ath01100	Pathway Name Metabolic pathways	ath:AT1G23820 ath:AT1G26570 ath:AT1G30620 ath:AT1G60810 ath:AT1G67750 ath:AT1G68530	Gene Name EFE; ethylene-forming enzyme AXS2; UDP-D-apiose/UDP-D-xylose synthase 2 SPDS1; spermidine synthase UGD1; UDP-glucose dehydrogenase 1 MUR4; NAD(P)-binding Rossmann-fold superfamily protein ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100	Metabolic pathways	ath:AT1G08200 ath:AT1G23820 ath:AT1G26570 ath:AT1G30620 ath:AT1G60810 ath:AT1G67750 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G21330	AXS2; UDP-D-apiose/UDP-D-xylose synthase 2 SPDS1; spermidine synthase UGD1; UDP-glucose dehydrogenase 1 MUR4; NAD(P)-binding Rossmann-fold superfamily protein ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100	Metabolic pathways	ath:AT1G23820 ath:AT1G26570 ath:AT1G30620 ath:AT1G60810 ath:AT1G67750 ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G21330	SPDS1; spermidine synthase UGD1; UDP-glucose dehydrogenase 1 MUR4; NAD(P)-binding Rossmann-fold superfamily protein ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100	Metabolic pathways	ath:AT1G26570 ath:AT1G30620 ath:AT1G60810 ath:AT1G67750 ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	UGD1; UDP-glucose dehydrogenase 1 MUR4; NAD(P)-binding Rossmann-fold superfamily protein ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G30620 ath:AT1G60810 ath:AT1G67750 ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	MUR4; NAD(P)-binding Rossmann-fold superfamily protein ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G60810 ath:AT1G67750 ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	ACLA-2; ATP-citrate lyase A-2 Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G67750 ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	Pectate lyase family protein KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G68530 ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	KCS6; 3-ketoacyl-CoA synthase 6 Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G71695 ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	Peroxidase superfamily protein DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT1G75270 ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	DHAR2; dehydroascorbate reductase 2 HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways Metabolic pathways Metabolic pathways Metabolic pathways Metabolic pathways	ath:AT1G76490 ath:AT2G21330 ath:AT2G24200	HMG1; hydroxy methylglutaryl CoA reductase 1 FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways Metabolic pathways Metabolic pathways Metabolic pathways	ath:AT2G21330 ath:AT2G24200	FBA1; fructose-bisphosphate aldolase 1
ath01100 ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways Metabolic pathways Metabolic pathways	ath:AT2G24200	
ath01100 ath01100 ath01100 ath01100 ath01100	Metabolic pathways Metabolic pathways		LADA: Citaral antinamentidas: forth contain
ath01100 ath01100 ath01100 ath01100	Metabolic pathways	ath:AT2G37130	LAP1; Cytosol aminopeptidase family protein
ath01100 ath01100 ath01100			Peroxidase superfamily protein
ath01100 ath01100 ath01100		ath:AT2G43590	Chitinase family protein
ath01100 ath01100		ath:AT3G06350	MEE32; dehydroquinate dehydratase, putative / shikimate dehydrogenase
ath01100			, , , , , , , , , , , , , , , , , , , ,
ath01100	Metabolic pathways	ath:AT3G12120	FAD2; fatty acid desaturase 2
	Metabolic pathways	ath:AT3G12120	O-Glycosyl hydrolases family 17 protein
~	Metabolic pathways	ath:AT3G15300	dCTP pyrophosphatase-like protein
	Metabolic pathways	ath:AT3G25400	Polyketide synthase, encylreductase family protein
	·		
	Metabolic pathways	ath:AT4G08870	ARGAH2; Arginase/deacetylase superfamily protein
atn01100	Metabolic pathways	ath:AT4G26220	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
