

Primer name	Enzyme name	Enzyme Id		Primer sequence
A_C15_B08	oleoyl-[acyl-carrier-protein] hydrolase	ec:3.1.2.14_A	Forward	GCTTTCTACTGTCCTCATCTACAAC
			Reverse	GCTTCGAGTCTATGGGTGATG
A_E21_C11	methionine adenosyltransferase	ec:2.5.1.6_A_1	Forward	TTTTCACGCTTCAGGTTTCT
			Reverse	CATACGGGCACTTTGGAAG
A_M18_G09	alcohol dehydrogenase	ec:1.1.1.1_A	Forward	GCGAATTTTGCAGTCAAGG
			Reverse	TGAAACCACAGCAAAGGAA
A_M19_G10	methionine adenosyltransferase	ec:2.5.1.6_A_2	Forward	CCTTCCATTTCCGCCCT
			Reverse	CCATTGTCTGTGTTTGTTGATACTT
A_N13_G07	H ⁺ -transporting two-sector ATPase	ec:3.6.3.14_A	Forward	TGACAACAAGGGAAGGGAAAT
			Reverse	GGCAGCAGAGCATCAAGAAT
A_O01_H01	phospholipase D	ec:3.1.4.4_A	Forward	GATACTCCATTCCATTCACTTTTC
			Reverse	TGTTTCCTCCATCTCTGCTC
ADP-glucose	glucose-1-phosphate adenylyltransferase	ec:2.7.7.27_A	Forward	ATCTGCACCCATCAGCAATGAA
			Reverse	CCTCGATATCTGCCTCCTTCCA
A-K05-F03	senescence-associated protein	A-K05-F03_A	Forward	CGTCGTGAGACAGGTTAGTT
			Reverse	GGCGTTCAGTCATAATCCA
ANTHOCYAN-D-P13	leucocyanidin oxygenase	ec:1.14.11.19_D_1	Forward	GTGAATAAAGAGAAGGTGAGGA
			Reverse	AGAAAAGTGCCCAAGAAATC
Antocyan_D	leucocyanidin oxygenase	ec:1.14.11.19_D_2	Forward	GACCCATTTTCCCTCACA
			Reverse	CACTTTCATCCTCCACAACA
At1g2141_D	ubiquitin protein ligase	ec:6.3.2.19_D	Forward	CCTCCTTGATCCCTTTTTTCAC
			Reverse	AAACCATTGCCTTCACCTAAGA
At5g28840_B	GDP-mannose 3,5-epimerase	ec:5.1.3.18_B	Forward	ACCGATTTGAAGTGGAGCTTG
			Reverse	ACGAGATTGAAGGATGGCCTG
B_B24_A12	alpha-amylase, galactinol---sucrose galactosyltransferase	ec:3.2.1.0_B	Forward	CAACCCGACCCCAAGACC
			Reverse	CTGGAATAGATGGCGTGAAGGTT
B_C08_B04	pantothenate kinase	ec:2.7.1.33_B	Forward	TCGCAAGAGGGACAGAGATA
			Reverse	ACATACTGGGGATTAGGGAAGC
B_C12_B06	adenosine kinase	ec:2.7.1.20_B	Forward	CCTTTCTGCTCCATTTATCTGT
			Reverse	CGTGCTTCGGTTTCATTTC

B_G23_D12	phosphopyruvate hydratase	ec:4.2.1.11_B_1	Forward	CAACCCACGGAGAGATCAG
			Reverse	CGCAGTGGAGAGACAGAGG
B_I06_E03	phospholipase D	ec:3.1.4.4_B	Forward	GCTCGCTCACCTTTCCTTCG
			Reverse	GCAGCCAGCAAGGGGACAAA
B-A14-A07	lipoxygenase	ec:1.13.11.12_B	Forward	CTCGGCTACAGACATTACTGG
			Reverse	TCGTTCTCTACTTCCCTCAA
BETA-GAL-D-B19	beta-galactosidase	ec:3.2.1.23_D	Forward	CAACAATGCGATTACAGAG
			Reverse	TCTCCGCCAATCTCTTCA
B-gluc_B	pyruvate kinase	ec:2.7.1.40_B_1	Forward	CAGCTGCCAAGAGTGCATCAAT
			Reverse	CAAGGACGATGTTGTGTCGTGATG
B-gluc_C	raucaffricine beta-glucosidase	ec:3.2.1.125_C	Forward	TGGGATATTCCCAATGTTTGC
			Reverse	CGATCACCAAATCCCAGAAGC
Biotin_1B	acetyl-CoA carboxylase	ec:6.4.1.2_B_1	Forward	CTCCTTCAAATGTCCCTGCTA
			Reverse	TGGGGCAGAAGAACGGTAAAA
Biotin_3B	acetyl-CoA carboxylase	ec:6.4.1.2_B_2	Forward	CTCCTTCAAATGTCCCTGCTC
