AGL20, SOC1, ATSOC1	AGAMOUS-like 20	Knowtator curated
AT2G46340	SPA1	SPA (suppressor of phyA-105) protein family	Knowtator curated
AT2G46570	LAC6	laccase 6	Knowtator curated
AT2G46680	ATHB-7, ATHB7, HB-7	homeobox 7	Knowtator curated
AT2G47450	CAO, CPSRP43	chloroplast signal recognition particle component (CAO)	Knowtator curated
AT3G01280	VDAC1, ATVDAC1	voltage dependent anion channel 1	Knowtator curated
AT3G02170	LNG2	longifolia2	Knowtator curated
AT3G02520	GRF7, GF14 NU	general regulatory factor 7	Knowtator curated
AT3G03220	ATEXPA13, EXP13, ATEXP13, ATHEXP ALPHA 1.22, EXPA13	expansin A13	Knowtator curated
AT3G03300	DCL2, ATDCL2 | DCL2	dicer-like 2	Knowtator curated
AT3G03450	RGL2	RGA-like 2	Knowtator curated
AT3G04120	GAPC, GAPC-1, GAPC1	glyceraldehyde-3-phosphate dehydrogenase C subunit 1	Knowtator curated
AT3G04610	FLK	RNA-binding KH domain-containing protein	Knowtator curated
AT3G04740	SWP, MED14, ATMED14	RNA polymerase II transcription mediators	Knowtator curated
AT3G04810	ATNEK2, NEK2	NIMA-related kinase 2	Knowtator curated
AT3G05030	NHX2, ATNHX2	sodium hydrogen exchanger 2	Knowtator curated
AT3G05040	HST, HST1	ARM repeat superfamily protein	Knowtator curated
AT3G05970	LACS6, ATLACS6	long-chain acyl-CoA synthetase 6	Knowtator curated
AT3G06010	ATCHR12	Homeotic gene regulator	Knowtator curated
AT3G06120	MUTE	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Knowtator curated

AT3G06370	NHX4, ATNHX4	sodium hydrogen exchanger 4	Knowtator curated
AT3G06420	ATG8H	Ubiquitin-like superfamily protein	Knowtator curated
AT3G07040	RPM1, RPS3	NB-ARC domain-containing disease resistance protein	Knowtator curated
AT3G08720	ATPK19, ATS6K2, S6K2, ATPK2 | ATPK19, ATPK2	serine/threonine protein kinase 2	Knowtator curated
AT3G08730	ATPK1, ATPK6, ATS6K1, PK6, PK1, S6K1	protein-serine kinase 1	Knowtator curated
AT3G08940	LHCB4.2	light harvesting complex photosystem II	Knowtator curated
AT3G09220	LAC7	laccase 7	Knowtator curated
AT3G09520	ATEXO70H4, EXO70H4	exocyst subunit exo70 family protein H4	Knowtator curated
AT3G09650	HCF152, CRM3	Tetratricopeptide repeat (TPR)-like superfamily protein	Knowtator curated
AT3G09810	IDH-VI	isocitrate dehydrogenase VI	Knowtator curated
AT3G10525	LGO, SMR1	LOSS OF GIANT CELLS FROM ORGANS	Knowtator curated
AT3G11220	ELO1	Paxneb protein-related	Knowtator curated
AT3G11440	ATMYB65, MYB65	myb domain protein 65	Knowtator curated
AT3G11540	SPY	Tetratricopeptide repeat (TPR)-like superfamily protein	Knowtator curated
AT3G11900	ANT1	aromatic and neutral transporter 1	Knowtator curated
AT3G12110	ACT11	actin-11	Knowtator curated
AT3G12200	AtNek7, Nek7 | Nek7	NIMA-related kinase 7	Knowtator curated
AT3G12280	RBR1, RBR, RB, ATRBR1, RB1 | RBR1	retinoblastoma-related 1	Knowtator curated
AT3G12580	HSP70, ATHSP70	heat shock protein 70	Knowtator curated
AT3G12680	HUA1	floral homeotic protein (HUA1)	Knowtator curated
AT3G12750	ZIP1	zinc transporter 1 precursor	Knowtator curated
AT3G12930	NULL	Lojap-related protein	regulated protein Baerenfaller et al. (2012)
AT3G13065	SRF4	STRUBBELIG-receptor family 4	Knowtator curated
AT3G13470	NULL	TCP-1/cpn60 chaperonin family protein	regulated protein Baerenfaller et al. (2012)
AT3G13730	CYP90D1	cytochrome P450, family 90, subfamily D, polypeptide 1	Knowtator curated

AT3G13920	EIF4A1, RH4, TIF4A1 | EIF4A1	eukaryotic translation initiation factor 4A1	regulated protein Baerenfaller et al. (2012)
AT3G13960	AtGRF5, GRF5	growth-regulating factor 5	Knowtator curated
AT3G14090	ATEXO70D3, EXO70D3	exocyst subunit exo70 family protein D3	Knowtator curated
AT3G14350	SRF7	STRUBBELIG-receptor family 7	Knowtator curated
AT3G14390	NULL	Pyridoxal-dependent decarboxylase family protein	regulated protein Baerenfaller et al. (2012)
AT3G14440	NCED3, ATNCED3, STO1, SIS7	nine-cis-epoxycarotenoid dioxygenase 3	Knowtator curated
AT3G14940	ATPPC3, PPC3	phosphoenolpyruvate carboxylase 3	Knowtator curated
AT3G15030	TCP4, MEE35 | TCP4	TCP family transcription factor 4	Knowtator curated
AT3G15170	CUC1, ANAC054, ATNAC1	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Knowtator curated
AT3G15190	NULL	chloroplast 30S ribosomal protein S20, putative	regulated protein Baerenfaller et al. (2012)
AT3G15210	ATERF-4, ERF4, RAP2.5, ATERF4	ethylene responsive element binding factor 4	Knowtator curated
AT3G15270	SPL5	squamosa promoter binding protein-like 5	Knowtator curated
AT3G15356	NULL	Legume lectin family protein	regulated protein Baerenfaller et al. (2012)
AT3G15540	IAA19, MSG2	indole-3-acetic acid inducible 19	Knowtator curated
AT3G15730	PLDALPHA1, PLD	phospholipase D alpha 1	Knowtator curated
AT3G16240	DELTA-TIP, TIP2;1, DELTA-TIP1, AQP1, ATTIP2;1	delta tonoplast integral protein	Knowtator curated
AT3G16470	JR1	Mannose-binding lectin superfamily protein	Knowtator curated
AT3G16530	NULL	Legume lectin family protein	regulated protein Baerenfaller et al. (2012)
AT3G16640	TCTP	translationally controlled tumor protein	Knowtator curated
AT3G16830	TPR2	TOPLESS-related 2	Knowtator curated
AT3G16850	NULL	Pectin lyase-like superfamily protein	regulated protein Baerenfaller et al. (2012)
AT3G16857	ARR1, RR1	response regulator 1	Knowtator curated
AT3G17860	JAZ3, JAI3, TIFY6B	jasmonate-zim-domain protein 3	Knowtator curated
AT3G18010	WOX1	WUSCHEL related homeobox 1	Knowtator curated
AT3G18990	VRN1, REM39	AP2/B3-like transcriptional factor family protein	Knowtator curated