ath01100	Metabolic pathways	ath:AT4G30920	LAP2; Cytosol aminopeptidase family protein
	Metabolic pathways	ath:AT4G33150	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional
ath01100	Metabolic pathways	ath:AT4G35160	O-methyltransferase family protein
ath01100	Metabolic pathways	ath:AT4G37970	CAD6; cinnamyl alcohol dehydrogenase 6
ath01100	Metabolic pathways	ath:AT4G39010	GH9B18; glycosyl hydrolase 9B18
ath01100	Metabolic pathways	ath:AT5G03300	ADK2; adenosine kinase 2
ath01100	Metabolic pathways	ath:AT5G06060	NAD(P)-binding Rossmann-fold superfamily protein
ath01100	Metabolic pathways	ath:AT5G20830	SUS1; sucrose synthase 1
ath01100	Metabolic pathways	ath:AT5G21100	Plant L-ascorbate oxidase
ath01100	Metabolic pathways	ath:AT5G37600	GSR_1; hypothetical protein
	Metabolic pathways	ath:AT5G40150	Peroxidase superfamily protein
	Metabolic pathways	ath:AT5G60340	AAK6; P-loop containing nucleoside triphosphate hydrolases superfamily
	,		protein
ath01100	Metabolic pathways	ath:ArthCp002	psbA; photosystem II protein D1
	Metabolic pathways	ath:ArthCp007	atpA; ATP synthase CF1 alpha subunit
		 	
	Metabolic pathways	ath:ArthCp018	psbC; photosystem II 44 kDa protein psaA; photosystem I P700 chlorophyll a apoprotein A1
	Metabolic pathways	ath:ArthCp022	
ath01100	Metabolic pathways	ath:ArthCp053	petB; cytochrome b6
ath01110	Biosynthesis of secondary metabolites	ath:AT1G05010	EFE; ethylene-forming enzyme
ath01110	Biosynthesis of secondary metabolites	ath:AT1G19640	JMT; jasmonic acid carboxyl methyltransferase
ath01110	Biosynthesis of secondary metabolites	ath:AT1G60810	ACLA-2; ATP-citrate lyase A-2
ath01110	Biosynthesis of secondary metabolites	ath:AT1G68530	KCS6; 3-ketoacyl-CoA synthase 6
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:AT2G19500	CKX2; cytokinin oxidase 2
ath01110	Biosynthesis of secondary metabolites	ath:AT2G21330	FBA1; fructose-bisphosphate aldolase 1
ath01110	Biosynthesis of secondary metabolites	ath:AT2G24190	SDR2; NAD(P)-binding Rossmann-fold superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT2G26710	BAS1; Cytochrome P450 superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT2G36750	UGT73C1; UDP-glucosyl transferase 73C1
ath01110	Biosynthesis of secondary metabolites	ath:AT2G37130	Peroxidase superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT3G06350	MEE32; dehydroquinate dehydratase, putative / shikimate dehydrogenase
-+b01110	Diagonathasia of associate a contribute	-th.AT4C00070	ADCAUS. Assissand/deportulation property of the control of
ath01110	Biosynthesis of secondary metabolites	ath:AT4G08870	ARGAH2; Arginase/deacetylase superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT4G26220	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT4G33150	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme
	Biosynthesis of secondary metabolites	ath:AT4G35160	O-methyltransferase family protein

KEGG Pathway	Pathway Name	KEGG Gene ID	Gene Name
ath01110	Biosynthesis of secondary metabolites	ath:AT4G37970	CAD6; cinnamyl alcohol dehydrogenase 6
ath01110	Biosynthesis of secondary metabolites	ath:AT5G06060	NAD(P)-binding Rossmann-fold superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT5G20830	SUS1; sucrose synthase 1
ath01110	Biosynthesis of secondary metabolites	ath:AT5G40150	Peroxidase superfamily protein
ath01110	Biosynthesis of secondary metabolites	ath:AT5G60340	AAK6; P-loop containing nucleoside triphosphate hydrolases superfamily
			protein
ath04075	Plant hormone signal transduction	ath:AT1G74890	ARR15; response regulator 15
ath04075	Plant hormone signal transduction	ath:AT2G25490	EBF1; EIN3-binding F box protein 1
ath04075	Plant hormone signal transduction	ath:AT3G11410	PP2CA; protein phosphatase 2CA
ath04075	Plant hormone signal transduction	ath:AT3G63010	GID1B; alpha/beta-Hydrolases superfamily protein
