

| KEGG Pathway | Pathway Name       | KEGG Gene ID  | Gene Name                                                                          |
|--------------|--------------------|---------------|------------------------------------------------------------------------------------|
| ath01100     | Metabolic pathways | ath:AT1G05260 | RCI3; Peroxidase superfamily protein                                               |
| ath01100     | Metabolic pathways | ath:AT1G07440 | NAD(P)-binding Rossmann-fold superfamily protein                                   |
| ath01100     | Metabolic pathways | ath:AT1G08250 | ADT6; aroenate dehydratase 6                                                       |
| ath01100     | Metabolic pathways | ath:AT1G15710 | prephenate dehydrogenase family protein                                            |
| ath01100     | Metabolic pathways | ath:AT1G20510 | OPCL1; OPC-8:0 CoA ligase1                                                         |
| ath01100     | Metabolic pathways | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                                  |
| ath01100     | Metabolic pathways | ath:AT1G29930 | CAB1; chlorophyll A/B binding protein 1                                            |
| ath01100     | Metabolic pathways | ath:AT1G32550 | FdC2; 2Fe-2S ferredoxin-like superfamily protein                                   |
| ath01100     | Metabolic pathways | ath:AT1G51680 | 4CL1; 4-coumarate:CoA ligase 1                                                     |
| ath01100     | Metabolic pathways | ath:AT1G52760 | LysoPL2; lysophospholipase 2                                                       |
| ath01100     | Metabolic pathways | ath:AT1G60810 | ACLA-2; ATP-citrate lyase A-2                                                      |
| ath01100     | Metabolic pathways | ath:AT1G67980 | CCOAMT; caffeoyl-CoA 3-O-methyltransferase                                         |
| ath01100     | Metabolic pathways | ath:AT1G71695 | Peroxidase superfamily protein                                                     |
| ath01100     | Metabolic pathways | ath:AT1G76490 | HMG1; hydroxy methylglutaryl CoA reductase 1                                       |
| ath01100     | Metabolic pathways | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                               |
| ath01100     | Metabolic pathways | ath:AT2G06050 | OPR3; oxophytodienoate-reductase 3                                                 |
| ath01100     | Metabolic pathways | ath:AT2G16500 | ADC1; arginine decarboxylase 1                                                     |
| ath01100     | Metabolic pathways | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                             |
| ath01100     | Metabolic pathways | ath:AT2G24200 | LAP1; Cytosol aminopeptidase family protein                                        |
| ath01100     | Metabolic pathways | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                                             |
| ath01100     | Metabolic pathways | ath:AT2G38050 | DET2; 3-oxo-5-alpha-steroid 4-dehydrogenase family protein                         |
| ath01100     | Metabolic pathways | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                                        |
| ath01100     | Metabolic pathways | ath:AT3G07010 | Pectin lyase-like superfamily protein                                              |
| ath01100     | Metabolic pathways | ath:AT3G14310 | PME3; pectin methylesterase 3                                                      |
| ath01100     | Metabolic pathways | ath:AT3G25400 | dCTP pyrophosphatase-like protein                                                  |
| ath01100     | Metabolic pathways | ath:AT3G25760 | AOC1; allene oxide cyclase 1                                                       |
| ath01100     | Metabolic pathways | ath:AT3G45770 | Polyketide synthase, enoylreductase family protein                                 |
| ath01100     | Metabolic pathways | ath:AT3G53260 | PAL2; phenylalanine ammonia-lyase 2                                                |
| ath01100     | Metabolic pathways | ath:AT3G54420 | EP3; homolog of carrot EP3-3 chitinase                                             |
| ath01100     | Metabolic pathways | ath:AT3G61510 | ACS1; ACC synthase 1                                                               |
| ath01100     | Metabolic pathways | ath:AT3G62750 | BGLU8; beta glucosidase 8                                                          |
| ath01100     | Metabolic pathways | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                                           |
| ath01100     | Metabolic pathways | ath:AT4G08870 | ARGAH2; Arginase/deacetylase superfamily protein                                   |
| ath01100     | Metabolic pathways | ath:AT4G17830 | Peptidase M20/M25/M40 family protein                                               |
| ath01100     | Metabolic pathways | ath:AT4G21990 | APR3; APS reductase 3                                                              |
| ath01100     | Metabolic pathways | ath:AT4G25420 | GA20OX1; 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein   |
| ath01100     | Metabolic pathways | ath:AT4G25700 | BETA-OHASE_1; beta-hydroxylase 1                                                   |