			Reverse	TGGGGCAGAAGAACGGTAAAA
C_C04_B02	adenosylmethionine decarboxylase, arginine decarboxylase	ec:4.1.1.50_C	Forward	TCAAATCCAATCGCAGAAAC
			Reverse	TTCCACTTCACTCCTTTCCTT
C_D14_B07	digalactosyldiacylglycerol synthase	ec:2.4.1.241_C	Forward	CAGCAGAAAGGCGGAGGA
			Reverse	GGAATACATCAAGAGGGAAAAGA
C_D19_B10	mitogen-activated protein kinase kinase kinase	ec:2.7.11.25_C	Forward	GTCTCAAGAGGGAGCCGTTAG
			Reverse	CAAGGGGAGGAGGGAAAGCA
C_I19_E10	pyruvate kinase	ec:2.7.1.40_C	Forward	TGATTTTATTGCCTTGTCGTT
			Reverse	GGCTTCCAACTCTCTATCTT
C_N01_G01	amidase	ec:3.5.1.4_C	Forward	AGCCAAACGCAGAATAGAAG
			Reverse	GCAGCAAATCTTCTTGGGTTC
Cellulose	cellulose synthase (UDP-forming)	ec:2.4.1.12_A	Forward	CTGTTTTGCCTTCCCATCAACC
			Reverse	CCCTTCTCATTCCACCAACCAC
Cellulose_B	cellulose synthase (UDP-forming)	ec:2.4.1.12_B	Forward	GCAGAATGCAATAAGCGAGCAA
			Reverse	TCAGGTCCTTAGGTGGGCTTT
C-H22-D11	aldo/keto reductase family protein	C-H22-D11_C	Forward	GGAAGTGTCGAGGAATGAGA

			Reverse	CTGGGCTGTATGGGTATG
Chalcone_D	naringenin-chalcone synthase	ec:2.3.1.74_D_1	Forward	GGCGAAGACCGAGGAGTTT
			Reverse	CCCAAAAAGCAATCAAAGAATGG
Chloroplast_C	acetyl-CoA carboxylase	ec:6.4.1.2_C	Forward	AAATGCAGTCTTCTATGTTGCC
			Reverse	GGTTCAGGGATGATGCCG
Citrate_A	ATP citrate synthase / citrate (Si)-synthase	ec:2.3.3.8_A_1	Forward	GCAAGACAGATCCAAGATACACG
			Reverse	GTTCTAAGAGTATAGGAGGCACT
Citrate_B	ATP citrate synthase / citrate (Si)-synthase	ec:2.3.3.8_A_2	Forward	AAAGCACTTGCCTGAAGATCCA
			Reverse	ACAGTGTAGTATCTTGCTTCAGTC
C-J08-E04	pyridoxine biosynthesis	C-J08-E04_C	Forward	TACCCCGAACCCCTCTTGT
			Reverse	GTGACGCCTGCTGATGCT
C-O09-H05	UDP-glycosyltransferase	C-O09-H05_C	Forward	TTAGCAAGACCCCAAGCAAA
			Reverse	GAGCGAAAACTCAAATCCATT
Cysteine_A	phospholipase A2	ec:3.1.1.4_A	Forward	ATGGCTCTATTGCAATACCACA
			Reverse	TGGTGTGGCTGTTGTTGGAT
Cysteine_D	phospholipase A2	ec:3.1.1.4_D	Forward	ATGGCTCTATTGCAATACCACG
			Reverse	TGGTGTGGCTGTTGTTGGAT
D_A03_A02	asparaginase	ec:3.5.1.1_D	Forward	TCAGGGAGGGGATTGATGAGC
			Reverse	GTGGGTGGCGATGGGTTGG
D_D01_B01	superoxide dismutase	ec:1.15.1.1_D	Forward	CTTCCACCAGCATTTCAGT
			Reverse	CTCTTACAGGACCACATTCCA
D_D23_B12	NADH dehydrogenase (ubiquinone)	ec:1.6.5.3_D	Forward	CCACCAAGCACTCATTCTCT
			Reverse	CTCATACCCCGAACCATTTC
D_I24_E12	arginine decarboxylase	ec:4.1.1.19_D	Forward	CAGCCTCACCAACACCATC
			Reverse	GACATTCGGGTCCACTTC
D-B23-A12	naringenin-chalcone synthase	ec:2.3.1.74_D_2	Forward	GGCGAAGACCGAGGAGTTT
			Reverse	CCCAAAAAGCAATCAAAGAATGG
D-E16-C08	arabidopsis response regulator 1	D-E16-C08_D	Forward	AGTGACAACTGCTGATGGAG
			Reverse	GAAAGGACGAGGAAGATGAAG