ath04075	Plant hormone signal transduction	ath:AT5G18030	SAUR-like auxin-responsive protein family
ath00195	Photosynthesis	ath:ArthCp002	psbA; photosystem II protein D1
ath00195	Photosynthesis	ath:ArthCp007	atpA; ATP synthase CF1 alpha subunit
ath00195	Photosynthesis	ath:ArthCp018	psbC; photosystem II 44 kDa protein
ath00195	Photosynthesis	ath:ArthCp022	psaA; photosystem I P700 chlorophyll a apoprotein A1
ath00195	Photosynthesis	ath:ArthCp053	petB; cytochrome b6
ath04712	Circadian rhythm	ath:AT1G01060	LHY; Homeodomain-like superfamily protein
ath04712	Circadian rhythm	ath:AT1G22770	GI; gigantea protein (GI)
ath04712	Circadian rhythm	ath:AT1G68050	FKF1; flavin-binding, kelch repeat, f box 1
ath04712	Circadian rhythm	ath:AT5G24470	PRR5; two-component response regulator-like protein
ath04712	Circadian rhythm	ath:AT5G62430	CDF1; cycling DOF factor 1
ath00940	Phenylpropanoid biosynthesis	ath:AT1G71695	Peroxidase superfamily protein
ath00940	Phenylpropanoid biosynthesis	ath:AT2G37130	Peroxidase superfamily protein
ath00940	Phenylpropanoid biosynthesis	ath:AT4G26220	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
ath00940	Phenylpropanoid biosynthesis	ath:AT4G37970	CAD6; cinnamyl alcohol dehydrogenase 6
ath00940	Phenylpropanoid biosynthesis	ath:AT5G40150	Peroxidase superfamily protein
ath00520	Amino sugar and nucleotide sugar	ath:AT1G08200	AXS2; UDP-D-apiose/UDP-D-xylose synthase 2
	metabolism		
ath00520	Amino sugar and nucleotide sugar	ath:AT1G26570	UGD1; UDP-glucose dehydrogenase 1
	metabolism		
ath00520	Amino sugar and nucleotide sugar	ath:AT1G30620	MUR4; NAD(P)-binding Rossmann-fold superfamily protein
	metabolism		
ath00520	Amino sugar and nucleotide sugar	ath:AT2G43590	Chitinase family protein
	metabolism		
ath00480	Glutathione metabolism	ath:AT1G23820	SPDS1; spermidine synthase
ath00480	Glutathione metabolism	ath:AT1G75270	DHAR2; dehydroascorbate reductase 2
ath00480	Glutathione metabolism	ath:AT2G24200	LAP1; Cytosol aminopeptidase family protein
ath00480	Glutathione metabolism		LAP2; Cytosol aminopeptidase family protein
ath01230	Biosynthesis of amino acids		FBA1; fructose-bisphosphate aldolase 1
ath01230	Biosynthesis of amino acids	ath:AT3G06350	MEE32; dehydroquinate dehydratase, putative / shikimate dehydrogenase
-+-01220	Discountly sain of service spaids	-+b.AT4C00070	ADC ALID: A minor of deceated and a superferred to make in
ath01230 ath01230	Biosynthesis of amino acids		ARGAH2; Arginase/deacetylase superfamily protein
ath01230 ath04141	Biosynthesis of amino acids		GSR_1; hypothetical protein HSP20-like chaperones superfamily protein
au 104141	Protein processing in endoplasmic reticulum	ath:AT1G07400	processing chaperones superidinily protein
ath04141	Protein processing in endoplasmic	ath:AT1G75950	SKP1; S phase kinase-associated protein 1
au 104141	reticulum	aui.A110/3930	Jon 1, 5 phase khase-associated photein 1
ath04141	Protein processing in endoplasmic	ath:AT5G02490	Hsp70-2; Heat shock protein 70 (Hsp 70) family protein
au104141	reticulum	atii.A13002490	113970-2, Heat shock protein 70 (1139 70) fallilly protein
ath04141	Protein processing in endoplasmic	ath:AT5G02500	HSC70-1; heat shock cognate protein 70-1
au 104141	reticulum	atii.A13002300	113070-1, Heat Shock Cognate protein 70-1
ath04145	Phagosome	ath:AT1G20010	TUB5; tubulin beta-5 chain
ath04145	Phagosome		TUA1; alpha-1 tubulin
ath04145	Phagosome		TUB1; tubulin beta-1 chain
ath04144	Endocytosis	ath:AT1G75780	RABA3; RAB GTPase homolog A3
ath04144	Endocytosis		Hsp70-2; Heat shock protein 70 (Hsp 70) family protein
ath04144	Endocytosis		HSC70-1; heat shock cognate protein 70-1
ath00500	Starch and sucrose metabolism		O-Glycosyl hydrolases family 17 protein
ath00500	Starch and sucrose metabolism		GH9B18; glycosyl hydrolase 9B18