| ath01100     | Metabolic pathways | ath:AT4G26220 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein           |
| ath01100     | Metabolic pathways | ath:AT4G30920 | LAP2; Cytosol aminopeptidase family protein                                        |
| ath01100     | Metabolic pathways | ath:AT4G34050 | CCoAOMT1; S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| ath01100     | Metabolic pathways | ath:AT4G34880 | Amidase family protein                                                             |
| ath01100     | Metabolic pathways | ath:AT5G04950 | NAS1; nicotianamine synthase 1                                                     |
| ath01100     | Metabolic pathways | ath:AT5G13700 | PAO1; polyamine oxidase 1                                                          |
| ath01100     | Metabolic pathways | ath:AT5G41670 | 6-phosphogluconate dehydrogenase family protein                                    |

| KEGG Pathway | Pathway Name                          | KEGG Gene ID  | Gene Name                                                                          |
|--------------|---------------------------------------|---------------|------------------------------------------------------------------------------------|
| ath01100     | Metabolic pathways                    | ath:AT5G42650 | AOS; allene oxide synthase                                                         |
| ath01100     | Metabolic pathways                    | ath:AT5G43860 | CLH2; chlorophyllase 2                                                             |
| ath01100     | Metabolic pathways                    | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                  |
| ath01100     | Metabolic pathways                    | ath:AT5G48300 | ADG1; ADP glucose pyrophosphorylase 1                                              |
| ath01100     | Metabolic pathways                    | ath:AT5G48930 | HCT; hydroxycinnamoyl-CoA shikimate/quininate hydroxycinnamoyl transferase         |
| ath01100     | Metabolic pathways                    | ath:AT5G54810 | TSB1; tryptophan synthase beta-subunit 1                                           |
| ath01100     | Metabolic pathways                    | ath:AT5G58700 | PLC4; phosphatidylinositol-specific phospholipase C4                               |
| ath01100     | Metabolic pathways                    | ath:ArthCp028 | atpE; ATP synthase CF1 epsilon subunit                                             |
| ath01100     | Metabolic pathways                    | ath:ArthCp029 | atpB; ATP synthase CF1 beta subunit                                                |
| ath01100     | Metabolic pathways                    | ath:ArthCp030 | rbcl; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit                |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G05260 | RCI3; Peroxidase superfamily protein                                               |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G07440 | NAD(P)-binding Rossmann-fold superfamily protein                                   |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G08250 | ADT6; arogenate dehydratase 6                                                      |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G15710 | prephenate dehydrogenase family protein                                            |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G20510 | OPCL1; OPC-8:0 CoA ligase1                                                         |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G51680 | 4CL1; 4-coumarate:CoA ligase 1                                                     |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G52760 | LysoPL2; lysophospholipase 2                                                       |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G60810 | ACLA-2; ATP-citrate lyase A-2                                                      |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G67980 | CCOAMT; caffeoyl-CoA 3-O-methyltransferase                                         |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G71695 | Peroxidase superfamily protein                                                     |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT1G76490 | HMG1; hydroxy methylglutaryl CoA reductase 1                                       |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                               |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G06050 | OPR3; oxophytodienoate-reductase 3                                                 |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                             |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G36750 | UGT73C1; UDP-glucosyl transferase 73C1                                             |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                                             |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G38050 | DET2; 3-oxo-5-alpha-steroid 4-dehydrogenase family protein                         |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                                        |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT3G25760 | AOC1; allene oxide cyclase 1                                                       |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT3G53260 | PAL2; phenylalanine ammonia-lyase 2                                                |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT3G61220 | SDR1; NAD(P)-binding Rossmann-fold superfamily protein                             |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT3G61510 | ACS1; ACC synthase 1                                                               |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT3G62750 | BGLU8; beta glucosidase 8                                                          |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                                           |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G08870 | ARGAH2; Arginase/deacetylase superfamily protein                                   |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G17830 | Peptidase M20/M25/M40 family protein                                               |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G25420 | GA20OX1; 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein   |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G25700 | BETA-OHASE_1; beta-hydroxylase 1                                                   |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G26220 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein           |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT4G34050 | CCoAOMT1; S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G04950 | NAS1; nicotianamine synthase 1                                                     |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G41670 | 6-phosphogluconate dehydrogenase family protein                                    |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G42650 | AOS; allene oxide synthase                                                         |

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|--------------|---------------------------------------|---------------|------------------------------------------------------------------------------------|
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G43860 | CLH2; chlorophyllase 2                                                             |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G45340 | CYP707A3; cytochrome P450, family 707, subfamily A, polypeptide 3                  |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                  |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G48300 | ADG1; ADP glucose pyrophosphorylase 1                                              |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G48930 | HCT; hydroxycinnamoyl-CoA shikimate/quininate hydroxycinnamoyl transferase         |
| ath01110     | Biosynthesis of secondary metabolites | ath:AT5G54810 | TSB1; tryptophan synthase beta-subunit 1                                           |
| ath01110     | Biosynthesis of secondary metabolites | ath:ArthCp030 | rbcl; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit                |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT1G05260 | RCI3; Peroxidase superfamily protein                                               |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT1G51680 | 4CL1; 4-coumarate:CoA ligase 1                                                     |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT1G52760 | LysoPL2; lysophospholipase 2                                                       |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT1G67980 | CCOAMT; caffeoyl-CoA 3-O-methyltransferase                                         |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT1G71695 | Peroxidase superfamily protein                                                     |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT3G53260 | PAL2; phenylalanine ammonia-lyase 2                                                |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT4G26220 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein           |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT4G34050 | CCoAOMT1; S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| ath00940     | Phenylpropanoid biosynthesis          | ath:AT5G48930 | HCT; hydroxycinnamoyl-CoA shikimate/quininate hydroxycinnamoyl transferase         |
| ath01230     | Biosynthesis of amino acids           | ath:AT1G08250 | ADT6; argonate dehydratase 6                                                       |
| ath01230     | Biosynthesis of amino acids           | ath:AT1G15710 | prephenate dehydrogenase family protein                                            |
| ath01230     | Biosynthesis of amino acids           | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                               |
| ath01230     | Biosynthesis of amino acids           | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                             |
| ath01230     | Biosynthesis of amino acids           | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                                             |
| ath01230     | Biosynthesis of amino acids           | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                                           |
| ath01230     | Biosynthesis of amino acids           | ath:AT4G08870 | ARGAH2; Arginase/deacetylase superfamily protein                                   |
