

Additional data file 1: Identified ORFs and functional description

GENE NAME	SYSTEMATIC NAME	FUNCTIONAL DESCRIPTION (BRIEF)
AAD3	YCR107W	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
POT1	YIL160C	3-ketoacyl-CoA thiolase with broad chain length specificity, cleaves 3-ketoacyl-CoA into acyl-CoA and acetyl-CoA during beta-oxidation of fatty acids
LEU2	YCL018W	Beta-isopropylmalate dehydrogenase, catalyzes the third step in the leucine biosynthesis pathway
ALD3	YMR169C	Cytoplasmic aldehyde dehydrogenase, involved in beta-alanine synthesis; uses NAD ⁺ as the preferred coenzyme; very similar to Ald2p; expression is induced by stress and repressed by glucose
SFA1	YDL168W	Bifunctional enzyme containing both alcohol dehydrogenase and glutathione-dependent formaldehyde dehydrogenase activities, functions in formaldehyde detoxification and formation of long chain and complex alcohols
EEB1	YPL095C	Acyl-coenzymeA:ethanol O-acyltransferase responsible for the major part of medium-chain fatty acid ethyl ester biosynthesis during fermentation; possesses short chain esterase activity
YJL218W	YJL218W	Putative protein of unknown function, similar to bacterial galactoside O-acetyltransferases; induced by oleate in an OAF1/PIP2-dependent manner
ARO1	YDR127W	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids
ADH6	YMR318C	NADPH-dependent cinnamyl alcohol dehydrogenase family member with broad substrate specificity; may be involved in fusel alcohol synthesis or in aldehyde tolerance
ATF2	YGR177C	Alcohol acetyltransferase, may play a role in steroid detoxification; forms volatile esters during fermentation, which is important in brewing
ARO10	YDR380W	Phenylpyruvate decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway
PDC6	YGR087C	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, involved in amino acid catabolism
ALP1	YNL270C	Basic amino acid transporter, involved in uptake of cationic amino acids
ALD5	YER073W	Mitochondrial aldehyde dehydrogenase, involved in regulation or biosynthesis of electron transport chain components and acetate formation; activated by K ⁺ ; utilizes NADP ⁺ as the preferred coenzyme; constitutively expressed
ARO7	YPR060C	Chorismate mutase, catalyzes the conversion of chorismate to prephenate to initiate the tyrosine/phenylalanine-specific branch of aromatic amino acid biosynthesis
ADH3	YMR083W	Mitochondrial alcohol dehydrogenase isozyme III; involved in the shuttling of mitochondrial NADH to the cytosol under anaerobic conditions and ethanol production
ACS1	YAL054C	Acetyl-coA synthetase isoform which, along with Acs2p, is the nuclear source of acetyl-coA for histone acetylation; expressed during growth on nonfermentable carbon sources and under aerobic conditions
GRE2	YOL151W	NADPH-dependent methylglyoxal reductase (D-lactaldehyde dehydrogenase); stress induced (osmotic, ionic, oxidative, heat shock and heavy metals); regulated by the HOG pathway
HPA3	YEL066W	D-Amino acid N-acetyltransferase; similar to Hpa2p, acetylates histones weakly in vitro
BAP3	YDR046C	Amino acid permease involved in the uptake of cysteine, leucine, isoleucine and valine
HAT2	YEL056W	Subunit of the Hat1p-Hat2p histone acetyltransferase complex;
ILV5	YLR355C	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-

		chain amino acid biosynthesis, also required for maintenance of wild-type mitochondrial DNA
ARO4	YBR249C	3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthase, catalyzes the first step in aromatic amino acid biosynthesis and is feedback-inhibited by tyrosine or high concentrations of phenylalanine or tryptophan
ILV3	YJR016C	Dihydroxyacid dehydratase, catalyzes third step in the common pathway leading to biosynthesis of branched-chain amino acids
ADH2	YMR303C	Glucose-repressible alcohol dehydrogenase II, catalyzes the conversion of ethanol to acetaldehyde; involved in the production of certain carboxylate esters; regulated by ADR1
VBA3	YCL069W	Permease of basic amino acids in the vacuolar membrane /// Hypothetical protein
FDH1 ///		NAD(+)-dependent formate dehydrogenase, may protect cells from exogenous formate
FDH2	YOR388C	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
AAD10	YJR155W	Minor succinate dehydrogenase isozyme; homologous to Sdh1p, the major isozyme responsible for the oxidation of succinate and transfer of electrons to ubiquinone; induced during the diauxic shift in a Cat8p-dependent manner
YJL045W	YJL045W	Minor isoform of pyruvate decarboxylase, key enzyme in alcoholic fermentation, decarboxylates pyruvate to acetaldehyde, regulation is glucose- and ethanol-dependent, repressed by thiamine, involved in amino acid catabolism
PDC5	YLR134W	Acetyl-coA synthetase isoform which, along with Acs1p, is the nuclear source of acetyl-coA for histone acetylation; required for growth on glucose; expressed under anaerobic conditions
ACS2	YLR153C	High-affinity leucine permease, functions as a branched-chain amino acid permease involved in the uptake of leucine, isoleucine and valine
BAP2	YBR068C	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase), cytosolic enzyme that transfers an acetyl group from one acetyl-CoA molecule to another, forming acetoacetyl-CoA; involved in the first step in mevalonate biosynthesis
ERG10	YPL028W	Aromatic aminotransferase, catalyzes the first step of tryptophan, phenylalanine, and tyrosine catabolism
ARO9	YHR137W	Putative protein of unknown function with similarity to aldo/keto reductases; YMR041C is not an essential gene
YMR041C	YMR041C	Aromatic aminotransferase, expression is regulated by general control of amino acid biosynthesis
ARO8	YGL202W	3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) synthase, catalyzes the formation of HMG-CoA from acetyl-CoA and acetoacetyl-CoA; involved in the second step in mevalonate biosynthesis
ERG13	YML126C	Carbon source-responsive zinc-finger transcription factor, required for transcription of the glucose-repressed gene ADH2, of peroxisomal protein genes, and of genes required for ethanol, glycerol, and fatty acid utilization
ADR1	YDR216W	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine, low-affinity tryptophan and histidine transporter
TAT1	YBR069C	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis; expression is under general amino acid control
ILV1	YER086W	Mitochondrial aldehyde dehydrogenase, required for growth on ethanol and conversion of acetaldehyde to acetate; activity is K ⁺ dependent; utilizes NADP ⁺ or NAD ⁺ equally as coenzymes; expression is glucose repressed
ALD4	YOR374W	Mitochondrial malic enzyme, catalyzes the oxidative decarboxylation of malate to pyruvate, which is a key intermediate in sugar metabolism and a precursor for synthesis of several amino acids
MAE1	YKL029C	Cytosolic branched-chain amino acid aminotransferase; highly expressed during stationary phase and repressed during logarithmic phase
BAT2	YJR148W	NAD-dependent (2R,3R)-2,3-butanediol dehydrogenase, a zinc-containing medium-chain alcohol dehydrogenase, produces 2,3-butanediol from acetoin during fermentation
BDH1	YAL060W	Isopropylmalate isomerase, catalyzes the second step in the leucine biosynthesis pathway
LEU1	YGL009C	