ath00500	Starch and sucrose metabolism		SUS1; sucrose synthase 1
ath00500	Ascorbate and aldarate metabolism		UGD1; UDP-glucose dehydrogenase 1
uti100033	Macorpate and aluarate metabolism	[atti./110702/0	DODE, ODI BIUCOSC UCHYUIOSCHOSC I

KEGG Pathway	Pathway Name	KEGG Gene ID	Gene Name
ath00053	Ascorbate and aldarate metabolism	ath:AT1G75270	DHAR2; dehydroascorbate reductase 2
ath00053	Ascorbate and aldarate metabolism	ath:AT5G21100	Plant L-ascorbate oxidase
ath04016	MAPK signaling pathway	ath:AT2G25490	EBF1; EIN3-binding F box protein 1
ath04016	MAPK signaling pathway	ath:AT2G23430	MAPKKK17; mitogen-activated protein kinase kinase kinase 17
ath04016	MAPK signaling pathway	ath:AT2G32310	PP2CA; protein phosphatase 2CA
ath01250	Biosynthesis of nucleotide sugars	ath:AT1G08200	AXS2; UDP-D-apiose/UDP-D-xylose synthase 2
ath01250	Biosynthesis of nucleotide sugars	ath:AT1G26570	UGD1; UDP-glucose dehydrogenase 1
ath01250	Biosynthesis of nucleotide sugars	ath:AT1G20370	MUR4; NAD(P)-binding Rossmann-fold superfamily protein
ath04626	Plant-pathogen interaction	ath:AT1G50020	KCS6; 3-ketoacyl-CoA synthase 6
ath04626	Plant-pathogen interaction	ath:AT2G04880	ZAP1; zinc-dependent activator protein-1
ath00330	Arginine and proline metabolism	ath:AT1G23820	SPDS1; spermidine synthase
ath00330	Arginine and proline metabolism	ath:AT4G08870	ARGAH2; Arginase/deacetylase superfamily protein
ath00062	Fatty acid elongation	ath:AT1G68530	KCS6; 3-ketoacyl-CoA synthase 6
ath00062	Fatty acid elongation	ath:AT3G45770	Polyketide synthase, enoylreductase family protein
ath01240	Biosynthesis of cofactors	ath:AT1G26570	UGD1; UDP-glucose dehydrogenase 1
atii01240	Biosynthesis of Colactors	atii.A11G2G57G	AAK6; P-loop containing nucleoside triphosphate hydrolases superfamily
ath01240	Biosynthesis of cofactors	ath:AT5G60340	protein
ath01212	Fatty acid metabolism	ath:AT3G12120	FAD2; fatty acid desaturase 2
ath01212	Fatty acid metabolism	ath:AT3G45770	Polyketide synthase, enoylreductase family protein
ath00908	Zeatin biosynthesis	ath:AT2G19500	CKX2; cytokinin oxidase 2
ath00908	Zeatin biosynthesis	ath:AT2G36750	UGT73C1; UDP-glucosyl transferase 73C1
ath00270	Cysteine and methionine metabolism	ath:AT1G05010	EFE; ethylene-forming enzyme
ath00270	Cysteine and methionine metabolism	ath:AT1G23820	SPDS1; spermidine synthase
ath03040	Spliceosome		Hsp70-2; Heat shock protein 70 (Hsp 70) family pr
ath03040	Spliceosome	ath:AT5G02500	HSC70-1; heat shock cognate protein 70-1
ath00220	Arginine biosynthesis	ath:AT4G08870	ARGAH2; Arginase/deacetylase superfamily protein
ath00220	Arginine biosynthesis	ath:AT5G37600	GSR_1; hypothetical protein
	Pentose and glucuronate		
ath00040	1	ath:AT1G26570	UGD1; UDP-glucose dehydrogenase 1
- 11-00040	interconversions	- U. AT4 CC7750	Particle Land Court Court
ath00040	Pentose and glucuronate	ath:AT1G67750	Pectate lyase family protein
-+-00330	interconversions	a+b.ATEC02200	ADK2; adenosine kinase 2
ath00230	Purine metabolism	ath:AT5G03300	·
ath00230	Purine metabolism	ath:AT5G60340	AAK6; P-loop containing nucleoside triphosphate hydrolases super family
	Ctille and identify and air and air and	- U. ATAC2C220	protein
	Stilbenoid, diarylheptanoid and gingerol	ath:AT4G26220	
ath00945	biosynthesis		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
ath00592	alpha-Linolenic acid metabolism	ath:AT1G19640	JMT; jasmonic acid carboxyl methyltransferase
ath00941	Flavonoid biosynthesis		S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
ath01200	Carbon metabolism		FBA1; fructose-bisphosphate aldolase 1
ath00902	Monoterpenoid biosynthesis		SDR2; NAD(P)-binding Rossmann-fold superfamily protein
ath00960	Tropane, piperidine and pyridine alkaloid biosynthesis	ath:AT5G06060	NAD(P)-binding Rossmann-fold superfamily protein