| ath01230     | Biosynthesis of amino acids           | ath:AT4G17830 | Peptidase M20/M25/M40 family protein                                               |
| ath01230     | Biosynthesis of amino acids           | ath:AT5G54810 | TSB1; tryptophan synthase beta-subunit 1                                           |
| ath04075     | Plant hormone signal transduction     | ath:AT1G32640 | MYC2; Basic helix-loop-helix (bHLH) DNA-binding family protein                     |
| ath04075     | Plant hormone signal transduction     | ath:AT1G74950 | TIFY10B; TIFY domain/Divergent CCT motif family protein                            |
| ath04075     | Plant hormone signal transduction     | ath:AT3G11410 | PP2CA; protein phosphatase 2CA                                                     |
| ath04075     | Plant hormone signal transduction     | ath:AT3G16360 | AHP4; HPT phosphotransmitter 4                                                     |
| ath04075     | Plant hormone signal transduction     | ath:AT4G03400 | DFL2; Auxin-responsive GH3 family protein                                          |
| ath04075     | Plant hormone signal transduction     | ath:AT4G34760 | SAUR-like auxin-responsive protein family                                          |
| ath04075     | Plant hormone signal transduction     | ath:AT4G37390 | BRU6; Auxin-responsive GH3 family protein                                          |
| ath04016     | MAPK signaling pathway                | ath:AT1G05100 | MAPKKK18; mitogen-activated protein kinase kinase kinase 18                        |
| ath04016     | MAPK signaling pathway                | ath:AT1G32640 | MYC2; Basic helix-loop-helix (bHLH) DNA-binding family protein                     |
| ath04016     | MAPK signaling pathway                | ath:AT2G32510 | MAPKKK17; mitogen-activated protein kinase kinase kinase 17                        |
| ath04016     | MAPK signaling pathway                | ath:AT3G11410 | PP2CA; protein phosphatase 2CA                                                     |
| ath04016     | MAPK signaling pathway                | ath:AT3G61510 | ACS1; ACC synthase 1                                                               |
| ath00270     | Cysteine and methionine metabolism    | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                                             |
| ath00270     | Cysteine and methionine metabolism    | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                                        |
| ath00270     | Cysteine and methionine metabolism    | ath:AT3G61510 | ACS1; ACC synthase 1                                                               |
| ath00270     | Cysteine and methionine metabolism    | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                                           |

| KEGG Pathway | Pathway Name                                          | KEGG Gene ID  | Gene Name                                                                          |
|--------------|-------------------------------------------------------|---------------|------------------------------------------------------------------------------------|
| ath00270     | Cysteine and methionine metabolism                    | ath:AT5G04950 | NAS1; nicotianamine synthase 1                                                     |
| ath01200     | Carbon metabolism                                     | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                               |
| ath01200     | Carbon metabolism                                     | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                             |
| ath01200     | Carbon metabolism                                     | ath:AT5G41670 | 6-phosphogluconate dehydrogenase family protein                                    |
| ath01200     | Carbon metabolism                                     | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                  |
| ath01200     | Carbon metabolism                                     | ath:ArthCp030 | rbcl; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit                |
| ath00941     | Flavonoid biosynthesis                                | ath:AT1G67980 | CCOAMT; caffeoyl-CoA 3-O-methyltransferase                                         |
| ath00941     | Flavonoid biosynthesis                                | ath:AT4G26220 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein           |
| ath00941     | Flavonoid biosynthesis                                | ath:AT4G34050 | CCoAOMT1; S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| ath00941     | Flavonoid biosynthesis                                | ath:AT5G48930 | HCT; hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase       |
| ath00592     | alpha-Linolenic acid metabolism                       | ath:AT1G20510 | OPCL1; OPC-8:0 CoA ligase1                                                         |
| ath00592     | alpha-Linolenic acid metabolism                       | ath:AT2G06050 | OPR3; oxophytodienoate-reductase 3                                                 |
| ath00592     | alpha-Linolenic acid metabolism                       | ath:AT3G25760 | AOC1; allene oxide cyclase 1                                                       |