Deoxylul_A	1-deoxy-D-xylulose-5-phosphate synthase	ec:2.2.1.7_A	Forward	GCTGGACAATTGAACCGAATC
			Reverse	TCATAGACGACAGGCCAAG

Dihydroflav	dihydrokaempferol 4-reductase	ec:1.1.1.219_D	Forward	GAGCCATGAGCCGATGAAGC
			Reverse	TCTTTTGC GACTCCAATTTCTCG
Dihydroflav_A	dihydrokaempferol 4-reductase	ec:1.1.1.219_A	Forward	CTTGTC CAGGGTTCAGGCATCT
			Reverse	GGATGATCTATGTGCGGCTGAA
D-J04-E02	ABA deficient 2	D-J04-E02_D	Forward	CCACCATCCACAAAAAGGTTGT
			Reverse	GTTCCCTACACGGCAATCAAAG
D-K14-F07	lipoxygenase	ec:1.13.11.12_D	Forward	GGAGTCAAGGAACGGTAATG
			Reverse	GAATGAAGCACTGAGTATATTGTT
Enolase_B	phosphopyruvate hydratase	ec:4.2.1.11_B_2	Forward	GTTAGCAATGTGCTTGTATAGG
			Reverse	AGGCCGTTAGCAATGTTAACAT
ENOLASE-C	phosphopyruvate hydratase	ec:4.2.1.11_C	Forward	GTTAGCAATGTGCTTATATAGC
			Reverse	AGGCCGTTAGCAATGTTAACAC
Enoyl-acp_C	enoyl-[acyl-carrier-protein] reductase (NADH)	ec:1.3.1.9_C	Forward	TCAACGGCAGAGTCATTTTCC
			Reverse	CCTCTCAGATCAATGGGCAATC
Flavanone_D	flavanone 3-dioxygenase	ec:1.14.11.9_D	Forward	AGCATTCTTGAACCTCCCATTG
			Reverse	GGATGGTGGCAAGACATGGA
GADPH-BC05	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	ec:1.2.1.12_B	Forward	TCAACCACAGAGACATCAACA
			Reverse	ATCATTCCCAGCAGCACAG
GADPH-BDCONS	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	ec:1.2.1.12_B/D	Forward	ACCCTCAACAATACCAAACCTG
			Reverse	TCATTTCTGCCCCAAGTAA
GADPH-CCONS	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	ec:1.2.1.12_C	Forward	CTTCATCAGTGTAGCCGA
			Reverse	TTCCAACCCCTAATGTCTCT
GLUTAT-ALN179	glutathione transferase	ec:2.5.1.18_D	Forward	CACACTTTTCCTCTCCTTCAC
			Reverse	CATTTACACTGGCTGATCTGAG
Lipoxygen_A	lipoxygenase	ec:1.13.11.12_A	Forward	GACGCTCTTGAATGGACTAAGG
			Reverse	AATTCCCTTGCCAGTAAGTCCC
MALATE-JO5	malate dehydrogenase	ec:1.1.1.37_C	Forward	GTAATGAACTCACTATTCAACCAT
			Reverse	TTGGGGAAATCACTCTTCAACG
MALATE-PO5	malate dehydrogenase	ec:1.1.1.37_D	Forward	CCATTCATCATCTGCAACAAGT
			Reverse	TTGGGGAAATCACTCTTCAACT
MALONYL-ACYL-CONS	[acyl-carrier-protein] S-malonyltransferase	ec:2.3.1.39_D	Forward	ACAATGCCAGCTATAACCTTTCCA

			Reverse	CTCCCAGAATACCAGTTTATC
MONODEHYD-CONS	monodehydroascorbate reductase (NADH)	ec:1.6.5.4_D	Forward	GGGAATAGAAGAACGGAAGG
			Reverse	TGAAGAGGAAAAAGGTGGAA
NADP-malic	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	ec:1.1.1.40_B	Forward	AGCCCCTTGTGTGATGTGGAT
			Reverse	GGAGCAAAGAGGTGGGGAGTC
NADP-MALIC	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	ec:1.1.1.40_C	Forward	TGCCAAAAATACGGGAGTATC
			Reverse	GCAAGCAGAAGGACGAATAC
Oxoacylcar_B	3-oxoacyl-[acyl-carrier-protein] reductase	ec:1.1.1.100_B	Forward	AAACATCCAATGTTCCCCATGC
			Reverse	AAAGGAGGCGGAAGAAGTTT