ath00905	Brassinosteroid biosynthesis	ath:AT2G26710	BAS1; Cytochrome P450 superfamily protein
ath04146	Peroxisome	ath:AT2G28190	CSD2; copper/zinc superoxide dismutase 2
ath03060	Protein export	ath:AT1G48160	signal recognition particle 19 kDa protein, putative / SRP19
41103000	Trotein export	dtii.A11040100	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional
ath00310	Lysine degradation	ath:AT4G33150	enzyme
ath00310	Oxidative phosphorylation	ath:ArthCp007	atpA; ATP synthase CF1 alpha subunit
ath00190	Fructose and mannose metabolism	ath:AT2G21330	FBA1; fructose-bisphosphate aldolase 1
ath00051	i ructose and mannose metabolism		i bal, iractose bispriospriate aldolase 1
	Dhonylalaning turacing and thintanher		1
ati100400	Phenylalanine, tyrosine and tryptophan	ath:AT3G06350	MEES2: debudroquinate debudratase, nutativo / shikimate debudrasasase
	biosynthesis		MEE32; dehydroquinate dehydratase, putative / shikimate dehydrogenase
ath00020	biosynthesis Citrate cycle (TCA cycle)	ath:AT1G60810	ACLA-2; ATP-citrate lyase A-2
ath00020 ath00010	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis	ath:AT1G60810 ath:AT2G21330	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1
ath00020 ath00010 ath00380	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis Tryptophan metabolism	ath:AT1G60810 ath:AT2G21330 ath:AT4G35160	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1 O-methyltransferase family protein
ath00020 ath00010 ath00380 ath00030	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis Tryptophan metabolism Pentose phosphate pathway	ath:AT1G60810 ath:AT2G21330 ath:AT4G35160 ath:AT2G21330	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1 O-methyltransferase family protein FBA1; fructose-bisphosphate aldolase 1
ath00020 ath00010 ath00380 ath00030 ath01040	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis Tryptophan metabolism	ath:AT1G60810 ath:AT2G21330 ath:AT4G35160 ath:AT2G21330 ath:AT3G12120	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1 O-methyltransferase family protein FBA1; fructose-bisphosphate aldolase 1 FAD2; fatty acid desaturase 2
ath00020 ath00010 ath00380 ath00030	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis Tryptophan metabolism Pentose phosphate pathway Biosynthesis of unsaturated fatty acids	ath:AT1G60810 ath:AT2G21330 ath:AT4G35160 ath:AT2G21330 ath:AT3G12120 ath:AT5G37600	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1 O-methyltransferase family protein FBA1; fructose-bisphosphate aldolase 1
ath00020 ath00010 ath00380 ath00030 ath01040	biosynthesis Citrate cycle (TCA cycle) Glycolysis / Gluconeogenesis Tryptophan metabolism Pentose phosphate pathway	ath:AT1G60810 ath:AT2G21330 ath:AT4G35160 ath:AT2G21330 ath:AT3G12120 ath:AT5G37600	ACLA-2; ATP-citrate lyase A-2 FBA1; fructose-bisphosphate aldolase 1 O-methyltransferase family protein FBA1; fructose-bisphosphate aldolase 1 FAD2; fatty acid desaturase 2

KEGG Pathway	Pathway Name	KEGG Gene ID	Gene Name
ath00250	Alanine, aspartate and glutamate	ath:AT5G37600	GSR_1; hypothetical protein
	metabolism		
			AAK6; P-loop containing nucleoside triphosphate hydrolases superfamily
ath03008	Ribosome biogenesis in eukaryotes	ath:AT5G60340	protein
ath00910	Nitrogen metabolism	ath:AT5G37600	GSR_1; hypothetical protein
ath00240	Pyrimidine metabolism	ath:AT3G25400	dCTP pyrophosphatase-like protein
ath00999	Biosynthesis of various plant secondary	ath:AT3G06350	MEE32; dehydroquinate dehydratase, putative / shikimate dehydrogenase
	metabolites		
ath04120	Ubiquitin mediated proteolysis	ath:AT1G75950	SKP1; S phase kinase-associated protein 1
ath00061	Fatty acid biosynthesis	ath:AT3G45770	Polyketide synthase, enoylreductase family protein
ath00710	Carbon fixation in photosynthetic	ath:AT2G21330	FBA1; fructose-bisphosphate aldolase 1
	organisms		