| ath00592     | alpha-Linolenic acid metabolism                       | ath:AT5G42650 | AOS; allene oxide synthase                                                         |
| ath00945     | Stilbenoid, diarylheptanoid and gingerol biosynthesis | ath:AT1G67980 | CCOAMT; caffeoyl-CoA 3-O-methyltransferase                                         |
| ath00945     | Stilbenoid, diarylheptanoid and gingerol biosynthesis | ath:AT4G26220 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein           |
| ath00945     | Stilbenoid, diarylheptanoid and gingerol biosynthesis | ath:AT4G34050 | CCoAOMT1; S-adenosyl-L-methionine-dependent methyltransferases superfamily protein |
| ath00945     | Stilbenoid, diarylheptanoid and gingerol biosynthesis | ath:AT5G48930 | HCT; hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase       |
| ath00330     | Arginine and proline metabolism                       | ath:AT2G16500 | ADC1; arginine decarboxylase 1                                                     |
| ath00330     | Arginine and proline metabolism                       | ath:AT4G08870 | ARGAH2; Arginase/deacetylase superfamily protein                                   |
| ath00330     | Arginine and proline metabolism                       | ath:AT4G34880 | Amidase family protein                                                             |
| ath00330     | Arginine and proline metabolism                       | ath:AT5G13700 | PAO1; polyamine oxidase 1                                                          |
| ath00999     | Biosynthesis of various plant secondary metabolites   | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                                             |
| ath00999     | Biosynthesis of various plant secondary metabolites   | ath:AT3G62750 | BGLU8; beta glucosidase 8                                                          |
| ath00999     | Biosynthesis of various plant secondary metabolites   | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                                           |
| ath00999     | Biosynthesis of various plant secondary metabolites   | ath:AT5G04950 | NAS1; nicotianamine synthase 1                                                     |
| ath00190     | Oxidative phosphorylation                             | ath:AT1G01050 | PPa1; pyrophosphorylase 1                                                          |
| ath00190     | Oxidative phosphorylation                             | ath:ArthCp028 | atpE; ATP synthase CF1 epsilon subunit                                             |
| ath00190     | Oxidative phosphorylation                             | ath:ArthCp029 | atpB; ATP synthase CF1 beta subunit                                                |
| ath00400     | Phenylalanine, tyrosine and tryptophan biosynthesis   | ath:AT1G08250 | ADT6; arogenate dehydratase 6                                                      |
| ath00400     | Phenylalanine, tyrosine and tryptophan biosynthesis   | ath:AT1G15710 | prephenate dehydrogenase family protein                                            |
| ath00400     | Phenylalanine, tyrosine and tryptophan biosynthesis   | ath:AT5G54810 | TSB1; tryptophan synthase beta-subunit 1                                           |
| ath00710     | Carbon fixation in photosynthetic organisms           | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                               |
| ath00710     | Carbon fixation in photosynthetic organisms           | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                             |
| ath00710     | Carbon fixation in photosynthetic organisms           | ath:ArthCp030 | rbcl; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit                |
| ath00520     | Amino sugar and nucleotide sugar metabolism           | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                                  |
| ath00520     | Amino sugar and nucleotide sugar metabolism           | ath:AT3G54420 | EP3; homolog of carrot EP3-3 chitinase                                             |

| KEGG Pathway | Pathway Name                                | KEGG Gene ID  | Gene Name                                                           |
|--------------|---------------------------------------------|---------------|---------------------------------------------------------------------|
| ath00520     | Amino sugar and nucleotide sugar metabolism | ath:AT5G48300 | ADG1; ADP glucose pyrophosphorylase 1                               |
| ath00040     | Pentose and glucuronate interconversions    | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                   |
| ath00040     | Pentose and glucuronate interconversions    | ath:AT3G07010 | Pectin lyase-like superfamily protein                               |
| ath00040     | Pentose and glucuronate interconversions    | ath:AT3G14310 | PME3; pectin methylesterase 3                                       |
| ath00480     | Glutathione metabolism                      | ath:AT2G24200 | LAP1; Cytosol aminopeptidase family protein                         |
| ath00480     | Glutathione metabolism                      | ath:AT4G30920 | LAP2; Cytosol aminopeptidase family protein                         |