AT3G19150	KRP6, ICK4, ACK1	KIP-related protein 6	Knowtator curated
AT3G19710	BCAT4	branched-chain aminotransferase4	regulated protein Baerenfaller et al. (2012)
AT3G19820	DWF1, DIM, EVE1, DIM1, CBB1 | DWF1	cell elongation protein / DWARF1 / DIMINUTO (DIM)	Knowtator curated
AT3G20770	EIN3, AtEIN3	Ethylene insensitive 3 family protein	Knowtator curated
AT3G20780	ATTOP6B, BIN3, HYP6, RHL3, TOP6B	topoisomerase 6 subunit B	Knowtator curated
AT3G21640	TWD1, UCU2, FKBP42, ATFKBP42	FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Knowtator curated
AT3G22200	POP2, GABA-T, HER1 | POP2	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	Knowtator curated
AT3G23030	IAA2	indole-3-acetic acid inducible 2	Knowtator curated
AT3G23050	IAA7, AXR2	indole-3-acetic acid 7	Knowtator curated
AT3G23130	SUP, FON1, FLO10	C2H2 and C2HC zinc fingers superfamily protein	Knowtator curated
AT3G23580	RNR2, RNR2A	ribonucleotide reductase 2A	Knowtator curated
AT3G23630	ATIPT7, IPT7	isopentenyltransferase 7	Knowtator curated
AT3G23810	SAHH2, ATSAHH2	S-adenosyl-l-homocysteine (SAH) hydrolase 2	Knowtator curated
AT3G23890	TOPII, ATTOPII	topoisomerase II	Knowtator curated
AT3G23990	HSP60, HSP60-3B	heat shock protein 60	Knowtator curated
AT3G24140	FMA	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Knowtator curated
AT3G24225	CLE19, ESR19, ATCLE19	CLAVATA3/ESR-RELATED 19	Knowtator curated
AT3G24430	HCF101	ATP binding	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT3G24650	ABI3, SIS10	AP2/B3-like transcriptional factor family protein	Knowtator curated
AT3G24770	CLE41	CLAVATA3/ESR-RELATED 41	Knowtator curated
AT3G24810	ICK3, KRP5	Cyclin-dependent kinase inhibitor family protein	Knowtator curated
AT3G25520	ATL5, PGY3, OLI5, RPL5A | ATL5	ribosomal protein L5	Knowtator curated
AT3G25730	EDF3	ethylene response DNA binding factor 3	Knowtator curated
AT3G25760	AOC1, ERD12	allene oxide cyclase 1	Knowtator curated
AT3G27010	AT-TCP20, PCF1, TCP20, ATTCP20	TEOSINTE BRANCHED 1, cycloidea, PCF (TCP)-domain family protein 20	Knowtator curated
AT3G27280	ATPHB4, PHB4	prohibitin 4	Knowtator curated

AT3G27740	CARA	carbamoyl phosphate synthetase A	Knowtator curated
AT3G28220	NULL	TRAF-like family protein	regulated protein Baerenfaller et al. (2012)
AT3G28730	ATHMG, SSRP1, NFD, HMG	high mobility group	Knowtator curated
AT3G28917	MIF2	mini zinc finger 2	Knowtator curated
AT3G29030	ATEXPA5, ATEXP5, ATHEXP ALPHA 1.4, EXP5, EXPA5	expansin A5	Knowtator curated
AT3G29400	ATEXO70E1, EXO70E1	exocyst subunit exo70 family protein E1	Knowtator curated
AT3G33520	ATARP6, ARP6, SUF3, ESD1	actin-related protein 6	Knowtator curated
AT3G43210	TES, ATNACK2, NACK2	ATP binding microtubule motor family protein	Knowtator curated
AT3G43920	DCL3, ATDCL3	dicer-like 3	Knowtator curated
AT3G44200	ATNEK6, NEK6, IBO1	NIMA (never in mitosis, gene A)-related 6	Knowtator curated
AT3G44300	NIT2, AtNIT2	nitrilase 2	Knowtator curated
AT3G44310	NIT1, ATNIT1, NITI	nitrilase 1	Knowtator curated
AT3G44320	NIT3, AtNIT3	nitrilase 3	Knowtator curated
AT3G44590	NULL	60S acidic ribosomal protein family	regulated protein Baerenfaller et al. (2012)
AT3G44880	ACD1, LLS1, PAO	Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain	Knowtator curated
AT3G45030	NULL	Ribosomal protein S10p/S20e family protein	regulated protein Baerenfaller et al. (2012)
AT3G45140	LOX2, ATLOX2	lipoxygenase 2	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT3G45780	PHOT1, NPH1, JK224, RPT1	phototropin 1	Knowtator curated
AT3G46290	HERK1	hercules receptor kinase 1	Knowtator curated
AT3G47470	LHCA4, CAB4	light-harvesting chlorophyll-protein complex I subunit A4	Knowtator curated
AT3G47500	CDF3	cycling DOF factor 3	Knowtator curated
AT3G47620	AtTCP14, TCP14	TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14	Knowtator curated
AT3G48100	ARR5, ATRR2, IBC6, RR5	response regulator 5	Knowtator curated
AT3G48150	APC8, CDC23	anaphase-promoting complex subunit 8	Knowtator curated
AT3G48160	DEL1, E2L3, E2FE	DP-E2F-like 1	Knowtator curated
AT3G48190	ATM, ATATM	ataxia-telangiectasia mutated	Knowtator curated

AT3G48580	XTH11	xyloglucan endotransglucosylase/hydrolase 11	Knowtator curated
AT3G48750	CDKA;1, CDC2AAT, CDK2, CDC2, CDC2A, CDKA1	cell division control 2	Knowtator curated
AT3G49500	RDR6, SGS2, SDE1	RNA-dependent RNA polymerase 6	Knowtator curated
AT3G49670	BAM2	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT3G49920	VDAC5, ATVDAC5 | VDAC5	voltage dependent anion channel 5	Knowtator curated
AT3G50070	CYCD3;3	CYCLIN D3;3	Knowtator curated
AT3G50080	VFB2	VIER F-box proteine 2	Knowtator curated
AT3G50630	KRP2, ICK2	KIP-related protein 2	Knowtator curated
AT3G50660	DWF4, CYP90B1, CLM, SNP2, SAV1, PSC1	Cytochrome P450 superfamily protein	Knowtator curated
AT3G51240	F3H, TT6, F3'H | F3H	flavanone 3-hydroxylase	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT3G51550	FER	Malectin/receptor-like protein kinase family protein	Knowtator curated
AT3G51800	ATG2, EBP1, ATEBP1 | ATG2	metallopeptidase M24 family protein	Knowtator curated
AT3G52280	GTE6	general transcription factor group E6	Knowtator curated
AT3G52525	ATOFP6, OFP6	ovate family protein 6	Knowtator curated
AT3G52850	VSR1, BP-80, ATELP, BP80, BP80B, ATELP1, ATVSR1, GFS1, VSR1;1, BP80-1;1	vacuolar sorting receptor homolog 1	Knowtator curated
AT3G52910	AtGRF4, GRF4	growth-regulating factor 4	Knowtator curated
AT3G53130	LUT1, CYP97C1	Cytochrome P450 superfamily protein	Knowtator curated
AT3G53460	CP29	chloroplast RNA-binding protein 29	regulated protein Baerenfaller et al. (2012)
AT3G53560	NULL	Tetratricopeptide repeat (TPR)-like superfamily protein	regulated protein Baerenfaller et al. (2012)
AT3G53750	ACT3	actin 3	Knowtator curated
AT3G54090	FLN1	fructokinase-like 1	Knowtator curated
AT3G54180	CDC2B, CDKB1;1	cyclin-dependent kinase B1;1	Knowtator curated
AT3G54340	AP3, ATAP3	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT3G54710	ATCDT1B, CDT1B, CDT1	homolog of yeast CDT1 B homolog of yeast CDT1 B	Knowtator curated
AT3G54840	ARA6, ATRABF1, ARA-6, ATRAB5C | ARA6, RABF1	Ras-related small GTP-binding family protein	Knowtator curated