Pect_lyase_A	pectate lyase	ec:4.2.2.2_A_1	Forward	AACACGAGGAGGCACCAGA
			Reverse	CATTGAACCGATAAGAGAAGATG
Pectin_D	pectinesterase	ec:3.1.1.11_D	Forward	CGGTGATAATAGTGTTCCTTCT
			Reverse	ATAGGGAAAAATGTGGAGGTG
PECT-LY-ACO1	pectate lyase	ec:4.2.2.2_A_2	Forward	TGGAAGAAATGGAAGTGGAGA
			Reverse	TAAGAGAAGATGGTCTTGCACTC
PECT-LY-CON11	pectate lyase	ec:4.2.2.2_A_3	Forward	TGGAAGAAATGGAAGTGGAGA
			Reverse	TAAGAGAAGATGGTCTTGCACTT
PEROXID-CON15-1	peroxidase	ec:1.11.1.7_A_1	Forward	TTAGCATTTCTGATTGGTTGT
			Reverse	ATCTCGTGGCATTGTCTGGA
PEROXID-CON15-2	peroxidase	ec:1.11.1.7_A_2	Forward	TTAGCATTTCTGATTGGTTGT
			Reverse	ATCTCGTGGCATTGTCTGGG
PHOSPHOENOL	phosphoenolpyruvate carboxykinase (ATP)	ec:4.1.1.49_D	Forward	AACGCAAACTACAAGACAACC
			Reverse	GGCACACCCTCAACCTCA
PhosPiruv	phosphopyruvate hydratase	ec:4.2.1.11_B_3	Forward	ACCAAACCCACCTCACAAGCAT
			Reverse	CGTCGGATTGCCTCTGCTATCT
Protein_B	polygalacturonase	ec:3.2.1.15_B	Forward	GGGGTCAGGATCAAAACAG
			Reverse	CGTACCACATCCCTGTA
PROTEIN-A-B-CONS	beta-amylase	ec:3.2.1.2_A/B	Forward	GCACACATCTCCCTCTCCTC
			Reverse	AGAGACCACGAGCAACCACA
Prot-j01_D	phosphoprotein phosphatase	ec:3.1.3.16_D	Forward	GGTAGGGTTTCACAAAAAGTAATC
			Reverse	GAAATCGGGGAAAATATGGAG

PYROPHOSPH-D	6-phosphofructokinase	ec:2.7.1.11_D	Forward	TCTCCAATCACATCCCAATATG
			Reverse	CAGCCACCTCTTCAGCAA
Pyruvate_B1	beta-glucosidase	ec:3.2.1.21_B	Forward	CAGAAACATCGGCAACTTCAG
			Reverse	CTATGGTGGCAAGAGGAGAT
Pyruvate_B2	pyruvate kinase	ec:2.7.1.40_B_2	Forward	GAAGGCCGATAATGGCTCAG
			Reverse	GGTTGGTTCACAGACTCCAC
PYRUVATE-D-E17	pyruvate kinase	ec:2.7.1.40_B_3	Forward	TGTGTTATGCTAAGTGGGGAGA
			Reverse	AATCGAATGAATCTGTGGTAT
STEAROYL-D-B11-A06	acyl-[acyl-carrier-protein] desaturase	ec:1.14.19.2_D_1	Forward	CAACCCGTCCAGAAAGATAAAG
			Reverse	GCACTTCCCACTTACCAGA
Steroyl_D	acyl-[acyl-carrier-protein] desaturase	ec:1.14.19.2_D_2	Forward	GAAGGTGGGATGTTGAGAAGT
			Reverse	CGGATGATGTCTGCTTGA
Tetrafunct_D	dodecenoyl-CoA isomerase	ec:5.3.3.8_D	Forward	TTTCGGTTGACATTATTGATA
			Reverse	GTTGATTGGATGCTTTCTATT
Thiosulfate	3-mercaptopyruvate sulfurtransferase	ec:2.8.1.2_B	Forward	GTGCAACCCCATCAAACCTAGC
			Reverse	AAATTCCAGCCCCATTTCTGTCT
TYROSINE-A-F15-1	aromatic-L-amino-acid decarboxylase	ec:4.1.1.28_A_1	Forward	GACCCACATCCCATACTCCTTT
			Reverse	GGCTTGTTCCGCTCTTTCTC
TYROSINE-CONS	aromatic-L-amino-acid decarboxylase	ec:4.1.1.28_A_2	Forward	GACCCACATCCCATACTCCTTT
			Reverse	GGCTTGTTCCGCTCTTTCTG
TYROSINE-A-K15-2	aromatic-L-amino-acid decarboxylase	ec:4.1.1.28_A_3	Forward	GAGAAGAGAAATGAACTGGGAAGA
			Reverse	TGGGTTTAATGTTGTTGGATTT
Xylose_D	xylose isomerase	ec:5.3.1.5_D	Forward	ACTGGCGACCCTCAAACC
			Reverse	AACATCCGTGCTCTCTCTTC