| ath00480     | Glutathione metabolism                      | ath:AT5G41670 | 6-phosphogluconate dehydrogenase family protein                     |
| ath00195     | Photosynthesis                              | ath:AT1G32550 | FdC2; 2Fe-2S ferredoxin-like superfamily protein                    |
| ath00195     | Photosynthesis                              | ath:ArthCp028 | atpE; ATP synthase CF1 epsilon subunit                              |
| ath00195     | Photosynthesis                              | ath:ArthCp029 | atpB; ATP synthase CF1 beta subunit                                 |
| ath01240     | Biosynthesis of cofactors                   | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                   |
| ath01240     | Biosynthesis of cofactors                   | ath:AT2G36880 | MAT3; methionine adenosyltransferase 3                              |
| ath01240     | Biosynthesis of cofactors                   | ath:AT4G01850 | SAM-2; S-adenosylmethionine synthetase 2                            |
| ath00030     | Pentose phosphate pathway                   | ath:AT2G01290 | RPI2; ribose-5-phosphate isomerase 2                                |
| ath00030     | Pentose phosphate pathway                   | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                              |
| ath00030     | Pentose phosphate pathway                   | ath:AT5G41670 | 6-phosphogluconate dehydrogenase family protein                     |
| ath00220     | Arginine biosynthesis                       | ath:AT4G08870 | ARGAH2; Arginase/deacetylase superfamily protein                    |
| ath00220     | Arginine biosynthesis                       | ath:AT4G17830 | Peptidase M20/M25/M40 family protein                                |
| ath00260     | Glycine, serine and threonine metabolism    | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                         |
| ath00260     | Glycine, serine and threonine metabolism    | ath:AT5G54810 | TSB1; tryptophan synthase beta-subunit 1                            |
| ath04712     | Circadian rhythm                            | ath:AT1G01060 | LHY; Homeodomain-like superfamily protein                           |
| ath04712     | Circadian rhythm                            | ath:AT5G62430 | CDF1; cycling DOF factor 1                                          |
| ath00906     | Carotenoid biosynthesis                     | ath:AT4G25700 | BETA-OHASE_1; beta-hydroxylase 1                                    |
| ath00906     | Carotenoid biosynthesis                     | ath:AT5G45340 | CYP707A3; cytochrome P450, family 707, subfamily A, polypeptide 3   |
| ath00900     | Terpenoid backbone biosynthesis             | ath:AT1G76490 | HMG1; hydroxy methylglutaryl CoA reductase 1                        |
| ath00900     | Terpenoid backbone biosynthesis             | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                   |
| ath00380     | Tryptophan metabolism                       | ath:AT4G34880 | Amidase family protein                                              |
| ath00380     | Tryptophan metabolism                       | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                   |
| ath00280     | Valine, leucine and isoleucine degradation  | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                         |
| ath00280     | Valine, leucine and isoleucine degradation  | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                   |
| ath03013     | Nucleocytoplasmic transport                 | ath:AT1G10390 | Nucleoporin autopeptidase                                           |
| ath03013     | Nucleocytoplasmic transport                 | ath:AT5G60390 | GTP binding Elongation factor Tu family protein                     |
| ath00630     | Glyoxylate and dicarboxylate metabolism     | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                   |
| ath00630     | Glyoxylate and dicarboxylate metabolism     | ath:ArthCp030 | rbcl; ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit |
| ath00500     | Starch and sucrose metabolism               | ath:AT3G62750 | BGLU8; beta glucosidase 8                                           |
| ath00500     | Starch and sucrose metabolism               | ath:AT5G48300 | ADG1; ADP glucose pyrophosphorylase 1                               |
| ath00360     | Phenylalanine metabolism                    | ath:AT3G53260 | PAL2; phenylalanine ammonia-lyase 2                                 |
| ath00360     | Phenylalanine metabolism                    | ath:AT4G34880 | Amidase family protein                                              |
| ath01212     | Fatty acid metabolism                       | ath:AT3G45770 | Polyketide synthase, enoylreductase family protein                  |
| ath01212     | Fatty acid metabolism                       | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                   |
| ath01250     | Biosynthesis of nucleotide sugars           | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                   |
| ath01250     | Biosynthesis of nucleotide sugars           | ath:AT5G48300 | ADG1; ADP glucose pyrophosphorylase 1                               |
| ath04144     | Endocytosis                                 | ath:AT5G02500 | HSC70-1; heat shock cognate protein 70-1                            |