AT3G55120	TT5, A11, CFI	Chalcone-flavanone isomerase family protein	Knowtator curated
AT3G55150	ATEXO70H1, EXO70H1	exocyst subunit exo70 family protein H1	Knowtator curated
AT3G55370	OBP3	OBF-binding protein 3	Knowtator curated
AT3G55740	PROT2, ATPROT2	proline transporter 2	Knowtator curated
AT3G56150	EIF3C, ATEIF3C-1, EIF3C-1, ATTIF3C1, TIF3C1 | EIF3C	eukaryotic translation initiation factor 3C	Knowtator curated
AT3G57130	BOP1	Ankyrin repeat family protein / BTB/POZ domain-containing protein	Knowtator curated
AT3G57230	AGL16	AGAMOUS-like 16	Knowtator curated
AT3G57260	BGL2, PR2, BG2, PR-2	beta-1,3-glucanase 2	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT3G57290	EIF3E, TIF3E1, ATEIF3E-1, INT-6, ATINT6, INT6	eukaryotic translation initiation factor 3E	Knowtator curated
AT3G57530	CPK32, ATCPK32, CDPK32	calcium-dependent protein kinase 32	Knowtator curated
AT3G57860	UVI4-LIKE, OSD1	UV-B-insensitive 4-like	Knowtator curated
AT3G57920	SPL15	squamosa promoter binding protein-like 15	Knowtator curated
AT3G59380	FTA, PLP, ATFTA, PFT/PGGT-IALPHA	farnesyltransferase A	Knowtator curated
AT3G59400	GUN4	enzyme binding;tetrapyrrole binding	regulated protein Baerenfaller et al. (2012)
AT3G59900	ARGOS	auxin-regulated gene involved in organ size	Knowtator curated
AT3G60630	HAM2, ATHAM2, LOM2	GRAS family transcription factor	Knowtator curated
AT3G61140	FUS6, ATFUS6, CSN1, COP11, EMB78, ATSK31, SK31	26S proteasome, regulatory subunit Rpn7;Proteasome component (PCI) domain	Knowtator curated
AT3G61510	ACS1, AT-ACS1	ACC synthase 1	Knowtator curated
AT3G61850	DAG1	Dof-type zinc finger DNA-binding family protein	Knowtator curated
AT3G62980	TIR1	F-box/RNI-like superfamily protein	Knowtator curated
AT3G63280	ATNEK4, NEK4	NIMA-related kinase 4	Knowtator curated
AT3G63440	ATCKX6, CKX6, ATCKX7	cytokinin oxidase/dehydrogenase 6	Knowtator curated
AT3G63530	BB, BB2	RING/U-box superfamily protein	Knowtator curated
AT4G00150	HAM3, ATHAM3, LOM3	GRAS family transcription factor	Knowtator curated
AT4G00180	YAB3	Plant-specific transcription factor YABBY family protein	Knowtator curated
AT4G00850	GIF3	GRF1-interacting factor 3	Knowtator curated

AT4G02020	EZA1, SWN, SDG10	SET domain-containing protein	Knowtator curated
AT4G02390	APP, PARP1, ATPARP1, PP	poly(ADP-ribose) polymerase	Knowtator curated
AT4G02520	ATGSTF2, ATPM24.1, ATPM24, GST2, GSTF2	glutathione S-transferase PHI 2	regulated protein Baerenfaller et al. (2012)
AT4G02560	LD	Homeodomain-like superfamily protein	Knowtator curated
AT4G02570	ATCUL1, CUL1, AXR6 | CUL1	cullin 1	Knowtator curated
AT4G02780	GA1, ABC33, ATCPS1, CPS, CPS1	Terpenoid cyclases/Protein prenyltransferases superfamily protein	Knowtator curated
AT4G03390	SRF3	STRUBBELIG-receptor family 3	Knowtator curated
AT4G04020	FIB	fibrillin	regulated protein Baerenfaller et al. (2012)
AT4G04620	ATG8B	Ubiquitin-like superfamily protein	Knowtator curated
AT4G04780	MED21	mediator 21	Knowtator curated
AT4G05090	NULL	Inositol monophosphatase family protein	regulated protein Baerenfaller et al. (2012)
AT4G07400	VFB3	VIER F-box proteine 3	Knowtator curated
AT4G08150	KNAT1, BP, BP1	KNOTTED-like from Arabidopsis thaliana	Knowtator curated
AT4G08870	NULL	Arginase/deacetylase superfamily protein	regulated protein Baerenfaller et al. (2012)
AT4G08920	CRY1, BLU1, HY4, OOP2, ATCRY1	cryptochrome 1	Knowtator curated
AT4G08950	EXO	Phosphate-responsive 1 family protein	Knowtator curated
AT4G09000	GRF1, GF14 CHI	general regulatory factor 1	Knowtator curated
AT4G10340	LHCB5	light harvesting complex of photosystem II 5	Knowtator curated
AT4G10450	NULL	Ribosomal protein L6 family	regulated protein Baerenfaller et al. (2012)
AT4G10480	NULL	Nascent polypeptide-associated complex (NAC), alpha subunit family protein	regulated protein Baerenfaller et al. (2012)
AT4G10710	SPT16	global transcription factor C	Knowtator curated
AT4G11420	EIF3A, ATEIF3A-1, EIF3A-1, ATTIF3A1, TIF3A1	eukaryotic translation initiation factor 3A	Knowtator curated
AT4G11920	CCS52A2, FZR1	cell cycle switch protein 52 A2	Knowtator curated
AT4G12620	ORC1B, ATORC1B, UNE13	origin of replication complex 1B	Knowtator curated
AT4G13195	CLE44	CLAVATA3/ESR-RELATED 44	Knowtator curated

AT4G13250	NYC1	NAD(P)-binding Rossmann-fold superfamily protein	Knowtator curated
AT4G13260	YUC2	Flavin-binding monooxygenase family protein	Knowtator curated
AT4G13940	HOG1, EMB1395, SAHH1, MEE58, ATSAHH1 | HOG1, SAHH1	S-adenosyl-L-homocysteine hydrolase	Knowtator curated
AT4G14110	COP9, CSN8, FUS7, EMB143	COP9 signalosome, subunit CSN8	Knowtator curated
AT4G14550	IAA14, SLR	indole-3-acetic acid inducible 14	Knowtator curated
AT4G14560	IAA1, AXR5	indole-3-acetic acid inducible	Knowtator curated
AT4G14670	CLPB2	casein lytic proteinase B2	Knowtator curated
AT4G14700	ATORC1A, ORC1A	origin recognition complex 1	Knowtator curated
AT4G14713	PPD1, TIFY4A	TIFY domain/Divergent CCT motif family protein	Knowtator curated
AT4G14720	PPD2, TIFY4B	TIFY domain/Divergent CCT motif family protein	Knowtator curated
AT4G14960	TUA6	Tubulin/FtsZ family protein	regulated protein Baerenfaller et al. (2012)
AT4G15210	ATBETA-AMY, AT-BETA-AMY, RAM1, BMY1, BAM5 | ATBETA-AMY, AT-BETA-AMY, RAM1	beta-amylase 5	Knowtator curated
AT4G15440	HPL1, CYP74B2	hydroperoxide lyase 1	Knowtator curated
AT4G15530	PPDK	pyruvate orthophosphate dikinase	regulated protein Baerenfaller et al. (2012)
AT4G15560	CLA1, DEF, CLA, DXS, DXPS2	Deoxyxylulose-5-phosphate synthase	Knowtator curated
AT4G16340	SPK1	guanyl-nucleotide exchange factors;GTPase binding;GTP binding	Knowtator curated
AT4G16390	SVR7	pentatricopeptide (PPR) repeat-containing protein	regulated protein Baerenfaller et al. (2012)
AT4G16760	ACX1, ATACX1 | ACX1	acyl-CoA oxidase 1	Knowtator curated
AT4G16780	ATHB-2, HAT4, ATHB2, HB-2	homeobox protein 2	Knowtator curated
AT4G16845	VRN2	VEFS-Box of polycomb protein	Knowtator curated
AT4G17030	ATEXLB1, EXPR, AT-EXPR, ATEXPR1, ATHEXP BETA 3.1, EXLB1	expansin-like B1	Knowtator curated
AT4G17695	KAN3	Homeodomain-like superfamily protein	Knowtator curated
AT4G18100	NULL	Ribosomal protein L32e	regulated protein Baerenfaller et al. (2012)