YMR210W	YMR210W	Putative acyltransferase with similarity to Eeb1p and Eht1p, has a minor role in medium-chain fatty acid ethyl ester biosynthesis; may be involved in lipid metabolism and detoxification
YGL039W	YGL039W	Oxidoreductase, catalyzes NADPH-dependent reduction of the bicyclic diketone bicyclo[2.2.2]octane-2,6-dione (BCO2,6D) to the chiral ketoalcohol (1R,4S,6S)-6-hydroxybicyclo[2.2.2]octane-2-one (BCO2one6ol)
YGL157W	YGL157W	Oxidoreductase, catalyzes NADPH-dependent reduction of the bicyclic diketone bicyclo[2.2.2]octane-2,6-dione (BCO2,6D) to the chiral ketoalcohol (1R,4S,6S)-6-hydroxybicyclo[2.2.2]octane-2-one (BCO2one6ol)
THI3	YDL080C	Probable decarboxylase, required for expression of enzymes involved in thiamine biosynthesis; may have a role in catabolism of amino acids to long-chain and complex alcohols
ADH7	YCR105W	NADPH-dependent cinnamyl alcohol dehydrogenase family member with broad substrate specificity; may be involved in fusel alcohol synthesis
AYT1	YLL063C	Acetyltransferase; catalyzes trichothecene 3-O-acetylation, suggesting a possible role in trichothecene biosynthesis
TKL2	YBR117C	Transketolase; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids
TMT1	YER175C	Trans-aconitate methyltransferase, cytosolic enzyme that catalyzes the methyl esterification of 3-isopropylmalate, an intermediate of the leucine biosynthetic pathway, and trans-aconitate, which inhibits the citric acid cycle
ADH4	YGL256W	Alcohol dehydrogenase type IV, dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol dehydrogenases
ALD6	YPL061W	Cytosolic aldehyde dehydrogenase, activated by Mg ²⁺ and utilizes NADP ⁺ as the preferred coenzyme; required for conversion of acetaldehyde to acetate; constitutively expressed
CHA1	YCL064C	Catabolic L-serine (L-threonine) deaminase, catalyzes the degradation of both L-serine and L-threonine; required to use serine or threonine as the sole nitrogen source, transcriptionally induced by serine and threonine
TKL1	YPR074C	Transketolase; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids
BAT1	YHR208W	Mitochondrial branched-chain amino acid aminotransferase, homolog of murine ECA39; highly expressed during logarithmic phase and repressed during stationary phase
GRE3	YHR104W	Aldose reductase involved in methylglyoxal, d-xylose and arabinose metabolism; stress induced (osmotic, ionic, oxidative, heat shock, starvation and heavy metals); regulated by the HOG pathway
EHT1	YBR177C	Acyl-coenzymeA:ethanol O-acyltransferase that plays a minor role in medium-chain fatty acid ethyl ester biosynthesis; contains esterase activity; localizes to lipid particles and the mitochondrial outer membrane
ADH5	YBR145W	Alcohol dehydrogenase isoenzyme V; involved in ethanol production
ILV6	YCL009C	Regulatory subunit of acetolactate synthase, which catalyzes the first step of branched-chain amino acid biosynthesis; enhances activity of the Ilv2p catalytic subunit, localizes to mitochondria
MAK3	YPR051W	Catalytic subunit of N-terminal acetyltransferase of the NatC type; required for replication of dsRNA virus
ATF1	YOR377W	Alcohol acetyltransferase with potential roles in lipid and sterol metabolism; responsible for the major part of volatile acetate ester production during fermentation
ILV2	YMR108W	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid control
LEU9	YOR108W	Alpha-isopropylmalate synthase II (2-isopropylmalate synthase), catalyzes the first step in the leucine biosynthesis pathway; the minor isozyme, responsible for the residual alpha-IPMS activity detected in a leu4 null mutant
YPL113C	YPL113C	Putative dehydrogenase
AAD14	YNL331C	Putative aryl-alcohol dehydrogenase with similarity to <i>P. chrysosporium</i> aryl-

alcohol dehydrogenase; mutational analysis has not yet revealed a physiological role