| ath04626     | Plant-pathogen interaction                  | ath:AT4G36070 | CPK18; calcium-dependent protein kinase 18                          |

| KEGG Pathway | Pathway Name                                           | KEGG Gene ID  | Gene Name                                                                        |
|--------------|--------------------------------------------------------|---------------|----------------------------------------------------------------------------------|
| ath00908     | Zeatin biosynthesis                                    | ath:AT2G36750 | UGT73C1; UDP-glucosyl transferase 73C1                                           |
| ath00902     | Monoterpenoid biosynthesis                             | ath:AT3G61220 | SDR1; NAD(P)-binding Rossmann-fold superfamily protein                           |
| ath00053     | Ascorbate and aldarate metabolism                      | ath:AT1G26570 | UGD1; UDP-glucose dehydrogenase 1                                                |
| ath00620     | Pyruvate metabolism                                    | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                |
| ath00920     | Sulfur metabolism                                      | ath:AT4G21990 | APR3; APS reductase 3                                                            |
| ath00051     | Fructose and mannose metabolism                        | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                           |
| ath00650     | Butanoate metabolism                                   | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                |
| ath04070     | Phosphatidylinositol signaling system                  | ath:AT5G58700 | PLC4; phosphatidylinositol-specific phospholipase C4                             |
| ath00904     | Diterpenoid biosynthesis                               | ath:AT4G25420 | GA20OX1; 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein |
| ath00010     | Glycolysis / Gluconeogenesis                           | ath:AT2G21330 | FBA1; fructose-bisphosphate aldolase 1                                           |
| ath00960     | Tropane, piperidine and pyridine alkaloid biosynthesis | ath:AT1G07440 | NAD(P)-binding Rossmann-fold superfamily protein                                 |
| ath00905     | Brassinosteroid biosynthesis                           | ath:AT2G38050 | DET2; 3-oxo-5-alpha-steroid 4-dehydrogenase family protein                       |
| ath00460     | Cyanoamino acid metabolism                             | ath:AT3G62750 | BGLU8; beta glucosidase 8                                                        |
| ath00310     | Lysine degradation                                     | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                |
| ath00062     | Fatty acid elongation                                  | ath:AT3G45770 | Polyketide synthase, enoylreductase family protein                               |
| ath00130     | Ubiquinone and other terpenoid-quinone biosynthesis    | ath:AT1G51680 | 4CL1; 4-coumarate:CoA ligase 1                                                   |
| ath00240     | Pyrimidine metabolism                                  | ath:AT3G25400 | dCTP pyrophosphatase-like protein                                                |
| ath00562     | Inositol phosphate metabolism                          | ath:AT5G58700 | PLC4; phosphatidylinositol-specific phospholipase C4                             |
| ath03040     | Spliceosome                                            | ath:AT5G02500 | HSC70-1; heat shock cognate protein 70-1                                         |
| ath04141     | Protein processing in endoplasmic reticulum            | ath:AT5G02500 | HSC70-1; heat shock cognate protein 70-1                                         |
| ath03018     | RNA degradation                                        | ath:AT3G44260 | CAF1a; Polynucleotidyl transferase, ribonuclease H-like superfamily protein      |
| ath00250     | Alanine, aspartate and glutamate metabolism            | ath:AT2G38400 | AGT3; alanine:glyoxylate aminotransferase 3                                      |
| ath00071     | Fatty acid degradation                                 | ath:AT5G48230 | ACAT2; acetoacetyl-CoA thiolase 2                                                |
| ath00196     | Photosynthesis - antenna proteins                      | ath:AT1G29930 | CAB1; chlorophyll A/B binding protein 1                                          |
| ath00020     | Citrate cycle (TCA cycle)                              | ath:AT1G60810 | ACLA-2; ATP-citrate lyase A-2                                                    |
| ath00410     | beta-Alanine metabolism                                | ath:AT5G13700 | PAO1; polyamine oxidase 1                                                        |
| ath00061     | Fatty acid biosynthesis                                | ath:AT3G45770 | Polyketide synthase, enoylreductase family protein                               |
| ath00860     | Porphyrin metabolism                                   | ath:AT5G43860 | CLH2; chlorophyllase 2                                                           |
| ath01210     | 2-Oxocarboxylic acid metabolism                        | ath:AT4G17830 | Peptidase M20/M25/M40 family protein                                             |