AT4G18390	TCP2	TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2	Knowtator curated
AT4G18440	NULL	L-Aspartase-like family protein	regulated protein Baerenfaller et al. (2012)
AT4G18480	CHLI1, CH42, CH-42, CHL11, CHLI-1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	regulated protein Baerenfaller et al. (2012)
AT4G18510	CLE2	CLAVATA3/ESR-related 2	Knowtator curated
AT4G18710	BIN2, DWF12, UCU1, ATSK21, SK21 | BIN2	Protein kinase superfamily protein	Knowtator curated
AT4G18750	DOT4	Pentatricopeptide repeat (PPR) superfamily protein	Knowtator curated
AT4G18780	CESA8, IRX1, ATCESA8, LEW2	cellulose synthase family protein	Knowtator curated
AT4G18830	ATOFP5, OFP5	ovate family protein 5	Knowtator curated
AT4G18960	AG	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT4G19170	NCED4, CCD4	nine-cis-epoxycarotenoid dioxygenase 4	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT4G19640	ARA7, ARA-7, ATRABF2B, ATRAB5B, RABF2B, ATRAB-F2B, RAB-F2B	Ras-related small GTP-binding family protein	Knowtator curated
AT4G20270	BAM3	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT4G20380	LSD1	LSD1 zinc finger family protein	Knowtator curated
AT4G20910	HEN1, CRM2 | HEN1	double-stranded RNA binding protein-related / DsRBD protein-related	Knowtator curated
AT4G21070	ATBRCA1, BRCA1	breast cancer susceptibility1	Knowtator curated
AT4G21670	CPL1, FRY2, ATCPL1	C-terminal domain phosphatase-like 1	Knowtator curated
AT4G21750	ATML1	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	Knowtator curated
AT4G21980	APG8A, ATG8A	Ubiquitin-like superfamily protein	Knowtator curated
AT4G22130	SRF8	STRUBBELIG-receptor family 8	Knowtator curated
AT4G22270	MRB1, ATMRB1	Protein of unknown function (DUF3537)	Knowtator curated
AT4G22910	FZR2, CCS52A1	FIZZY-related 2	Knowtator curated
AT4G22920	ATNYE1, NYE1	non-yellowing 1	Knowtator curated
AT4G23600	CORI3, JR2	Tyrosine transaminase family protein	regulated protein Baerenfaller et al. (2012)

AT4G23810	WRKY53, ATWRKY53	WRKY family transcription factor	Knowtator curated
AT4G24150	AtGRF8, GRF8	growth-regulating factor 8	Knowtator curated
AT4G24510	CER2, VC2, VC-2	HXXXD-type acyl-transferase family protein	Knowtator curated
AT4G24520	ATR1, AR1 | ATR1	P450 reductase 1	Knowtator curated
AT4G24560	UBP16	ubiquitin-specific protease 16	Knowtator curated
AT4G24770	RBP31, ATRBP31, CP31, ATRBP33	31-kDa RNA binding protein	regulated protein Baerenfaller et al. (2012)
AT4G25100	FSD1, ATFSD1 | FSD1	Fe superoxide dismutase 1	regulated protein Baerenfaller et al. (2012)
AT4G25420	GA5, GA20OX1, AT2301, ATGA20OX1	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	Knowtator curated
AT4G26080	ABI1, AtABI1	Protein phosphatase 2C family protein	Knowtator curated
AT4G26110	NAP1;1, ATNAP1;1 | NAP1;1	nucleosome assembly protein1;1	Knowtator curated
AT4G26150	CGA1, GATA22, GNL	cytokinin-responsive gata factor 1	Knowtator curated
AT4G26200	ACS7, ATACS7	1-amino-cyclopropane-1-carboxylate synthase 7	Knowtator curated
AT4G27060	TOR1, SPR2, CN	ARM repeat superfamily protein	Knowtator curated
AT4G27090	NULL	Ribosomal protein L14	regulated protein Baerenfaller et al. (2012)
AT4G27440	PORB	protochlorophyllide oxidoreductase B	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT4G28510	ATPHB1, PHB1	prohibitin 1	Knowtator curated
AT4G28910	NINJA	novel interactor of JAZ	Knowtator curated
AT4G29040	RPT2a	regulatory particle AAA-ATPase 2A	Knowtator curated
AT4G29740	CKX4, ATCKX4	cytokinin oxidase 4	Knowtator curated
AT4G30270	MERI5B, MERI-5, XTH24, SEN4	xyloglucan endotransglucosylase/hydrolase 24	Knowtator curated
AT4G31120	SKB1, ATPRMT5 | PRMT5	SHK1 binding protein 1	Knowtator curated
AT4G31500	CYP83B1, SUR2, RNT1, RED1, ATR4	cytochrome P450, family 83, subfamily B, polypeptide 1	Knowtator curated
AT4G31540	ATEXO70G1, EXO70G1	exocyst subunit exo70 family protein G1	Knowtator curated
AT4G31700	RPS6, RPS6A	ribosomal protein S6	Knowtator curated
AT4G31840	ENODL15, AtENODL15	early nodulin-like protein 15	regulated protein Baerenfaller et al. (2012)
AT4G31920	ARR10, RR10	response regulator 10	Knowtator curated
AT4G32280	IAA29	indole-3-acetic acid inducible 29	Knowtator curated

AT4G32540	YUC, YUC1	Flavin-binding monooxygenase family protein	Knowtator curated
AT4G32551	LUG, RON2 | LUG	LisH dimerisation motif;WD40/YVTN repeat-like-containing domain	Knowtator curated
AT4G32570	TIFY8	TIFY domain protein 8	Knowtator curated
AT4G32810	CCD8, MAX4, ATCCD8	carotenoid cleavage dioxygenase 8	Knowtator curated
AT4G32830	AtAUR1, AUR1	ataurora1	Knowtator curated
AT4G32880	ATHB-8, ATHB8, HB-8	homeobox gene 8	Knowtator curated
AT4G34150	NULL	Calcium-dependent lipid-binding (CaLB domain) family protein	regulated protein Baerenfaller et al. (2012)
AT4G34160	CYCD3;1, CYCD3	CYCLIN D3;1	Knowtator curated
AT4G34290	NULL	SWIB/MDM2 domain superfamily protein	regulated protein Baerenfaller et al. (2012)
AT4G34350	CLB6, ISPH, HDR	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	Knowtator curated
AT4G34460	AGB1, ELK4, ATAGB1	GTP binding protein beta 1	Knowtator curated
AT4G34490	ATCAP1, CAP 1, CAP1	cyclase associated protein 1	Knowtator curated
AT4G34590	ATB2, GBF6, AtbZIP11, BZIP11	G-box binding factor 6	Knowtator curated
AT4G34650	SQS2	squalene synthase 2	Knowtator curated
AT4G34710	ADC2, SPE2, ATADC2	arginine decarboxylase 2	Knowtator curated
AT4G34740	ATASE2, CIA1, ATPURF2, ASE2	GLN phosphoribosyl pyrophosphate amidotransferase 2	Knowtator curated
AT4G35230	BSK1	BR-signaling kinase 1	Knowtator curated
AT4G35620	CYCB2;2	Cyclin B2;2	Knowtator curated
AT4G35800	NRPB1, RPB1, RNA_POL_II_LSRNA_POL_II_LS, RNA_POL_II_LS	RNA polymerase II large subunit	Knowtator curated
AT4G35850	NULL	Pentatricopeptide repeat (PPR) superfamily protein	regulated protein Baerenfaller et al. (2012)
AT4G35900	FD, FD-1, atbzip14	Basic-leucine zipper (bZIP) transcription factor family protein	Knowtator curated
AT4G36260	STY2, SRS2	Lateral root primordium (LRP) protein-related	Knowtator curated
AT4G36380	ROT3	Cytochrome P450 superfamily protein	Knowtator curated
AT4G36540	BEE2	BR enhanced expression 2	Knowtator curated
AT4G36800	RCE1	RUB1 conjugating enzyme 1	Knowtator curated
AT4G36870	BLH2, SAW1	BEL1-like homeodomain 2	Knowtator curated

AT4G36920	AP2, FLO2, FL1 | AP2	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT4G36930	SPT	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Knowtator curated
AT4G37120	SMP2	Pre-mRNA splicing Prp18-interacting factor	Knowtator curated
AT4G37490	CYC1, CYCB1;1, CYCB1	CYCLIN B1;1	Knowtator curated
AT4G37580	HLS1, COP3, UNS2	Acyl-CoA N-acyltransferases (NAT) superfamily protein	Knowtator curated
AT4G37630	CYCD5;1	cyclin d5;1	Knowtator curated
AT4G37650	SHR, SGR7	GRAS family transcription factor	Knowtator curated
AT4G37740	AtGRF2, GRF2	growth-regulating factor 2	Knowtator curated
AT4G37750	ANT, DRG, CKC, CKC1	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT4G37760	SQE3	squalene epoxidase 3	Knowtator curated
AT4G37790	HAT22	Homeobox-leucine zipper protein family	Knowtator curated
AT4G37910	mtHsc70-1	mitochondrial heat shock protein 70-1	Knowtator curated
AT4G37930	SHM1, STM, SHMT1	serine transhydroxymethyltransferase 1	Knowtator curated
AT4G38460	GGR	geranylgeranyl reductase	Knowtator curated
AT4G38600	KAK, UPL3	HEAT repeat ;HECT-domain (ubiquitin-transferase)	Knowtator curated
AT4G38630	RPN10, MCB1, ATMCB1, MBP1	regulatory particle non-ATPase 10	Knowtator curated
AT4G38850	SAUR_AC1, ATSAUR15, SAUR15, SAUR-AC1	SAUR-like auxin-responsive protein family	Knowtator curated
AT4G39400	BRI1, CBB2, DWF2, BIN1, ATBRI1	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT4G39680	NULL	SAP domain-containing protein	regulated protein Baerenfaller et al. (2012)
AT4G39920	POR, TFC C	C-CAP/cofactor C-like domain-containing protein	Knowtator curated
AT4G39950	CYP79B2	cytochrome P450, family 79, subfamily B, polypeptide 2	Knowtator curated
AT4G39990	ATRABA4B, ATRAB11G, ATGB3, RABA4B	RAB GTPase homolog A4B	Knowtator curated
AT4G40060	ATHB16, ATHB-16, HB16	homeobox protein 16	Knowtator curated
AT5G01040	LAC8	laccase 8	Knowtator curated
AT5G01190	LAC10	laccase 10	Knowtator curated
AT5G01270	CPL2, ATCPL2 | CPL2	carboxyl-terminal domain (ctd) phosphatase-like 2	Knowtator curated
AT5G01840	ATOFP1, OFP1	ovate family protein 1	Knowtator curated

AT5G02470	DPA	Transcription factor DP	Knowtator curated
AT5G02820	RHL2, BIN5	Spo11/DNA topoisomerase VI, subunit A protein	Knowtator curated
AT5G03260	LAC11	laccase 11	Knowtator curated
AT5G03280	EIN2, PIR2, CKR1, ERA3, ORE3, ORE2, ATEIN2	NRAMP metal ion transporter family protein	Knowtator curated
AT5G03290	IDH-V	isocitrate dehydrogenase V	Knowtator curated
AT5G03540	ATEXO70A1, EXO70A1 | EXO70A1	exocyst subunit exo70 family protein A1	Knowtator curated
AT5G03730	CTR1, SIS1, AtCTR1	Protein kinase superfamily protein	Knowtator curated
AT5G03840	TFL1, TFL-1	PEBP (phosphatidylethanolamine-binding protein) family protein	Knowtator curated
AT5G04200	AtMC9, MC9	metacaspase 9	Knowtator curated
AT5G04470	SIM	cyclin-dependent protein kinase inhibitors	Knowtator curated
AT5G05290	ATEXPA2, EXP2, ATEXP2, ATHEXP ALPHA 1.12, EXPA2	expansin A2	Knowtator curated
AT5G05390	LAC12	laccase 12	Knowtator curated
AT5G05410	DREB2A, DREB2	DRE-binding protein 2A	Knowtator curated
AT5G05440	PYL5, RCAR8	Polyketide cyclase/dehydrase and lipid transport superfamily protein	Knowtator curated
AT5G05690	CPD, CYP90A, CYP90, CBB3, DWF3, CYP90A1	Cytochrome P450 superfamily protein	Knowtator curated
AT5G05780	RPN8A, AE3, ATHMOV34 | RPN8A	RP non-ATPase subunit 8A	Knowtator curated
AT5G05920	DHS, EDA22 | DHS	deoxyhypusine synthase	Knowtator curated
AT5G06100	MYB33, ATMYB33	myb domain protein 33	Knowtator curated
AT5G06150	CYC1BAT, CYCB1;2	Cyclin family protein	Knowtator curated
AT5G06290	2-Cys Prx B, 2CPB	2-cysteine peroxiredoxin B	Knowtator curated
AT5G06820	SRF2	STRUBBELIG-receptor family 2	Knowtator curated
AT5G07130	LAC13	laccase 13	Knowtator curated
AT5G07180	ERL2	ERECTA-like 2	Knowtator curated
AT5G07200	YAP169, GA20OX3, ATGA20OX3	gibberellin 20-oxidase 3	Knowtator curated
AT5G07440	GDH2	glutamate dehydrogenase 2	Knowtator curated
AT5G07680	ANAC080, ANAC079, ATNAC4, NAC080 | ANAC080, NAC080	NAC domain containing protein 80	Knowtator curated

AT5G08790	ATAF2, anac081	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Knowtator curated
AT5G09360	LAC14	laccase 14	Knowtator curated
AT5G09440	EXL4	EXORDIUM like 4	Knowtator curated
AT5G09590	MTHSC70-2, HSC70-5	mitochondrial HSO70 2	Knowtator curated
AT5G09970	CYP78A7	cytochrome P450, family 78, subfamily A, polypeptide 7	Knowtator curated
AT5G10140	FLC, FLF, AGL25 | FLC	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT5G10250	DOT3	Phototropic-responsive NPH3 family protein	Knowtator curated
AT5G10360	EMB3010, RPS6B | EMB3010	Ribosomal protein S6e	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT5G10430	AGP4, ATAGP4	arabinogalactan protein 4	Knowtator curated
AT5G10450	GRF6, AFT1, 14-3-3lambda | GRF6	G-box regulating factor 6	Knowtator curated
AT5G10510	AIL6, PLT3 | AIL6	AINTEGUMENTA-like 6	Knowtator curated
AT5G11190	SHN3	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT5G11260	HY5, TED 5	Basic-leucine zipper (bZIP) transcription factor family protein	Knowtator curated
AT5G11300	CYC3B, CYC2BAT, CYCA2;2	mitotic-like cyclin 3B from Arabidopsis	Knowtator curated
AT5G11320	YUC4	Flavin-binding monooxygenase family protein	Knowtator curated
AT5G11530	EMF1	embryonic flower 1 (EMF1)	Knowtator curated
AT5G12250	TUB6	beta-6 tubulin	Knowtator curated
AT5G13060	ABAP1	ARMADILLO BTB protein 1	Knowtator curated
AT5G13150	ATEXO70C1, EXO70C1	exocyst subunit exo70 family protein C1	Knowtator curated
AT5G13680	ELO2, ABO1	IKI3 family protein	Knowtator curated
AT5G13840	FZR3	FIZZY-related 3	Knowtator curated
AT5G13910	LEP	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT5G13930	CHS, TT4, ATCHS	Chalcone and stilbene synthase family protein	Knowtator curated
AT5G13980	NULL	Glycosyl hydrolase family 38 protein	regulated protein Baerenfaller et al. (2012)
AT5G14740	CA2, CA18, BETA CA2	carbonic anhydrase 2	Knowtator curated
AT5G15090	VDAC3, ATVDAC3 | VDAC3	voltage dependent anion channel 3	Knowtator curated
AT5G15580	LNG1	longifolia1	Knowtator curated

AT5G15610	NULL	Proteasome component (PCI) domain protein	regulated protein Baerenfaller et al. (2012)
AT5G15840	CO, FG	B-box type zinc finger protein with CCT domain	Knowtator curated
AT5G16050	GRF5, GF14 UPSILON	general regulatory factor 5	Knowtator curated
AT5G16560	KAN, KAN1	Homeodomain-like superfamily protein	Knowtator curated
AT5G16690	ORC3, ATORC3	origin recognition complex subunit 3	Knowtator curated
AT5G16780	DOT2, MDF	SART-1 family	Knowtator curated
AT5G17000	NULL	Zinc-binding dehydrogenase family protein	regulated protein Baerenfaller et al. (2012)
AT5G17220	ATGSTF12, GST26, TT19, GSTF12	glutathione S-transferase phi 12	Knowtator curated
AT5G17420	IRX3, CESA7, ATCESA7, MUR10	Cellulose synthase family protein	Knowtator curated
AT5G17480	APC1, PC1	pollen calcium-binding protein 1	Knowtator curated
AT5G17490	RGL3	RGA-like protein 3	Knowtator curated
AT5G18170	GDH1	glutamate dehydrogenase 1	Knowtator curated
AT5G19180	ECR1	E1 C-terminal related 1	Knowtator curated
AT5G19530	ACL5	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Knowtator curated
AT5G19650	ATOFP8, OFP8	ovate family protein 8	Knowtator curated
AT5G19780	TUA5	tubulin alpha-5	Knowtator curated
AT5G20010	RAN-1, RAN1, ATRAN1	RAS-related nuclear protein-1	Knowtator curated
AT5G20320	DCL4, ATDCL4 | DCL4	dicer-like 4	Knowtator curated
AT5G20570	ROC1, RBX1, HRT1, ATRBX1	RING-box 1	Knowtator curated
AT5G20630	GLP3, GLP3A, GLP3B, ATGER3, GER3	germin 3	regulated protein Baerenfaller et al. (2012)
AT5G20730	NPH4, MSG1, IAA21, ARF7, TIR5, BIP | NPH4, MSG1, IAA21, ARF7, TIR5, BIP, IAA23, IAA25	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related	Knowtator curated
AT5G20850	ATRAD51, RAD51	RAS associated with diabetes protein 51	Knowtator curated
AT5G20900	JAZ12, TIFY3B	jasmonate-zim-domain protein 12	Knowtator curated
AT5G22220	E2F1, E2FB, ATE2FB	E2F transcription factor 1	Knowtator curated
AT5G22240	ATOFP10, OFP10	Ovate family protein	Knowtator curated
AT5G23010	MAM1, IMS3	methylthioalkylmalate synthase 1	Knowtator curated
AT5G23150	HUA2	Tudor/PWWP/MBT domain-containing protein	Knowtator curated

AT5G23570	SGS3, ATSGS3	XS domain-containing protein / XS zinc finger domain-containing protein-related	Knowtator curated
AT5G23820	NULL	MD-2-related lipid recognition domain-containing protein	regulated protein Baerenfaller et al. (2012)
AT5G24020	MIND, ARC11, ATMIND1	septum site-determining protein (MIND)	regulated protein Baerenfaller et al. (2012)
AT5G24630	BIN4	double-stranded DNA binding	Knowtator curated
AT5G24780	VSP1, ATVSP1	vegetative storage protein 1	Knowtator curated
AT5G25380	CYCA2;1	cyclin a2;1	Knowtator curated
AT5G25390	SHN2	Integrase-type DNA-binding superfamily protein	Knowtator curated
AT5G25610	RD22, ATRD22	BURP domain-containing protein	Knowtator curated
AT5G25620	YUC6	Flavin-binding monooxygenase family protein	Knowtator curated
AT5G25780	EIF3B-2, EIF3B, ATEIF3B-2	eukaryotic translation initiation factor 3B-2	Knowtator curated
AT5G25890	IAA28, IAR2	indole-3-acetic acid inducible 28	Knowtator curated
AT5G26667	PYR6	P-loop containing nucleoside triphosphate hydrolases superfamily protein	regulated protein Baerenfaller et al. (2012)
AT5G26860	LON_ARA_ARA, LON1	lon protease 1	Knowtator curated
AT5G27030	TPR3	TOPLESS-related 3	Knowtator curated
AT5G27150	NHX1, ATNHX, AT-NHX1, ATNHX1	Na+/H+ exchanger 1	Knowtator curated
AT5G27380	GSH2, GSHB	glutathione synthetase 2	Knowtator curated
AT5G28290	ATNEK3, NEK3	NIMA-related kinase 3	Knowtator curated
AT5G28640	AN3, GIF, GIF1, ATGIF1	SSXT family protein	Knowtator curated
AT5G33320	CUE1, PPT, ARAPPT	Glucose-6-phosphate/phosphate translocator-related	Knowtator curated
AT5G35750	AHK2, HK2	histidine kinase 2	Knowtator curated
AT5G36170	HCF109, ATPRFB	high chlorophyll fluorescent 109	Knowtator curated
AT5G37600	ATGSR1, GLN1;1, GSR 1, ATGLN1;1	glutamine synthase clone R1	regulated protein Baerenfaller et al. (2012)
AT5G38410	NULL	Ribulose bisphosphate carboxylase (small chain) family protein	regulated protein Baerenfaller et al. (2012)
AT5G38480	GRF3, RCI1	general regulatory factor 3	Knowtator curated
AT5G39570	NULL	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 25	regulated protein Baerenfaller et al. (2012)

		plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT3G29075.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink).	
AT5G39740	OLI7, RPL5B | RPL5B	ribosomal protein L5 B	Knowtator curated
AT5G40330	MYB23, ATMYB23, ATMYBRTF	myb domain protein 23	Knowtator curated
AT5G40770	ATPHB3, PHB3	prohibitin 3	Knowtator curated
AT5G40820	ATRAD3, ATR, ATATR	Ataxia telangiectasia-mutated and RAD3-related	Knowtator curated
AT5G40950	RPL27	ribosomal protein large subunit 27	regulated protein Baerenfaller et al. (2012)
AT5G41315	GL3, MYC6.2	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Knowtator curated
AT5G42190	ASK2, SKP1B	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 family protein	Knowtator curated
AT5G42630	KAN4, ATS	Homeodomain-like superfamily protein	Knowtator curated
AT5G42650	AOS, CYP74A, DDE2	allene oxide synthase	Knowtator curated | regulated protein Baerenfaller et al. (2012)
AT5G42800	DFR, TT3, M318	dihydroflavonol 4-reductase	Knowtator curated
AT5G42970	COP8, FUS4, EMB134, COP14, CSN4, FUS8, ATS4	Proteasome component (PCI) domain protein	Knowtator curated
AT5G43270	SPL2	squamosa promoter binding protein-like 2	Knowtator curated
AT5G43810	ZLL, PNH, AGO10 | ZLL	Stabilizer of iron transporter SufD / Polynucleotidyl transferase	Knowtator curated
AT5G44030	CESA4, IRX5, NWS2	cellulose synthase A4	Knowtator curated
AT5G44190	GLK2, ATGLK2, GPRI2	GOLDEN2-like 2	Knowtator curated
AT5G44200	CBP20, ATCBP20	CAP-binding protein 20	Knowtator curated
AT5G44340	TUB4	tubulin beta chain 4	Knowtator curated
AT5G44420	PDF1.2, PDF1.2A, LCR77	plant defensin 1.2	Knowtator curated
AT5G45890	SAG12	senescence-associated gene 12	Knowtator curated
AT5G45900	APG7, ATAPG7, ATG7, ATATG7	ThiF family protein	Knowtator curated
AT5G46210	CUL4, ATCUL4	cullin4	Knowtator curated

AT5G46280	MCM3	Minichromosome maintenance (MCM2/3/5) family protein	Knowtator curated
AT5G46700	TET1, TRN2	Tetraspanin family protein	Knowtator curated
AT5G46790	PYL1, RCAR12	PYR1-like 1	Knowtator curated
AT5G47930	NULL	Zinc-binding ribosomal protein family protein	regulated protein Baerenfaller et al. (2012)
AT5G48100	TT10, LAC15, ATLAC15	Laccase/Diphenol oxidase family protein	Knowtator curated
AT5G48480	NULL	Lactoylglutathione lyase / glyoxalase I family protein	regulated protein Baerenfaller et al. (2012)
AT5G48820	KRP3, ICK6 | ICK6	inhibitor/interactor with cyclin-dependent kinase	Knowtator curated
AT5G48930	HCT	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	Knowtator curated
AT5G50320	ELO3, HAG3, HAC8, ELP3, AtELP3	radical SAM domain-containing protein / GCN5-related N-acetyltransferase (GNAT) family protein	Knowtator curated
AT5G50670	SPL13B, SPL13	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	Knowtator curated
AT5G51020	CRL	crumpled leaf	Knowtator curated
AT5G51070	ERD1, CLPD, SAG15	Clp ATPase	Knowtator curated
AT5G51230	EMF2, VEF2, CYR1, AtEMF2	VEFS-Box of polycomb protein	Knowtator curated
AT5G51550	EXL3	EXORDIUM like 3	Knowtator curated
AT5G51600	PLE, ATMAP65-3, MAP65-3	Microtubule associated protein (MAP65/ASE1) family protein	Knowtator curated
AT5G51810	GA20OX2, AT2353, ATGA20OX2	gibberellin 20 oxidase 2	Knowtator curated
AT5G52110	HCF208, CCB2 | HCF208	Protein of unknown function (DUF2930)	Knowtator curated
AT5G52310	COR78, LTI78, RD29A, LTI140	low-temperature-responsive protein 78 (LTI78) / desiccation-responsive protein 29A (RD29A)	Knowtator curated
AT5G52340	ATEXO70A2, EXO70A2	exocyst subunit exo70 family protein A2	Knowtator curated
AT5G53200	TRY	Homeodomain-like superfamily protein	Knowtator curated
AT5G53210	SPCH	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	Knowtator curated
AT5G53660	AtGRF7, GRF7	growth-regulating factor 7	Knowtator curated
AT5G53950	CUC2, ANAC098, ATCUC2	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	Knowtator curated
AT5G54270	LHCB3, LHCB3*1	light-harvesting chlorophyll B-binding protein 3	Knowtator curated

AT5G54380	THE1	protein kinase family protein	Knowtator curated
AT5G54490	PBP1	pinoid-binding protein 1	Knowtator curated
AT5G54810	TSB1, TRPB, TRP2, ATTSB1	tryptophan synthase beta-subunit 1	Knowtator curated
AT5G54900	ATRBP45A, RBP45A	RNA-binding protein 45A	regulated protein Baerenfaller et al. (2012)
AT5G55250	IAMT1	IAA carboxylmethyltransferase 1	Knowtator curated
AT5G55470	ATNHX3, NHX3	Na+/H+ (sodium hydrogen) exchanger 3	Knowtator curated
AT5G55540	TRN1, LOP1	tornado 1	Knowtator curated
AT5G55920	OLI2	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	Knowtator curated
AT5G56350	NULL	Pyruvate kinase family protein	regulated protein Baerenfaller et al. (2012)
AT5G56650	ILL1	IAA-leucine resistant (ILR)-like 1	Knowtator curated
AT5G56660	ILL2	IAA-leucine resistant (ILR)-like 2	Knowtator curated
AT5G56860	GNC, GATA21	GATA type zinc finger transcription factor family protein	Knowtator curated
AT5G56950	NFA03, NFA3, NAP1;3	nucleosome assembly protein 1;3	Knowtator curated
AT5G56970	CKX3, ATCKX3	cytokinin oxidase 3	Knowtator curated
AT5G57030	LUT2	Lycopene beta/epsilon cyclase protein	Knowtator curated
AT5G57050	ABI2, AtABI2	Protein phosphatase 2C family protein	Knowtator curated
AT5G57090	EIR1, WAV6, ATPIN2, PIN2, AGR, AGR1	Auxin efflux carrier family protein	Knowtator curated
AT5G57290	NULL	60S acidic ribosomal protein family	regulated protein Baerenfaller et al. (2012)
AT5G57390	AIL5, CHO1, EMK	AINTEGUMENTA-like 5	Knowtator curated
AT5G57490	VDAC4, ATVDAC4	voltage dependent anion channel 4	Knowtator curated
AT5G57560	TCH4, XTH22	Xyloglucan endotransglucosylase/hydrolase family protein	Knowtator curated
AT5G58003	CPL4	C-terminal domain phosphatase-like 4	Knowtator curated
AT5G58140	PHOT2, NPL1	phototropin 2	Knowtator curated
AT5G58220	TTL	transthyretin-like protein	Knowtator curated
AT5G58230	MSI1, MEE70, ATMSI1	Transducin/WD40 repeat-like superfamily protein	Knowtator curated
AT5G58250	NULL	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown;	regulated protein Baerenfaller et al. (2012)

		LOCATED IN: thylakoid, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF2488 (InterPro:IPR019616); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink).	
AT5G58360	ATOFP3, OFP3	ovate family protein 3	Knowtator curated
AT5G58430	ATEXO70B1, EXO70B1	exocyst subunit exo70 family protein B1	Knowtator curated
AT5G58910	LAC16	laccase 16	Knowtator curated
AT5G59730	ATEXO70H7, EXO70H7	exocyst subunit exo70 family protein H7	Knowtator curated
AT5G59870	HTA6	histone H2A 6	regulated protein Baerenfaller et al. (2012)
AT5G60020	LAC17, ATLAC17	laccase 17	Knowtator curated
AT5G60410	ATSIZ1, SIZ1	DNA-binding protein with MIZ/SP-RING zinc finger, PHD-finger and SAP domain	Knowtator curated
AT5G60450	ARF4	auxin response factor 4	Knowtator curated
AT5G60600	GCPE, ISPG, CSB3, CLB4, HDS	4-hydroxy-3-methylbut-2-enyl diphosphate synthase	Knowtator curated
AT5G60690	REV, IFL, IFL1	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein	Knowtator curated
AT5G60880	BASL	breaking of asymmetry in the stomatal lineage	Knowtator curated
AT5G60910	AGL8, FUL	AGAMOUS-like 8	Knowtator curated
AT5G61010	ATEXO70E2, EXO70E2	exocyst subunit exo70 family protein E2	Knowtator curated
AT5G61430	ANAC100, ATNAC5, NAC100	NAC domain containing protein 100	Knowtator curated
AT5G61850	LFY, LFY3	floral meristem identity control protein LEAFY (LFY)	Knowtator curated
AT5G62000	ARF2, ARF1-BP, HSS, ORE14 | ARF2	auxin response factor 2	Knowtator curated
AT5G62230	ERL1	ERECTA-like 1	Knowtator curated
AT5G62300	NULL	Ribosomal protein S10p/S20e family protein	regulated protein Baerenfaller et al. (2012)
AT5G62690	TUB2	tubulin beta chain 2	regulated protein Baerenfaller et al. (2012)
AT5G62700	TUB3	tubulin beta chain 3	regulated protein Baerenfaller et al. (2012)

AT5G62790	DXR, PDE129 | DXR	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Knowtator curated
AT5G62920	ARR6	response regulator 6	Knowtator curated
AT5G63090	LOB	Lateral organ boundaries (LOB) domain family protein	Knowtator curated
AT5G63610	HEN3, CDKE;1, ATCDK8	cyclin-dependent kinase E;1	Knowtator curated
AT5G63800	MUM2, BGAL6	Glycosyl hydrolase family 35 protein	regulated protein Baerenfaller et al. (2012)
AT5G63860	UVR8	Regulator of chromosome condensation (RCC1) family protein	Knowtator curated
AT5G63880	VPS20.1	SNF7 family protein	Knowtator curated
AT5G63980	SAL1, ALX8, ATSAL1, HOS2, FRY1, RON1	Inositol monophosphatase family protein	Knowtator curated
AT5G64260	EXL2	EXORDIUM like 2	Knowtator curated
AT5G64630	FAS2, NFB01, NFB1, MUB3.9	Transducin/WD40 repeat-like superfamily protein	Knowtator curated
AT5G64800	CLE21	CLAVATA3/ESR-RELATED 21	Knowtator curated
AT5G65080	MAF5, AGL68	K-box region and MADS-box transcription factor family protein	Knowtator curated
AT5G65270	AtRABA4a, RABA4a	RAB GTPase homolog A4A	Knowtator curated
AT5G65310	ATHB5, ATHB-5, HB5	homeobox protein 5	Knowtator curated
AT5G65420	CYCD4;1	CYCLIN D4;1	Knowtator curated
AT5G65430	GRF8, 14-3-3KAPPA, GF14 KAPPA | GRF8, GF14 KAPPA | GRF8	general regulatory factor 8	Knowtator curated
AT5G65450	UBP17	ubiquitin-specific protease 17	Knowtator curated
AT5G65510	AIL7	AINTEGUMENTA-like 7	Knowtator curated
AT5G65700	BAM1	Leucine-rich receptor-like protein kinase family protein	Knowtator curated
AT5G65800	ACS5, CIN5, ETO2, ATACS5	ACC synthase 5	Knowtator curated
AT5G65930	ZWI, PKCBP, KCBP | ZWI	kinesin-like calmodulin-binding protein (ZWICHEL)	Knowtator curated
AT5G66030	ATGRIP, GRIP	Golgi-localized GRIP domain-containing protein	regulated protein Baerenfaller et al. (2012)
AT5G66400	RAB18, ATDI8	Dehydrin family protein	Knowtator curated
AT5G66870	ASL1, LBD36	ASYMMETRIC LEAVES 2-like 1	Knowtator curated
AT5G67030	ABA1, LOS6, NPQ2, ATABA1, ZEP, IBS3, ATZEP	zeaxanthin epoxidase (ZEP) (ABA1)	Knowtator curated
AT5G67100	ICU2	DNA-directed DNA polymerases	Knowtator curated

AT5G67250	SKIP2, VFB4	SKP1/ASK1-interacting protein 2	Knowtator curated
AT5G67260	CYCD3;2	CYCLIN D3;2	Knowtator curated
AT5G67500	VDAC2, ATVDAC2 | VDAC2	voltage dependent anion channel 2	Knowtator curated
ATCG00020	PSBA	photosystem II reaction center protein A	Knowtator curated
ATCG00040	MATK	maturase K	Knowtator curated
ATCG00140	ATPH	ATP synthase subunit C family protein	Knowtator curated
ATCG00160	RPS2	ribosomal protein S2	Knowtator curated
ATCG00170	RPOC2	DNA-directed RNA polymerase family protein	Knowtator curated
ATCG00180	RPOC1	DNA-directed RNA polymerase family protein	Knowtator curated
ATCG00190	RPOB	RNA polymerase subunit beta	Knowtator curated | regulated protein Baerenfaller et al. (2012)
ATCG00270	PSBD	photosystem II reaction center protein D	Knowtator curated
ATCG00340	PSAB	Photosystem I, PsaA/PsaB protein	Knowtator curated
ATCG00350	PSAA	Photosystem I, PsaA/PsaB protein	Knowtator curated
ATCG00380	RPS4	chloroplast ribosomal protein S4	Knowtator curated
ATCG00430	PSBG	photosystem II reaction center protein G	Knowtator curated
ATCG00480	ATPB, PB	ATP synthase subunit beta	Knowtator curated
ATCG00490	RBCL	ribulose-bisphosphate carboxylases	Knowtator curated
ATCG00500	ACCD	acetyl-CoA carboxylase carboxyl transferase subunit beta	Knowtator curated
ATCG00540	PETA	photosynthetic electron transfer A	Knowtator curated
ATCG00560	PSBL	photosystem II reaction center protein L	Knowtator curated
ATCG00570	PSBF	photosystem II reaction center protein F	Knowtator curated
ATCG00580	PSBE	photosystem II reaction center protein E	Knowtator curated
ATCG00650	RPS18	ribosomal protein S18	Knowtator curated
ATCG00660	RPL20	ribosomal protein L20	Knowtator curated
ATCG00670	CLPP1, PCLPP	plastid-encoded CLP P	Knowtator curated
ATCG00680	PSBB	photosystem II reaction center protein B	Knowtator curated
ATCG00700	PSBN	photosystem II reaction center protein N	Knowtator curated
ATCG00790	RPL16	ribosomal protein L16	Knowtator curated
ATCG00890	NDHB.1	NADH-Ubiquinone/plastoquinone (complex I) protein	Knowtator curated
ATCG01070	NDHE	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	Knowtator curated
ATCG01080	NDHG	NADH:ubiquinone/plastoquinone oxidoreductase,	Knowtator curated

		chain 6	
ATCG01120	RPS15	chloroplast ribosomal protein S15	Knowtator curated | regulated protein Baerenfaller et al. (2012)
ATCG01130	YCF1.2	Ycf1 protein	Knowtator curated
ATCG01250	NDHB.2	NADH-Ubiquinone/plastoquinone (complex I) protein	Knowtator curated
ATCG01310	RPL2.2	ribosomal protein L2	Knowtator curated
ATMG00110	CCB206	cytochrome C biogenesis 206	Knowtator curated
ATMG00130	ORF121A	hypothetical protein	Knowtator curated
ATMG00150	ORF116	hypothetical protein	Knowtator curated
ATMG00210	RPL5	ribosomal protein L5	Knowtator curated
ATMG00500	ORF141	hypothetical protein	Knowtator curated
ATMG00520	MATR	Intron maturase, type II family protein	Knowtator curated
ATMG00590	ORF313	Cytochrome b/b6 protein	Knowtator curated
ATMG00640	ORF25	hydrogen ion transporting ATP synthases, rotational mechanism;zinc ion binding	Knowtator curated
ATMG00660	ORF149	hypothetical protein	Knowtator curated
ATMG00760	ORF109B	hypothetical protein	Knowtator curated
ATMG01200	ORF294	hypothetical protein	Knowtator curated
ATMG01210	ORF101B	hypothetical protein	Knowtator curated
ATMG01220	ORF113	hypothetical protein	Knowtator curated
ATMG01360	COX1	cytochrome oxidase	Knowtator curated